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636.642 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd
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                                                      M. catarrhalis BAS
Moraxella catarrha
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    Novel human diagno
                  Drosophila melanog
                                Moraxella catarrha
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AAR08067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M. catarrhalis BASB019 protein sequence #1.
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This sequence is a Moraxella catarrhalis BASB019 protein of the invention. The sequences can be used for diagnosis of disease, staging of disease, or determining response of an infectious organism to drugs. The polynucleotides may be used as a source for hybridisation probes, and for screening of genetic mutations, serotype, organism or strain case, and as identification, identification of mutation in BASB013 sequences, and as components of arrays which are useful for diagnostic and prognostic components of arrays which are useful for diagnostic and prognostic purposes. The polypeptides can be used to produce antibodies, and as a target for the screening of antimicrobial drugs. The polypeptides can be used in vaccine formulations, and to identify agonists and antagonists. The polypeptides, antibodies, agonists and antagonists. The polypeptides can be used for the treatment and prevention of (which are bacteristatic) are used for the treatment and prevention of diseases including bacterial infection, otitis media in infants and
                                                                                                                                                                                                                                                                                                                                                                                                                    W09957277-A2
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                                                                                                                                                                                                          catarrhalis used to prepare vaccines against bacterial infections
                                                                                                                                                                                                                       Novel BASB019 polynucleotides and polypeptides from Moraxella
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Best Local S
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                                   Claim 3; Fig 3; 101pp; English
                                                                      Novel BASB019 polynucleotides and polypeptides from Moraxella catarrhalis used to prepare vaccines against bacterial infections
                                                                                                                                                                                      Ruelle J;
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This sequence is a Moraxella catarrhalis BASB019 protein of the

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                                                                                          (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
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                                                                                                                                                             98GB-0009683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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В

03-MAY-1999;

99WO-EP03038.

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AAY55092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Screening of genetic mutations, serotype, organism or strain
CC identification, identifications of mutation in BASBO13 sequences, and as
CC components of arrays which are useful for diagnostic and prognostic
CC target for the screening of antimicrobial drugs. The polypeptides can be used to produce antibodies, and as a
CC also be used in vaccine formulations, and to identify agonists and
CC (which are bacteristatic) are used for the treatment and prevention of
CC diseases including bacterial infection, otitis media in infants and
CC (which are bacteristatic) are used for the treatment and prevention of
CC diseases including bacterial infection, otitis media in infants and
CC (inflaren, pneumonia in the elderly, sinusitis, nosocomial infections and
CC accumulation in the middle ear, auditive nerve damage, delayed speech
CC infection. They are also used in the prevention of adhesion of bacteria
CC infection of the upper respiratory tract and middle ear
CC infection of mounds, and to thus prevent tissue damage and/or block the
CC the implantation of in-dwelling devices or by other surgical techniques.
CC and it is no longer common to isolate M. catarrhalis attained remaitically,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                        genetic mutation screening; antibody production; vaccine; otitis media; bacterial infection; pneumonia; sinusitis; nosocomial infection; invasive disease; delayed speech learning; bacteria adhesion prevention; upper respiratory tract infection; middle ear infection; therapy.
11-NOV-1999,
                                     W09957277-A2.
                                                                           Moraxella catarrhalis.
                                                                                                                                                                  BASB019 protein; diagnosis; infectious organism; genetic mutation screening; antibody production;
                                                                                                                                                                                                                              M. catarrhalis BASB019 protein sequence #4.
                                                                                                                                                                                                                                                                                     01-MAR-2000
                                                                                                                                                                                                                                                                                                                                  AAY55092;
                                                                                                                                                                                                                                                                                                                                                            AAY55092 standard; Protein; 172 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and it is no longer common to isolate M. catarrhalis strains that are resistant to standard antibiotics. The BASB019 products of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               can be used screen for new antibacterial compounds that may target these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence is a Moraxella catarrhalis BASB019 protein of the invention. The sequences can be used for diagnosis of disease, staging of disease, or determining response of an infectious organism to drugs. The polynucleotides may be used as a source for hypridisation probes, and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; Fig 3; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    catarrhalis used to prepare vaccines against bacterial infections
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Pred. No.
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cc screening of genetic mutations, scrotype, organism or strain cc identification, identification of mutation in BASB013 sequences, and as cc identification, identification of mutation in BASB013 sequences, and as a components of arrays which are used to produce antibodies, and as a components of arrays which are used to produce antibodies, and as a cupurposes. The polypeptides can be used to produce antibodies, and as a can be used in vaccine formulations, and to identify agonists and components of the polypeptides, antibodies, agonists and antagonists and components. The polypeptides, antibodies, agonists and antagonists and components of the polypeptides, antibodies, agonists and prevention of components. The polypeptides can the component of the treatment and prevention and components in the elderly, sinusitis, nosocomial infections and components of diseases including bacterial infection, vitis media with hearing loss, fluid components of diseases, chronic otitis media with hearing loss, fluid components of diseases, chronic otitis media with hearing loss, fluid components of diseases, chronic otitis media with hearing loss, fluid components of diseases, chronic otitis media with hearing loss, fluid components of diseases, chronic otitis media with hearing loss, fluid components of diseases, chronic otitis media with hearing loss, fluid components of the middle ear and middle ear commonents of the prevention of adhesion of bacteria components of the prevention of adhesion of bacteria components of the prevent tissue damage and/or block the proteins on wounds, and to thus prevent tissue damage and/or block the proteins on wounds, and to thus prevent tissue damage and/or block the proteins on of pathogenesis in infections initiated other than by comman progression of pathogenesis in infections initiated other than by component of the decrease of the component of the decrease of the component of the component
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Fig 3; 101pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             resistant bacteria
BASB019 protein; diagnosis; infectious organism; auditive nerve damage; genetic mutation screening; antibody production; vaccine; otitis media; bacterial infection; pneumonia; sinusitis; nosocomial infection; invasive disease; delayed speech learning; bacteria adhesion prevention; upper respiratory tract infection; middle ear infection; therapy.
                                                                                                                                                                                                                                                                                                                       AAY55093 standard; Protein; 16 AA
                                                                                                                                                                M. catarrhalis BASB019 protein sequence fragment.
                                                                                                                                                                                                                        01-MAR-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 AA;
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; Pred. No. 3.2e-56;
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RESULT 6
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      KW XXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence is a fragment of a Moraxella catarrhalis BASBO19 protein of the invention. The sequences can be used for diagnosis of disease, or determining response of an infectious organism to staging of disease, or determining response of an infectious organism to drugs. The polynucleotides may be used as a source for hybridisation probes, and for screening of genetic mutations, serotype, organism or probes, and for screening of genetic mutations, serotype, organism or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   speech learning, infection of the upper respiratory tract and middle ear speech learning, infection of the upper respiratory tract and middle ear infection. They are also used in the prevention of adhesion of bacteria to eukaryotic matrix proteins on in-dwelling devices, or to extracellular to eukaryotic matrix proteins on in-dwelling devices or block the proteins on wounds, and to thus prevent tissue damage and/or block the proteins on wounds, and to thus prevent tissue damage and/or block the proteins on wounds, and to thus prevent tissue damage and/or block the proteins on by other surgical techniques, the implantation of in-dwelling devices or by other surgical techniques, the implantation of in-dwelling devices or by other surgical techniques, the implantation of in-dwelling devices or by other surgical techniques, and it is no longer common to isolate M. catarrhalis strains that are and it is no longer common to isolate M. catarrhalis strains that are and it is no longer common to isolate M. catarrhalis strains that are and it is no longer common to isolate M. catarrhalis strains that are can be used screen for new antibacterial compounds that may target these can be used screen for new antibacterial compounds that may target these
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                                                                                                                                                                                                                                                      AAY57577 standard; peptide; 16 AA.
                                                                                    Moraxella catarrhalis BASB020 specific peptide SEQ ID NO:13.
otitis media; pneumonia; sinusitis; anti-inflammatory; auditory;
                           Moraxella catarrhalis; BASB020; diagnosis; vaccine; infection;
                                                                                                                                             02-MAR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 100.0%; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15;
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100.0%; Pred. No. 4.8e-07
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RESULT 7
AAY5504
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XX AAY5
AC AAY5
XX AAY5
DT 01-M
DT 01-M
XX XX
XX MX MASH
KW BASH
KW BASH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Columes of other genes that have any symbol to the Stable of Orliner genes and polypoptides are used as research of comparison genes are used as research to the mann diseases. Probes comprising BASBO20 nucleotide sequences can be constructed to conduct efficient screening of genetic mutations, compounds the used in the discovery and development of antibacterial compounds. The polypeptides and polynucleotides are used to block the continual physical interaction between a gram negative and/or gram positive bacteria to the mammalian host. The polynucleotides encoding certain compounds to the mammalian host. The polynucleotides encoding certain comportable regions of bacterial cell surface protein are used in color than on variable regions of bacterial cell surface protein are used in convariable regions of bacterial cell surface protein are used in convariable regions of bacterial cell surface protein are used in convariable regions of bacterial composition with M.catarrhalis to dientify protein apitops able to provoke a prophylactic or therapeutic composition comprising an antibody can be used for treating humans with mann with diseases such as sinusitis, otitis media and nosocomial conversed to the converse of t
                                                                                                                                                                                                                                                                                                                                                                                                                               Вþ
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a peptide specific for a BASB020 protein, isolated from Moraxella catarrhalis, used in an example from the present invention. BASB020 polynucleotide fragments may be used as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-062301/05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Moraxella catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNAs and genomic clones encoding BASB020 and to isolate cDNA and clones of other genes that have high sequence identity to BASB020 \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hybridisation probes for RNA, cDNA and genomic DNA to isolate full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 9; Page 69; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel peptides useful as vaccines for Moraxella infections such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thonnard J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                        BASB019 protein; diagnosis; infectious organism; auditive nerve damage; genetic mutation screening; antibody production; vaccine; otitis media; bacterial infection; pneumonia; sinusitis; nosocomial infection;
                                                                                                                                                                                        01-MAR-2000
                                                                                                                                                                                                                                            AAY55094;
                                                                                                                                                                                                                                                                                              AAY55094 standard; Protein; 14 AA.
                                                                                                                                    M. catarrhalis BASB019 protein sequence fragment
     invasive disease; delayed speech learning;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 158 NEEAWSQNRRAELSY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 media, pneumonia, sinusitis etc.,
                                                                                                                                                                                                                                                                                                                                                                                                                               N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98GB-0010285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-EP03257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 15;
; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 21; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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RESULT 8
AAY57578

AAY57578 standard; peptide; 14 AA

XXX DXXX

02-MAR-2000 AAY57578;

(first entry)

Moraxella catarrhalis; BASB020; diagnosis; vaccine; infection Moraxella catarrhalis BASB020 specific peptide SEQ ID NO:14. 밁

1 YTGVAPLVDNDETV 14

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Matches
                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                             polypeptides can also be used in vaccine formulations, and to identify agonists and antagonists. The polypeptides, antibodies, agonists and antagonists (which are bacteristatic) are used for the treatment and prevention of diseases including bacterial infection, othits media in infants and children, pneumonia in the elderly, sinusitis, nosocomial infections and invasive diseases, chronic othits media with hearing loss, fluid accumulation in the middle ear, auditive nerve damage, delayed speech learning, infection of the upper respiratory tract and middle ear infection. They are also used in the prevention of adhesion of bacteria to eukaryotic matrix proteins on in-dwelling devices, or to extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Moraxella catarrhalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   upper respiratory tract infection; middle ear infection; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and as components of arrays which are useful for diagnostic and prognostic purposes. The polypeptides can be used to produce antibodies, and as a target for the screening of antimicrobial drugs. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-062148/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-NOV-1999
                                                                                                                                                                                                       proteins on wounds, and to thus prevent tissue damage and/or block the normal progression of pathogenesis in infections initiated other than by the implantation of in-dwelling devices or by other surgical techniques. The frequency of Moraxella catarrhalis infections has risen dramatically, and it is no longer common to isolate M. catarrhalis strains that are resistant to standard antibiotics. The BASB019 products of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probes, and for screening of genetic mutations, serotype, organism or strain identification, identification of mutation in BASB013 sequences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                staging of disease, or determining response of an infectious organism drugs. The polynucleotides may be used as a source for hybridisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 8; Page 70; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 catarrhalis used to prepare vaccines against bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel BASB019 polynucleotides and polypeptides from Moraxella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence is a fragment of a Moraxella catarrhalis BASB019 protein of the invention. The sequences can be used for diagnosis of disease,
                                                                                                                          Sequence
                                                                                                                                                                    resistant bacteria.
                                                             Local Similarity
                                                                                                                                                                                        be used screen for new antibacterial compounds that may target these
46 YTGVAPLVDNDETV 59
                                           14;
                                                                                                                          14
                                           Conservative
                                                                                                                            AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-EP03038
                                                             8.1%;
                                              0,
                                                               Score 14;
Pred. No.
                                              Mismatches
                                                                   DB 21;
, 3.7e-06;
                                                                                       21;
                                                                                     Length 14;
                                              0;
                                              Gaps
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RESULT 9
                                                                                                                                                                                                                             ABB64563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a peptide specific for a BASB020 CC protein, isolated from Moraxella catarrhalis, used in an example from CC the present invention. BASB020 polynucleotide fragments may be used as CC hybridisation probes for RNA. CDNA and genomic DNA to isolate full-length CC clones and genomic clones encoding BASB020 and to isolate cDNA and genomic Clones of other genes that have high sequence identity to BASB020 gene. CC The BASB020 polynucleotides and polypeptides are used as research compared to conduct efficient screening of genetic mutations. CC constructed to conduct efficient screening of genetic mutations. CC sequences can be used in the discovery of the distribution. The polynucleotide sequences can be used in the discovery and development of antibacterial compounds. The polypeptides and polynucleotides are used to block the initial physical interaction between a gram negative and/or gram positive bacteria to the mammalian host. The polynucleotides encoding certain compounds of bacterial cell surface protein are used to polynucleotide constructs which are useful for genetic immunisation conjuncted against BASB020 can be used for treating an antibody confidence and polynucleotide sequences. A therapeutic composition comprising an antibody confidence affected against BASB020 can be used for treating humans with
                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                    Drosophila; developmental biology; cell signalling; insecticide;
                                                                              Drosophila melanogaster polypeptide SEQ ID NO 20481.
                                                                                                                            26-MAR-2002
                                                                                                                                                                   ABB64563;
                                                                                                                                                                                                   ABB64563 standard; Protein; 2168 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      otitis media; pneumonia; sinusitis; anti-inflammatory; auditory; antibacterial; immune response; immunisation; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 9; Page 69; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9958684-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Moraxella catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       catarrhalis diseases such as sinusitis, otitis media and nosocomial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000-062301/05
                                                                                                                                                                                                                                                                                                                                        46 YTGVAPLVDNDETV 59
                                                                                                                                                                                                                                                                                                    1 YTGVAPLVDNDETV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptides useful as vaccines for Moraxella infections such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       media, pneumonia, sinusitis etc.,
                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 AA;
                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98GB-0010285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-EP03257.
                                                                                                                                                                                                                                                                                                                                                                                              8.1%; Score 14;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                              3.7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                 DB 21;
                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                               Length 14;
                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                      0,
RESULT 10
ABG22196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                  (HYSE-) HYSEQ INC
                                                      31-MAR-2000;
23-AUG-2000;
                                                                                                                                                     11-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventiuseful in developmental biology and in elucidating cell signalling a cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL101840-ABL16175) and the encoded proteins (ABB7377-ABB72072).
                                                                                                              30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                           WO200175067-A2
                                                                                                                                                                                                                                                                                                                            Novel human diagnostic protein #22187.
                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                        ABG22196;
                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG22196 standard; Protein; 139 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                   food supplement; medical imaging;
                                                                                                                                                                                                                                                                                    Human; chromosome mapping;
                                                                                                                                                                                                                                                                                                                                                                    18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 20481; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ABL08666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200171042-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           979 AAAAAALSV 987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 AAAAAALSV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2168 AA;
                                                      2000US-0540217
2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adams M,
                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-191637P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.2%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PWD,
                                                                                                                                                                                                                                                               gene mapping; gene therapy;
maging; diagnostic; genetic 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 9;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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DB 22; ). 18;

The invention

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0; Indels Length 2168;

0;

Gaps

0

forensic;

IJ

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RESULT 11
AAG18977
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to isolated polynucleotide (I) and CC polymerase (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinate control of the contr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                      25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                   Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                        25-FEB-2000; 2000EP-0301439.
                                                                                                                                                                                                                                                                 EP1033405-A2
                                                                                                                                                                                                                                                                                                      Zea mays subsp. mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                               termination sequence;
                                                                                                                                                                                                                                                                                                                                                                                                                               Zea mays protein fragment SEQ ID NO: 20601.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAG18977 standard; Protein; 158 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAS86383.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 AAAAAALS 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20; SEQ ID No 52555; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 AAAAAALS 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                    99US-0121825.
99US-0123180.
99US-0123548.
99US-0125788.
99US-0126264.
99US-0126785.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                 corn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 8;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22;
o. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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         06-JUL-1
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19-APR-1999;
99US-0139750.
99US-0139763.
99US-0139891.
99US-0140353.
99US-0140695.
99US-0140893.
99US-0140893.
99US-0141287.
99US-0141287.
99US-0141287.
99US-0142154.
99US-014255.
99US-0142890.
99US-0142890.
99US-0142890.
99US-0142890.
99US-0142890.
99US-0142897.
99US-0142897.
99US-0143542.
99US-0144085.
99US-0144085.
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99US-0139453

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99US-0139459

99US-0139460

99US-0139461

99US-0139463
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990S-0137222.

990S-0137528.

990S-0137502.

990S-0137724.

990S-0138044.

990S-0138047.

990S-0138047.
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99US-0136021.
99US-0136392.
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99US-0134370.
99US-0134768.
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99US-0128714.
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21-JUL-1999 22-JUL-1999 22-JUL-1999 22-JUL-1999 22-JUL-1999 23-JUL-1999 23-JUL-1999 23-JUL-1999 26-JUL-1999 27-JUL-1999 27-JUL-1999

> 99US-0145087. 99US-0145089. 99US-0145192. 99US-0145145. 99US-0145218.

99US-0145088 99US-0145085

99US-0145224. 99US-0145276. 99US-0145913. 99US-0145918. 99US-0145919. 99US-0145951. 19-JUL-1999 19-JUL-1999 19-JUL-1999 19-JUL-1999 19-JUL-1999 20-JUL-1999 20-JUL-1999 21-JUL-1999 21-JUL-1999

990S-0144331 990S-0144332 990S-0144333 990S-0144334 990S-0144352 990S-0144352 990S-0144632 990S-0144814 990S-0144814

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RESULT 12
ABB62221
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Вр
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Best Local S
Matches 8
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21-OCT-1999;
21-OCT-1999;
21-OCT-1999;
22-OCT-1999;
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26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
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14-OCT-1999;
14-OCT-1999;
14-OCT-1999;
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22-OCT-1999;
25-OCT-1999;
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28-OCT-1999;
29-OCT-1999;
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13-OCT-1999;
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                                                                                                                                                                                                                                                                    Drosophila melanogaster polypeptide SEQ ID NO 13455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-OCT-1999;
25-OCT-1999;
                                                                                                                                                                                                                                      Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
                                                                                                                                                                                                                                                                                                              ABB62221;
                                                                                                                                                                                                                                                                                                                                  ABB62221 standard; Protein; 306 AA.
       \mbox{New} isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                 WPI; 2001-656860/75.
N-PSDB; ABL06324.
                                                                                                                        23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                WO200171042-A2
                                                                                                                                                                                                                   Drosophila melanogaster
                                                                                                                                                                                                                                                                                         26-MAR-2002 (first entry)
                                                                                 Venter JC, Adams M,
                                                                                                  (PEKE ) PE CORP NY.
                                                                                                                                                       23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                            27-SEP-2001.
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                                                                                                                                                                                                                                                                                                                                                                                     27 AAAAAALS
                                                                                                                                                                                                                                                                                                                                                                                                8 AAAAAALS 15
                                                                                                                                                                                                                                                                                                                                                                                                                              8;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                             4.7%; Score 8; DB 2 ilarity 100.0%; Pred. No. 15; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0159293

99US-0159294

99US-0159329

99US-0159330

99US-0159331

99US-0159637

99US-0159588

99US-0160767

99US-0160767

99US-0160770

99US-0160814

99US-0160814

99US-0160814

99US-0160815

99US-0160815

99US-0160815

99US-0160816

99US-0160816

99US-0161816

99US-0161816

99US-0161406

99US-0161406

99US-0161406

99US-0161406

99US-0161369

99US-0161369

99US-0161369

99US-0161361

99US-0161361
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 8; DB 21;
Pred. No. 15;
                                                                                  Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 158;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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10-AUG-1999;
11-AUG-1999;
11-AUG-1999;
13-AUG-1999;
16-AUG-1999;
16-AUG-1999;
20-AUG-1999;
20-AUG-1999;
23-AUG-1999;
23-AUG-1999;
24-AUG-1999;
27-AUG-1999;
28-EP-1999;
29-EP-1999;
29-EP-1999;
29-EP-1999;
29-EP-1999;
29-EP-1999;
29-EP-1999;
29-EP-1999;
29-EP-1999;
20-CCT-1999;
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06-CCT-1999;
01-CCT-1999;
01-CCT-1999;
01-CCT-1999;
01-CCT-1999;
01-CCT-1999;
01-CCT-1999;
01-CCT-1999;
01-CCT-1999;

99US-0148684 99US-0149175 99US-0149175 99US-0149723 99US-0149922 99US-0150864 99US-0150866 99US-0151066 99US-0151066 99US-0151086 99US-0151303 99US-0153763 99US-0154018 99US-0154018 99US-0155486 99US-0155486 99US-0155486 99US-0155486 99US-0157763 99US-0157763 99US-0157763 99US-0157763 99US-0157763 27-JUL-1999;
28-JUL-1999;
02-AUG-1999;
02-AUG-1999;
03-AUG-1999;
04-AUG-1999;
05-AUG-1999;
05-AUG-1999;
06-AUG-1999;
06-AUG-1999;
06-AUG-1999;
09-AUG-1999;

99US-0146386.
99US-0146388.
99US-0147038.
99US-0147038.
99US-0147703.
99US-01471302.
99US-01471302.
99US-014714703.
99US-0147476.
99US-0147416.
99US-0147416.
99US-0147416.
99US-0147418.
99US-0147418.

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ABG11084
ID ABG;
XX
AC ABG;
XX
DT 18-1
DX Nov;
XX
KW Hum,
KW Hoo,
XX
XX
PN W02:
XX
PN W0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II), (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical
                                                                                                                                                                                                                                                                                                                                               Claim 20; SEQ ID No 41443; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                        biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; chromosome mapping; gene mapping; food supplement; medical imaging; diagnos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABG11084;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human diagnostic protein #11075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABG11084 standard; Protein; 436 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-639362/73.
)B; AAS75271.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 IAAAAAAL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0649167
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.00.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g; gene mapping; gene therapy; forensic;
imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                      Novel Neisserial polypeptides predicted to be useful antigens for
                                                                                                                                                       Petersen J,
Tettelin H,
                                                                                                                                                                                Fraser C,
                                                                                                                      N-PSDB; AAZ53150
                                                                                                                                                                                                                                                       09-OCT-1998;
                                                                                                                                                                                                                                                                                                                  01-MAY-1998;
31-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and animo acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                      (GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                 09-OCT-1998;
                                                                                                                                                                                                                                                                            09-OCT-1998;
                                                                                                                                                                                                                                                                                         02-SEP-1998;
02-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                      30-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                   W09957280-A2
                                                                                                                                                                                                                                                                                                                                                                                                                          Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenlo; diagnosis; immunogenic; infection; meningitis; septi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY74388 standard; Protein; 452 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY74388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                               2000-062150/05.
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                                                                                                                                                                                                                    CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 AAAAAALS 15
                                                                               and diagnostics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          meningitidis ORF 081 protein sequence SEQ ID NO:252.
                                                                                                                                                                             Galeotti C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              436 AA;
                                                                                                                                                      Venter JC;
                                                                                                                                                                    Pizza M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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98US-0094869.
98US-0098994.
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98US-0103796
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98US-0103749.
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Rappuoli R,
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Ratti
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Scalato E,
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Scarselli M;
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AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ55473 represent PCR primers used in the exemplification of the present invention. The

Claim 2; Page 267; 1453pp; English.

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                              discloses genomic DNA sequences (ABL16176-ABL30511), essequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                             useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABIL16176-ABIJ30511), expressed DNA
                                                                                                                                                                          capable of detecting 1000 or more genes from Drosophila.
                                                                                                                                                                                                                       Disclosure; SEQ ID NO 2526; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                    New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                    N-PSDB; ABL02681.
                                                                                                                                                                                                                                                                                                                                                                    Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                               (PEKE ) PE CORP NY.
 Sequence
                                                The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                           The invention relates to an isolated nucleic acid detection reagent
                                                                               (ABB57737-ABB72072)
                             itp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          289 AAAAAALS 296
                                                                                                                                                                                                                                                                                                                                      2001-656860/75.
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    545 AA;
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2000US-0614150.
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                                                                                                                                                                                                                                                                       detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
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Pred. No.
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o. 39;
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Query Match

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AAU75084;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB67264;
                                                                                                                                                                                                                                             capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL101840-ABL16175) and the encoded proteins
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11-JUL-2000; 2000US-0614150
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                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 28584; 21pp + Sequence Listing; English
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                                                                                                                                                                                             at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                        The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                   (ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Venter JC, Adams M,
                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                         genes from Drosophila and
AAU75084 standard; Protein; 606 AA
                                                                                                                                                                                                                                                                                                                                                                              interactions
                                                                                                                               Local
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8; Conserve
                                                               AAAAALS
                                                                                                                                                                       545 AA;
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                                                                                                                    Conservative
                                                                                                                              4.7%; Score 8;
100.0%; Pred. No
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                                                                                                                                   No.
                                                                                                                                              DB 22;
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                                                                                                                                                                 isolated regulatory element from the nucleic acid sequences and a plant cell or seed transformed with the nucleic acid. An isolated regulatory element from these nucleotide molecules is useful for expressing an exogenous gene in plant cells. The nucleotide sequences of the invention and vectors containing these sequences are useful for expressing an injustive trait loci (QTL) tagging, QTL mapping, DNA fingerprinting and in marker assisted selection, in forage and turf grass improvement, palatability, regrowth after cutting and grazing, cold tolerance, tiller survival and plant persistence. The present sequence represents the perennial ryegrass 4-coumarate Co-A-ligase 1 (LP4CL1) protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                 This invention represents purified or isolated nucleic acid and protein sequences of enzymes involved in lignin biosynthesis. The enzymes of the invention are 4 coumarate CoA-ligase (4CL), cinnamoyl-CoA reductase (CCR) and cinnamyl alcohol dehydrogenase (CAD) from a ryegrass (Lollum sp.) or fescue (Festuca sp.). The invention comprises an (Lollum sp.) or fescue (Festuca sp.) and cinnamyl alcohol dehydrogenase (CAD) from a ryegrass (Lollum sp.) or fescue (Festuca sp.).
                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 13; Fig 2; 148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel nucleic acid encoding enzymes involved in lignin biosynthetic pathway from ryegrass or fescue species useful for modifying lignin biosynthesis in plants and as a molecular genetic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Perennial ryegrass; lignin; 4 coumarate COA-ligase; QTL; lignin biosynthesis; enzyme; cinnamoyl-COA reductase; CCR; cinnamyl alcohol dehydrogenase; CAD; molecular genetic marker; qualitative trait loci; tagging; QTL mapping; DNA fingerprinting; marker assisted selection; forage improvement; turf grass improvement; dry matter digestibility; herbage quality; palatability; regrowth; cold tolerance; drought tolerance; tiller survival; plant persistence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-JUN-2000; 2000AU-0008154.
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                                                                                      Local
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13 QIAAAAAA 20
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                                                                                     Similarity
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                                                                                                                                       .606 AA;
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100.0%; Pred. No.
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RESULT 18
ABB70398
ID ABB70:
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XX Droso;
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XW Pharm
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Drosophila; developmental biology; cell signalling; insecticide;
                                                              Drosophila melanogaster polypeptide SEQ ID NO 27429
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                                                                                                                                26-MAR-2002
                                                                                                                                                                                            ABB66879;
                                                                                                                                                                                                                                         ABB66879 standard; Protein; 637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB70398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pharmaceutical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB70398 standard; Protein; 624 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity les 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                        158 AAAAAALS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001-656860/75.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           8 AAAAAALS 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     624 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adams M,
                                                                                                                          (first entry)
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2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 8; DB 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        capable of detecting 1000 or more genes from Drosophila. The inventueseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLG175-ABL30511), expressed DNA sequences (ABLG1840-ABL16175) and the encoded proteins (ABB73737-ABB73072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 27429; 21pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent
                                                                                                                      Oryza sativa
                                                                                                                                            Rice; Oryza sativa var. Kinmaze; acetolactic acid synthase; enzyme; herbicide resistance; pyrimidinylcarboxy-based herbicide; plant.
                                                                                                                                                                                                           30-AUG-2002
                                                                                                                                                                                                                                                         ABB81482 standard; Protein;
(TSUB ) KUMIAI CHEM IND CO LTD
                                                                       06-JUN-2002
                                                                                              WO200244385-A1.
                       29-NOV-2000; 2000JP-0362630
                                               16-NOV-2001; 2001WO-JP10014
                                                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                acetolactic acid synthase protein SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                     461 AAAAAALS 468
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                                                                                                                                                                                                                                                                                                                                                                  Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                            AAAAAALS 15
                                                                                                                                                                                                                                                                                                                                                                                                                  637
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2000US-0614150
                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
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                                                                                                                                                                                                                                                           644 AA
                                                                                                                                                                                                                                                                                                                                                                              Score 8;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                           Length 637;
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RESULT 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     resistance against PC-based herbicides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene encoding acetolactic acid synthase, useful in providing ne of plants with high resistance against pyrimidinylcarboxy-based
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NAAG-) NAT INST AGROBIOLOGICAL SCI.
                    This invention relates to novel nucleic acid and protein sequences of mutant acetohydroxyacid synthase (AHS) enzymes that can be used to create herbicide resistance green plants. The encoded AHAS exhibits resistance to at least one herbicide as compared to the wild-type, and has a serine-asparagine substitution at amino acid 627. The sequences of
                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU10024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU10024 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        herbicides
                                                                                                                                                                                                                                                                                                                                                                                              Rice; AHS; acetohydroxyacid synthase; sulphonylurea herbicide; herbicide resistance; weed control; imidazolinone; EC.4.1.3.18
                                                                                                                                                                                                                                                                                                                                                                                                                                     Rice acetohydroxyacid synthase (AHS) wild type protein sequence
                                                                                                                                                                                                                                                                                              09-MAY-2001; 2001WO-US15072
                                                                                                                                                                                                                                                                                                                                               WO200185970-A2
                                                                                                                            herbicide resistant rice
                                                                                                                                       Novel gene encoding a functional acetohydroxyacid synthase gene which imparts resistance to at least one herbicide, used for producing
                                                                                                                                                                                                                                           (LOUU ) UNIV LOUISIANA STATE & AGRIC & MECH COLL.
                                                                                                                                                                                                                                                                      10-MAY-2000; 2000US-203434P
                                                                                                                                                                                                                                                                                                                      15-NOV-2001
                                                                                                    Example 29; Page 117-119; 157pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  644 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 8;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   644
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the invention are useful creating herbicide resistance plants,

these plants it is easier to control the growth of weeds in the

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RESULT 22
AAU10025
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Best Local
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                                                                                                                       mutant acetohydroxyacid synthase (AHS) enzymes that can be used to create herbicide resistance green plants. The encoded AHAS exhibits resistance to at least one herbicide as compared to the wild type, and has a serine-asparagine substitution at amino acid 627. The sequences of the invention are useful creating herbicide resistance plants, by planting these plants it is easier to control the growth of weeds in the vicinity of a plant by applying a herbicide which normally inhibits AHAS. The sequences can be used for producing rice plants having resistance to at least one herbicide which normally inhibits AHAS in the wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vicinity of a plant by applying a herbicide which normally inhibits AHAS. The sequences can be used for producing rice plants having resistance to at least one herbicide which normally inhibits AHAS in the wild-type plant, such herbicides may be particularly inidazolinone or sulphonylurea herbicides. The production of plant having resistance to AHAS inhibiting herbicide allows the development of new herbicides which target AHAS, reducing the risk of weeds becoming resistant. The present sequence represents the wild type protein sequence of the rice AHS.
                           plant, such herbicides may be particularly imidazolinone or sulphonylurea herbicides. The production of plant having resistance to AHAS inhibiting herbicide allows the development of new herbicides which target AHAS, reducing the risk of weeds becoming resistant. The present
                                                                                                                                                                                                                                                                                                                                                                  This invention relates to novel nucleic acid and protein sequences
                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 121-123; 157pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel gene encoding a functional acetohydroxyacid synthase gene which imparts resistance to at least one herbicide, used for producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Croughan TP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-MAY-2001; 2001WO-US15072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rice; AHS; acetohydroxyacid synthase; sulphonylurea herbicide; herbicide resistance; weed control; imidazolinone; EC.4.1.3.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    herbicide resistant rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ABK14658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rice herbicide resistant AHS protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-MAY-2002
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          represents
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8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAAAAALS
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the sequence of the mutant protein sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 8;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGRIC & MECH COLL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                              English.
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. 53;
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210 AAAAAALS 8 AAAAAALS 15 Matches

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Mismatches

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ABB59430
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Matches 8; Conserv
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                                             Sequence
                                                                                                     (ABB57737-ABB72072)
                                                                                                        useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLO1810-6-ABL30511), expressed DNA sequences (ABL01810-6-ABL30511), and the encoded proteins
                                                                    at ftp.wipo.int/pub/published_pct_sequences
                                                                                 specification,
                                                                                         The sequence data for this patent did not form
                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent
                                                                                                                                                                                                            Disclosure; SEQ ID NO 5082; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                            New isolated nucleic
                                                                                                                                                                                                                                                                                     N-PSDB; ABL03533.
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11-JUL-2000; 2000US-0614150
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                                                                                                                                                                                                                                       interactions
                                                                                                                                                                                                                                                 genes from Drosophila
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Similarity 100.0%;
8; Conservative
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                                             662 AA;
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                                                                                                                                                                                                                                              detection reagent for detecting for elucidating cell signalling
           Score 8;
Pred. No.
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      DB 55;
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53;
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and cell-cell
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RESULT 24
ABB57802
RESULT 25
ABB60943
ID ABB6C
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AC ABB6C
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DT 26-M2
DT 26-M2
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                                                                                                                                                                                                                                                                                                                               The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid
genes from Drosophila and
interactions -
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                                        Drosophila melanogaster polypeptide SEQ ID NO 9621.
                                                                                                                                                                                                                                                                                                       Sequence
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11-JUL-2000;
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            Drosophila; developmental biology; cell signalling;
                                                                                              ABB60943;
                                                                                                                        ABB60943 standard; Protein; 1412 AA
                                                                   26-MAR-2002
                                                                                                                                                                                                                                              Local Similarity es 8; Conserv
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                                                                                                                                                                                                                                                                                                       1164 AA;
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ative 0; Mismatches
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               insecticide;
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RESULT 26
ABB64682
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
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genes from Drosophila and
                      23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150
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                                                                                                                                    Drosophila melanogaster
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                                                                                                                                                                           Drosophila; developmental biology; cell signalling; insecticide;
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                                                       genes from Drosophila and
                                                                    New isolated nucleic acid
                                                                                            N-PSDB;
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                                                                                                                                                                                                                                                                                      Drosophila melanogaster
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8; Conserv
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                                                                                                                                PWD,
                                                     detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cel
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The invention relates

to an isolated nucleic acid detection reagent

ligand and a TCR was studied using purified MHC-single peptide complexes (e.g. AAW04633-37) and an antigen specific TCR-zeta chimeric receptor expressed on the surface of a basophil cell line. AAT43774-77 are primer

Disclosure; SEQ ID NO 16689; 21pp + Sequence Listing;

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RESULT 28
AAW04637
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                                       Novel specific inhibitors of the interaction between a T-cell receptor (TCR) and a MHC peptide ligand, are identified by: (a) incubating responder cells that express TCR with a MHC ligand which stimulates the cells, and a test cpd.; (b) monitoring a signal produced by the cell when the TCR and MHC peptide ligand interact; and (c) comparing this signal with a control signal from a similar system lacking the test cpd. The specific inhibitors are potentially useful for blocking T-cells that cause autoimmune diseases (e.g. diabetes, rheumatoid arthritis, Grave's disease etc.), organ transplant rejection or other T cell mediated conditions. The interaction between a specific MHC peptide
                                                                                                                                                                                                                                                                  Specific inhibitors of interaction between T cell receptor and MHC peptide ligand - identified by incubating receptor expressing cells with ligand and test cpd., and measuring change in interaction to detect cpds. potentially useful for blocking disease related T cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                primer; PCR; polymerase chain reaction; specific inhibitor; T-cell receptor; TCR; MHC; ligand; autoimmune diseas; diabetes; rheumatoid arthritis; Grave's disease; organ transplant rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                              Barouch DH,
                                                                                                                                                                                                                                       Example -; Page 3; 21pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9636881-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Null peptide that complexes with A2 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW04637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW04637 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  specification, but was obtained in electroni
at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                               (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-MAY-1995;
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8; Conser
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                                                                                                                                                                                                                                                                                                                                                                                              Jakobsen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide;
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                                                                                                                                                                                                                                                                                                                                                                                             BK, Vessey SJR,
                                                                                                                                                                                                                                       English.
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AA
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). 1.9e+02;
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RESULT 29
AAW61561
ID AAW61
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XX T-CC
DE Synth
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RESULT 30
AAR84046
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CTL clone
                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The biotinylated peptides AAW61559-W61561 were used in a peptide binding assay to test the peptide interactions of a Teel epitope derived from malaria can be used in an immunogenic composition. The T-cell epitope elicits an anti-malarial T-cell response in mammals of diverse genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 11; 38pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New immunogenic compositions for malaria - comprise malaria derived peptide comprising universal T-cell epitope which elicits anti-malarial T-cell response
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biotinylated peptide GYR(A)6L.
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                                                AAR84046 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                      backgrounds. The composition can be used as a vaccine to confer prophylactic or therapeutic immunity against malaria. They may also be used to inhibit the propagation of a malarial organism in a susceptible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-413810/35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAAAAAL 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nardin E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                peptide; 13 AA.
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100.0%; Pr
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                                                                                                                                                                                                                                                                                                                        4.18;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 anti-malarial; prophylactic immunity
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                                                                                                                                                                                                                                                                                            DB 19;
o. 11;
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                                                                                                                                                                                                                                                                                                                   Length 10
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                                                                                                                                                                                                                                                                                                                                               RESULT 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A peptide of 7-30 amino acids capable of binding to a murine MHC class II mol. (i.e. AAR84018-47) covalently linked to 1-3 hapten mols. can be used for treating contact sensitivity, or desensitising a mammal to a contact allergen (e.g. urushiol of poison ivy/oak). The peptide-hapten cpds. disrupt the normal proliferation of hapten-specific T cells, or alter the T cell mediated delayed type hypersensitivity response to the hapten, resulting if offering a property of the sense of the
                      Autoimmune disease; pACT59; pACT74; pACT36; pACT60; murine; T-cell; PKA; mouse; A-kinase anchoring protein 79; cAMP-dependent protein kinase; postsynaptic density; AKAP79; human forebrain; transcriptional activator; interleukin 2; T-cell activation; calcineurin; T-cell clonal expansion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gefter ML, Wilson KJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murine; MHC class II; binding peptide; haptenated peptides; contact; sensitivity; desensitising; mammal; allergen; ivy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-MAY-1996
     calcium/calmodulin
                                                                                                                                                   AKAP79 A37-50 mutation.
                                                                                                                                                                                                 13-JAN-1997
                                                                                                                                                                                                                                                 AAW02569;
                                                                                                                                                                                                                                                                                               AAW02569 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   resulting in effective desensitisation to the hapten.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example; Fig 2; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haptenated peptide(s) capable of binding for treating contact dermatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1995-358583/46
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7; Conserv
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94US-0222206.
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     dependent protein
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Pred. No.
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     phosphatase;
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o. 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 13;
          T-cell response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   II MHC molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                                                                        CC anchoring protein 79 (AKAP79). AKAP79 (see AAM05264 for wild type CC residues 37-50) is responsible for anchoring cAMP-dependent protein kinase CC (PKA) to specific intracellular sites. AKAP79 is predominantly present CC in postsynaptic densities in the human forebrain. The pathways that CC involve AKAP79 are important in many cell types and have been implicated in many cell functions, including the transcriptional activation of the cC interleukin 2 gene that is important in T-cell activation. AKAP allso binds to calcineurin (see AAW02536), which is a calcium/calmodulin CC dependent protein phosphatase associated with T-cell activation. By binding both pKA and calcineurin, AKAP79 co-localises a kinase and CC phosphatase which may regulate flux through a specific signalling CC pathway. The AKAP79 binding sequences can be used to develop products for use in the treatment of autoimmune related conditions. The AKAP79 binding squences can be used to develop products of use in the treatment of autoimmune related conditions. The AKAP79 cc-localises a kinase and for stimulating activated T-cells for selected clonal CC expansion. The proteins can also be used in a method for enhancing CC in T-cell biology and activation of the immune response.
                                                             Matches
                                                                        Query Match
Best Local (
                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New modulators of anchoring protein function - used to develop prods. for use in the treatment of auto-immune-related conditions.
                                                                                                                                                                                                                                                                                                                                                                                                             AAW02565-W02569 represent mutants of residues 37-50 of the A-kinase anchoring protein 79 (AKAP79). AKAP79 (see AAW05264 for wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 11; Page 34; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-268608/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Coghlan VM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-JUL-1995;
23-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W09616172-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ICOS-) ICOS CORP.
(OREG-) STATE OF OREGON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              autoimmune related disease; therapy; immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYOR-)
                            æ
                                                         Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UNIV OREGON HEALTH
                AAAAAAL 14
                                                                                                                      14
                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallatin WM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95US-0503226.
94US-0344227.
95US-0404731.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95WO-US16039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Arg40Ala"
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Lys50Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Lys45Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "Lys42Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Arg39Ala"
                                                     4.1%; Score 7; 1
100.0%; Pred. No.
tive 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Lys41Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Howard ML,
                                                        Mismatches
                                                                     DB 17;
o. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lockerbie RO
                                                        0:
                                                                                   Length 14
                                                     0;
                                                   Gaps
                                                     0,
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RESULT 33 AAR84047

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G

Query Match Best Local Matches

Similarity

4.1%; Score 7; DB 21; 100.0%; Pred. No. 15; Live 0; Mismatches

Length 14;

0;

Gaps

0;

Conservative

8 AAAAAAL 14

ΧX

AAR84047 standard; peptide; 16

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AAB14909
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                                         and calcineurin and so colocalises a kinase and a phosphatase that may regulate flux through a specific signalling pathway. Calcineurin is a Ca2+/calmodulin-dependent protein phosphatase which is involved in many intracellular signalling pathways. It participates in regulation of IL-2 expression following T cell stimulation in T cells. Calcineurin-binding peptides derived from AKAP 79 may be used to inhibit calcineurin activity in a cell. The peptides are useful for treating graft rejection following organ transplantation and for treating T cell-mediated disorders. Calcineurin deletion mutants which bind AKAP 79 are useful for defining an AKAP 79 binding site, for stimulating the immune response, stimulating activated T cells for selected clonal expansion, or for enhancing T cell responses to experimental stimuli for evaluation of early events in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-NOV-1994;
15-MAR-1995;
17-JUL-1995;
                                                                                                                                                                                                                                                           The present sequence is a mutant peptide derived from A-kinase anchor protein 79 (AKAP 79). It is expressed as a poly-histidine tag fusion protein and can thus be purified to homogeneity by nickel affinity chromatography. AKAP 79 binds both cAMP-dependent protein kinase (PKA)
 Sequence
                               T cell biology and activation of the
                                                                                                                                                                                                                                                                                                                                                       Example 11; Column 21; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                     Novel calcineurin deletion mutant having calcineurin polypeptide sequence and binding A-kinase anchor proteins, for treating graft rejection following organ transplantation and T cell-mediated disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; calcineurin-binding peptide; A-kinase anchor protein; AKAP; AKAP 79; immunostimulant; interleukin 2 expression modulation; graft rejection; transplantation; T cell-mediated disorder; mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-578541/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lockerbie RO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ICOS-) ICOS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-SEP-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mutant peptide AKAP 79 A37-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB14909;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB14909 standard; Peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallatin WM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94US-0344227
95US-0404731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lai Y,
                                 immune
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                             response
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RESULT 34
ABB27942
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Matches
                                                                                                                                                                                                                                            Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           urushiol; poison; oak.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murine; MHC class II; binding peptide; haptenated peptides;
contact; sensitivity; desensitising; mammal; allergen; ivy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murine MHC class II binding peptide E5:10:PDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR84047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1995-358583/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gefter ML,
Wilson KJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-FEB-1995;
01-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9526980-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                               Haptenated peptide(s) capable of binding for treating contact dermatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (IMMU-) IMMULOGIC PHARM CORP.
                                Human; microarray; single exon probe; gene expression; breast;
                                                                              01-FEB-2002
                                                                                                     ABB27942;
                                                                                                                                                                                                                                                                                                                                                                                                       Example; Fig 2; 85pp; English.
                                                       Human peptide #593 encoded by breast cell single exon nucleic acid
                                                                                                                            ABB27942 standard; Peptide; 21 AA
                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                              l Similarity
7; Conserv
                                                                                                                                                                                                 IAAAAAA 13
                                                                                                                                                                                                                                                                               16
                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gelber C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                             (first entry)
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94US-0222206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95WO-US04121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "amidated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "acylated"
                                                                                                                                                                                                                                          4.1%; Score 7;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Greenstein
                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'n,
                                                                                                                                                                                                                                             DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hackett CJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Class II MHC molecules
                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                        Length 16
                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                RESULT 35
                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
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21-SEP-2000;
27-SEP-2000;
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26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a peptide encoded by a single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a spatially-addressable set of single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 27; SEQ ID NO 10910; 327pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-496933/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JAN-2001; 2001WO-US00662
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                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probe of the invention.
WO200157277-A2
                                                            Human; foetal liver; gene expression; single exon nucleic acid probe
                                                                                                                               04-FEB-2002 (first entry)
                                                                                              Peptide #5276 encoded by human foetal liver single exon probe
                                                                                                                                                                ABB37770;
                                                                                                                                                                                                 ABB37770 standard; Peptide; 21 AA
                                                                                                                                                                                                                                                                                                               130 NYLLGKG 136
                                                                                                                                                                                                                                                                                  4 NYLLGKG 10
                                                                                                                                                                                                                                                                                                                                                Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                               21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000GB-0024263
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2000US-0608408
                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                   4.1%; Score 7;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen W,
                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rank DR;
                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                DB 22;
                                                                                                                                                                                                                                                                                                                                                                                  Length 21;
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RESULT 36
AAM53912
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Best Local
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 fetal liver. The present sequence is a peptide encoded by a succleic acid probe of the invention.

Note: The sequence data for this patent did not form part of printed specification, but was obtained in electronic format from WIFO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                        04-FEB-2000;
                                                                                                                           W0200157275-A2
                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                               AAM53912;
                                                                               30-JAN-2001; 2001WO-US00667
                                                                                                    09-AUG-2001.
                                                                                                                                                                        epilepsy; cancer.
                                                                                                                                                                                  microarray; Alzheimer's
                                                                                                                                                                                            Human; brain expressed exon;
                                                                                                                                                                                                               Human brain expressed single exon probe encoded protein SEQ ID
                                                                                                                                                                                                                                          05-NOV-2001
                                                                                                                                                                                                                                                                                    AAM53912 standard; Protein; 21 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Penn
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30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                    130 NYLLGKG 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genome-derived single exon nucleic acid probes useful for zing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                              4
                                                                                                                                                                                                                                                                                                                                                                                          Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                              NYLLGKG 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                       21 AA;
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                        (first entry)
                                                       2000US-0180312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000GB-0024263.
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2000US-0207456.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ID NO 30405; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DK,
                                                                                                                                                                                                                                                                                                                                                                                                   4.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen W,
                                                                                                                                                                                 disease;
                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                   Score 7; I
                                                                                                                                                                                           gene expression analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                multiple
                                                                                                                                                                                                                                                                                                                                                                                                              DB
                                                                                                                                                                                                                                                                                                                                                                                                              22;
                                                                                                                                                                              sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                              Length 21;
                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     format directly
                                                                                                                                                                                           probe;
                                                                                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                NO:
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                    04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
                                                                                            Penn
                                                                                                                                      04-OCT-2000;
                                                                                                                                               21-SEP-2000;
27-SEP-2000;
                                                                                                                (MOLE-)
                                                                                                                                                                                                                          30-JAN-2001;
                                                                                                                                                                                                                                              09-AUG-2001
                                                                                                                                                                                                                                                                   WO200157276-A2
                                                                                                                                                                                                                                                                                        Homo
                                                                                                                                                                                                                                                                                                             mlcroarray; cancer;
                                                                                                                                                                                                                                                                                                                     Human; bone marrow expressed exon; gene expression analysis; probe;
                                                                                                                                                                                                                                                                                                                                         Human bone marrow expressed probe encoded protein SEQ ID NO: 31170.
                                                                                                                                                                                                                                                                                                                                                                  06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                       AAM70864;
                                                                                                                                                                                                                                                                                                                                                                                                            AAM70864 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              epilepsy and cancers. The present sequence is a protein encoded by one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides a number of single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                brains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 4; SEQ ID NO: 26017; 650pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity les 7; Conserv
                                                                       2001-488900/53.
                                                                                            SG,
                                                                                                                                                                                                                                                                                       sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 NYLLGKG 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 NYLLGKG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exon nucleic acid probes
                                                                                                                MOLECULAR DYNAMICS INC
                                                                                           Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21
                                                                                                                                              2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                             2000US-0180312.
2000US-0207456.
2000US-0608408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                     2000GB-0024263
                                                                                                                                                                                                                         2001WO-US00668
                                                                                                                                                                                                                                                                                                                                                                  (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,
                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                                            leukaemia; lymphoma;
                                                                                                                                                                                                                                                                                                                                                                 entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.1%; Score 7; DB 22; 100.0%; Pred. No. 22;
                                                                                          Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                           21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                           Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                           Å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for analyzing gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                            myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expressed in the human
on in brain cell samples,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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of.

0;

The present invention provides a number of single

exon

nucleic English.

acid

Human genome-derived single exon nucleic acid probes useful

Example 4;

SEQ ID NO:

31170; 658pp + Sequence Listing;

gene

expression

Τ'n

human

bone

marrow

for

Ъ QΥ

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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
Query Match
Best Local Similarity
                                                                                                                The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a
                                                                                                                                                                                                                                                       Claim 27; SEQ ID No 23534; 487pp; English.
                                                                                                                                                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells - \,
                                                                                                                                                                                                                                                                                                                                WPI; 2001-488901/53.
                                                                                                                                                                                                                                                                                                                                                              Penn
                                                                                                                                                                                                                                                                                                                                                                                          (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JAN-2001; 2001WO-US00670.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200157278-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide #5142 encoded by probe for measuring cervical gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAM18708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM18708 standard; Protein; 21 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein encoded by one of the probes of the invention.
                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUN-2000;
                                                                                       specification,
                                                                       ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130 NYLLGKG 136
                                                                                       The sequence data for this patent did not form part of the printed fication, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 NYLLGKG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                              Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 AA;
                                             21
                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.1%;
100.0%;
4.1%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                              Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 7; 1
Pred. No.
 Score Pred.
                                                                                                                                                                                                                                                                                                                                                              Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
 . No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
22;
 DB 22;
. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22;
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               Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                           밁
                                                                                              δÃ
                             ABG40662
                                           RESULT 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                Query Match
Best Local :
                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                           04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                           The present invention relates to single exon nucleic acid probes (SENP: see AA131315-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM26577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM26577 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide #614 encoded by probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-OCT-2001
                                                                                                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human placenta \dot{}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200157272-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probe; microarray; human; placenta; antenatal diagnosis;
ABG40662;
                     ABG40662 standard;
                                                                                                                                                                Sequence
                                                                                                                                                                                   human genetic disorders.
                                                                                                                                                                                                                                                             Claim 27; SEQ ID No 26846; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JAN-2001;
                                                                                                                     Local Similarity
nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                         sg,
                                                                                                                                                                                                                                                                                                                   2001-488897/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130 NYLLGKG 136
                                                                                                130 NYLLGKG 136
                                                                           4 NYLLGKG
                                                                                                                                                                                                                                                                                                                                                             MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NYLLGKG
                                                                                                                                                                                                                                                                                                                                         Hanzel DK,
                                                                                                                                                                21 AA;
                                                                                                                                                                                                                                                                                                                                                                                  ; 2000US-0234687.
; 2000US-0236359.
; 2000GB-0024263.
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; 2000US-0608408.
; 2000US-0632366.
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                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0180312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001WO-US00663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10
                     Peptide;
                                                                                                                                 100.0%;
                                                                                                                                                                                                                                                                                                                                         Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                      0;
                       21
                                                                                                                                Score 7;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                          Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                       Mismatches
                                                                                                                                 DB 22;
o. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                        0
                                                                                                                                            Length 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                        0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
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19-AUG-2002

(first entry)

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CC nucleid acid expressed in the human lung; measuring gene expression in a CC sample derived from human lung; comprising (a) contacting the array with CC a collection of detectably labeled nucleic acids derived from human lung; comprising (a) contacting the array with CC mRNA, and (b) measuring the label detectably bound to each probe of CC the array; identifying exons in a eukaryotic genome, comprising CC (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, comprising (a) identifying exons from genomic sequences of the above mentioned microarray; assigning exons to a single exon probe, comprising (a) identifying exons from genomic sequence by the method comprising (a) identifying exons from genomic sequence by the method comprising (a) identifying exons from genomic sequence by the method comprising the expression of each of the exons in several common pattern of compression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one concession analysis, and for identifying exons in a gene, particularly cusing human lung derived mRNA and for the study of lung disease (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary disease concession, neutrofibromatosis, thebrous sclerosis, Canther's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                  haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomtosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic
                                                                                                             fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease
Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 27; SEQ ID No 30327; 634pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probes. Also included are a microarray comprising the novel set of probes; the novel set of probes which hybridise at high stringency to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                measure gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spatially-addressable set of single exon nucleic acid probes, used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-114183/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JAN-2001; 2001WO-US00665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human peptide encoded by genome-derived single exon probe SEQ ID 30327
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                 Sequence
                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences.
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                                                                               130 NYLLGKG 136
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cardiotrophin-1 conserved hypothet protein T6D22.4 [i probable peptidogl peptidoglycan-asso cysteine synthase peptidoglycan-asso
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E75613 D95860 E72629 A98330 AD2953 B70765 C70675 C70675 E87310 S63604 B97509 S387509 S387509 S387509 S387509 S387509

G86214 G81653 I49153 A84250 JC4808 A82752 E71495 H72036

C86588 AG2727 A85577 H90725 AI0592 F72550 T52661 AE3013 B98271 D75351

\$05508 H84115 T30575 AI2675 B87367 F84401 I57039 AB3431

\$23053 \$28125 A37185 D72689 H97457 \$26596 E84770 A39065

## ALIGNMENTS

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submitted to GenBank, June 2000
A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Kitajina, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigu J.D.; Jungueira, M.L.; Kemper, E.L.; Kitajina, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigu Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, H.A.; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunces, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.M.; F.G.; Nunces, L.R.; Oliveira, M.A.; de Nosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; A; Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  outer membrane protein P6 precursor XF1896 [imported] - Xylella fastidiosa (strain 9a5c) C;Species: Xylella fastidiosa (c;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 C;Accession: E82625 R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: I-176 <LDD>
A;Residues: I-200; Howe, D.C.; Rogers, J.E.; Arroyo, J.; Eisenstein, B.I.
Mol. Microbiol. 5, 2021-2029, 1991
Mol. Microbiol. 5, 2021-2029, 1991
A;Title: Characterization of a Legionella pneumophila gene encoding a lipoprotein antige
A;Reference number: S16631; MUID:92114778; PMID:1766377
A;Accession: S16631
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A;Accession: A60337
A;Status: preliminary
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R; Ludwig, B.; Schmid, A.; Marre,
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C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: strain 9a5c R; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carraso, B.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: The genome sequence of the plant pathogen Xylella fastidiosa. A;Reference number: A82515; MUID:20365717; PMID:10910347 A;Note: for a complete list of authors see reference number A59328 below
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A; Title: Cloning, genetic analysis, and nucleotide sequence of a determinant coding for
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A; Status: preliminary
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A; Residues: 1-176 < ENG>
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                                                                       A; Contents: annotation C; Genetics:
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A; Residues: 1-186 <SIM>
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conserved hypothetical protein SMa0520 [imported] - Sinorhizobium meliloti (strain C;Species: Sinorhizobium meliloti C;Date: 24-Aug-2001 #sequence remission -
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A;Title: The Drosophila toucan (too) gene is required in A;Reference number: 217769; MUID:98090047; PMID:9362455 A;Accession: T13806
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C;Species: Drosophila melanogaster
C;Species: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Ju1-2000 C;Accession: H72296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sugar-phosphate isomerase - Thermotoga maritima (strain MSB8)
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A; Residues: 1-2176 <GRA>
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Development 124, 4917-4926, 1997
                                                                                                                                                                                                    A; Experimental source: strain MSB8 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                            Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Genetics:
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                                                                                                                                                            A; Gene: TM1080 C; Superfamily: galactoside O-acetyltransferase
                                                                                                                                                                                                                                         A;Cross-references: GB:AE001768; GB:AE000512; NID:g4981619; PIDN:AAD36157.1; PID:g498
                                                                                                                                                                                                                                                                                                                                             A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome A;Reference number: A72200; MUID:99287316; PMID:10360571
                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Nelson, K.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Species: Thermotoga maritima
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A; Residues: 1-143 <ARN>
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                                                                                                                                                                                                                                                                                                                                                                                          Nature 399,
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                                      130 NYLLGKGI 137
20 NYLLGKGI 27
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100.0%;
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L00.0%; Pred. No. 4.9;
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C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 03-Jun-2002
C:Accession: H81777
                                                                    UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-dlamino-pimelate-D-alanyl-D-alanine
                                                                                                        RESULT
H81777
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C; Keywords:
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A; Residues: 1-381 <KIT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Title: Sequence analysis and overexpression of a pectin lyase A; Reference number: JC7650; MUID:21119720; PMID:11272833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: JC7650; PC7125

R;Kitamoto, N.; Yoshino-Yasuda, S.; Ohmiya, K.; Tsukagoshi, N.
Biosci. Biotechnol. Biochem. 65, 209-212, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pectin lyase (EC 4.2.2.10) - Aspergillus oryzae
C;Species: Aspergillus oryzae
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 02-Nov-2001
C;Accession: JC7650; pc7125
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A,Experimental source: strain 1021, megaplasmid pSyma
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
habault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
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R; Barnett, )
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A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot A; Reference number: A95262; MUID:21396509; PMID:11481432
A; Accession: B95296
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A; Residues: 1-280 < KUR>
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                                                                                                                                                                                                       C; Superfamily: D-alanyl-D-alanine carboxypeptidase
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A; Cross-references: GB:
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I40455
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C;Keywords:
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A; Residues: 1-452 < PAR>
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                                                                                                                                        Query Match
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                     88 AAAALSVL 95
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4.7%; Score 8; 1 100.0%; Pred. No.

DB 2;

Length 491;

0;

Mismatches

0;

Indels

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Gaps

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A;Cross-references: EMBL:234883; NID:g1805667; PIDN:CAA84366.1; PID:g509467 R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber C.; Bron, S.; Brouschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galiech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili A;Reference number: A69580; MUID:98044033; PMID:9384377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Bacillus subtilis
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 21-Jul-2000
C;Accession: I40455; D69673; S49132
R;Tognoni, A; Franchi, E; Magistrelli, C.; Colombo, E.; Cosmina, P.; Grandi, Microbiology 141, 645-648, 1995
A; Status: nucleic acid sequence not shown; translation not shown
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A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: H81777
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Pred. No.
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12;
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Cell 61, 85-99, 1990
A;Title: The Drosophila 74EF early puff contains E74, a A;Reference number: A90912; MUID:90199900; PMID:2107982 A;Accession: A34692 A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Genetics:
A;Gene: ditE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DitE protein [imported] - Pseudomonas abietaniphila C;Species: Pseudomonas abietaniphila C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000 C;Accession: T50939
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C; Superfamily: dipeptide transport protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathoa;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: G82981
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                                                                                                                       N;Alternate names: ets-related protein E74A
C;Speciles: Drosophila melanogaster
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 24-Sep-1998
C;Accession: A34692
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A; Residues: 1-547 < MAR>
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A; Residues: 1-526 <STO>
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                                                                           R;Burtis, K.C.; Thumm
Cell 61, 85-99, 1990
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A;Experimental source: strain BKME-9; ATCC700689
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8; Conserv
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                                                                                                        Thummel, C.S.; Jones, C.W.; Karim, F.D.; Hogness, D.S
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A.; Larbig,
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RESULT 12
T13049
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A;Cross references: GB:M37082; NID:g157307; PID:g157308
C;Genetics:
A;Gene: E74
A;Cross references: FlyBase:FBgn0000567
C;Superfamily: ets DNA-binding domain homology
C;Keywords: alternative splicing; DNA binding; nucleus;
F;735-815/Domain: ets DNA-binding domain homology <ETS>
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C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
                                                                                                                                                                                                                            Biochim. Biophys. Acta 495, 388-392, 1977
A;Title: Structure of a peptide antifreeze and mechanism A;Reference number: A03192; MUID:78060969; PMID:588591
A;Accession: A03192
                                                                                                                                                                                                                                                                                                                                              antifreeze protein 3 - winter flounder
C; Species: Pseudopleuronectes americanus (winter flounder)
C; Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change
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A; Residues: 1-2715 <TRE>
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A; Accession: T13049
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R; Treisman, J.E.;
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                                                                                                                                                      C; Keywords: antifreeze
                                                                                                                                                                                                                                                                                                        R; DeVries, A.L.; Lin, Y.
                                                                                                                                                                                                                                                                                                                              C; Accession: A03192
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                                                                                                                                                                        ;Superfamily: antifreeze
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Matches 8; Conserv
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les 8; Conserv
                                                                        Local Similarity
es 7; Conserv
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AAAAAL
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100.0%;
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100.0%; Pred. No.
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G:Genetics.
A;Introns: 19/2
A;Introns: 19/2
C;Superfamily: antifreeze protein
C;Keywords: antifreeze; plasma; tandem repeat
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-44/Domain: propeptide #status predicted <PRO>
- ^=-82/Product: antifreeze protein A #status predicted <MAT>
                          antifreeze protein A - winter flounder (*) Species: Pseudopleuronectes americanus (winter flounder) C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 24-Oct-2000 C;Accession: S02326; JH0627
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A;Residues: 1-82 <DA2>
A;Experimental source: clones 4-2b and 2A-7c
A;Note: the authors translated the codon AGC for residue 24 as Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:M62412; GB:M62416; NID:g213592; PIDN:AAA49471.1; PID:g213593 R;Davles, P.L.; Roach, A.H.; Hew, C.L. Proc. Natl. Acad. Sci. U.S.A. 79, 335-339, 1982 A;Title: DNA sequence coding for an antifreeze protein precursor from winter flounder. A;Reference number: A03194; MUID:82197490; PMID:6952188
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A;Residues: 1-40 <CHA>
C;Superfamily: antifreeze protein
C;Keywords: antifreeze; blocked amino end
F;l/Modified site: blocked amino end (Met) #status experimental
       R; Scott, G.K.; Davies,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antifreeze protein A precursor - winter flounder
C;Species: Pseudopleuronectes americanus (winter flounder)
C;Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change
C;Accession: JS0704; A03194
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R;Chakrabartty, A.; Hew, C.L.;
Can. J. Zool. 66, 403-408, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antifreeze protein GS-8 - grubby sculpin
C;Species: Myoxocephalus aenaeus (grubby sculpin)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 24-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-82 <DA1>
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A; Accession: S07046
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Best Local :
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Conservative (
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P.L.; Kao, M.H.; Fletcher, G.L.
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100.0%; Pred. No
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A; Molecule type: DNA
A; Residues: 1-82 < DAV>
                                                                                                                     R;Davies, P.L.; Hough, C.; Scott, G.K.; Ng, N.; White, B.N.; Hew, C.L. J. Biol. Chem. 259, 9241-9247, 1984
A;Reference number: A05161; MUID:84264559; PMID:6086629
                                                                                                                                                                                             antifreeze protein B precursor - winter flounder (:Speciles: Pseudopleuronectes americanus (winter flounder) C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 24-Oct-2000 C:Accession: A05161
A; Introns: 19/2
                     C; Genetics:
                                       A; Cross-references:
                                                                                                         A; Accession: A05161
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                                                                                                                                                                                                                                                                                                            RESULT 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antifreeze protein (clone 4-2c) - winter flounder C;Species: Pseudopleuronectes americanus (winter flounder) C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 24-Oct-2000
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A; Residues: 1-82 <DAV>
A; Cross-references: GB: M62417;
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Gene 112, 163-170, 1992
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C;Keywords: antifreeze
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A;Title: Differential amplification of antifreeze protein genes in the Pleuronectinae
A;Reference number: S02326; MUID:88259236; PMID:3133486
A;Accession: S02326
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A; Residues: 1-82 < DAV>
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A;Accession: JH0627
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A; Residues: 1-82 <SCO>
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163-170,
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                                GB:L00138; GB:J00929; NID:g343126; PIDN:AAB59964.1; PID:g457351
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A; Gene: AFP
C; Superfamil:
C; Keywords:
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C;Species: Pseudopleuronectes americanus (winter flounder)
C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 24-Oct-2000
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C;Keywords: antifreeze
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C;Superfamily: antifreeze protein
C;Keywords: antifreeze
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C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 24-Oct-2000
C;Accession: I51125
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                                                                                                                                                                                                                                                                                                                                                                                                                   R;Pickett, M.; Scott, G.; Davies, P.; Wang, N.; Joshi, S.; Hew, C. Eur. J. Biochem. 143, 35-38, 1984
A;Title: Sequence of an antifreeze protein precursor.
A;Reference number: IS1125; MUID:84285392; PMID:6547905
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A; Residues: 1-82 <DAV>
oppF homolog, kgmB 5'-region -
C; Species: Streptomyces tenebra
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A; Residues: 1-82 <PIC>
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                                    A55846
                                                     RESULT
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100.0%; Pred. No.
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100.0%; Pred. No.
                 Streptomyces tenebrarius (fragment)
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hypothetical protein Rv2719c - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2000 C;Accession: B70533

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A;Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230 A;Accession: B70533

A;Cross-references: GB:296072; GB:AL123456; NID:g3261793; PIDN:CAB09460.1; PID:g21820

A; Experimental source: strain H37Rv

A; Molecule type: DNA A; Residues: 1-165 <COL>

A;Status: preliminary; nucleic acid sequence not shown;

translation not shown

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

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R.Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alo Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Hulzar, L. Nature 408, 816-820, 2000

Nature 408, 816-820, 2000

A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim A; Liu, J.R.; Liu, S.X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzi, C.A.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallaker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein F309.23 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001 C;Accession: F86299
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A; Residues: 1-87 <HOL>
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A; Residues: 1-150 <STO>
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17 AAAAAAL 23
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7; Conserva
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100.0%; Pred. No.
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omp16 protein - Brucella abortus
C; Species: Brucella abortus
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C;Superfamily: outer membrane protein A
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A; Residues: 1-168 <STO>
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A;Accession: G83525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            outer membrane protein OprL precursor PA0973 [1mported] - Pseudomonas aeruginosa (strair C;Species: Pseudomonas aeruginosa (c;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: G83525
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A; Residues: 1-167 <LIM>
A; Cross-references: EMBL: Z50191
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A; Accession: S58217
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C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 26-Aug-1999
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, K.; Lim,
                                                                                DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AE2405
                                                                                                                                                                            R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata
DNA Res. 8, 205-213, 2001
A;Cross-references: GB:BA000019; PIDN:BAB76496.1; PID:g17133934; GSPDB:GN00179 A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
                                                 A; Molecule type: DNA
A; Residues: 1-170 < KUR>
                                                                                                                                                                                                                                                   C; Accession: AE2405
                                                                                                                                                                                                                                                                                                                               hypothetical protein all4797 [imported] - Nostoc sp. (strain PCC 7120)
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C; Superfamily: outer membrane protein A
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A;Title: The genome sequence of the facultative intracellular pathogen Brucella melit. A;Reference number: Ab3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptidoglycan-associated lipoprotein [imported] - Brucella melitensis (strain 16M) C;Species: Brucella melitensis C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Mar-2002
                                                                                                                                                                                                                                                           C; Genetics:
                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AE008917; PIDN:AAL51521.1; PID:g17982237; GSPDB:GN00190
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A; Residues: 1-168 < KUR>
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A;Title: Molecular cloning, nucleotide sequence, and occurrence of a 16.5-kilodalton A;Reference number: 140346; MUID:94341863; PMID:8063379
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C;Accession: I40346
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A; Residues: 1-168 < RES>
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153 WSQNRRA 159
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A;Gene: pal; excC
A;Map position: 17 min
A;Map position: 17 min
C;Superfamily: outer membrane protein A
C;Keywords: lipid binding; lipoprotein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-173/Product: peptidoglycan-associated lipoprotein #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; B.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: D64810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross references: GB:X05123; NID:g42256; PIDN:CAA28771.1; PID:g42257
R;Lazzaroni, J.C.; Portalier, R.
Mol. Microbiol. 6, 735-742, 1992
A;Title: The excC gene of Escherichia coli K-12 required for cell envelope integrity end A;Reference number: S20546; MUID:92244043; PMID:1574003
A;Accession: S20547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Nucleotide sequence of the gene for the peptidoglycan-associated lipoprotein of A;Reference number: A27534; MUID:87133578; PMID:3545827 A;Accession: A27534
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C;Date: 30-Sep-1988 *sequence_revision 30-Sep-1988 *text_change 01-Mar-2002
C;Accession: A27534; S20547; D64810
R;Chen, R; Henning, U.
Eur. J. Biochem. 163, 73-77, 1987
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C;Species: Escherichia coli
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A; Gene: all4797
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A; Residues: 1-173 < CHE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AE000177; GB:U00096; NID:g1786955; PIDN:AAC73835.1; PID:g1786962; A;Experimental source: strain K-12, substrain MG1655 C;Comment: This lipoprotein of unknown function is very strongly associated with the pef C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X65796; NID:g41358; PIDN:CAA46673.1; PID:g41360 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V
                                                                          C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 01-Mar-2002
C;Accession: A85577
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose,
                                                                                                                                                           peptidoglycan-associated lipoprotein [imported] - Escherichia coli (strain 0157:H7, C;Species: Escherichia coli
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A; Residues: 1-173 <BLAT>
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A; Residues: 1-173 <LAZ>
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
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100.0%; Pred. N
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                                                                                   J.D.; Rose, D.J.; Mayhev
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A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: A85577
A;Status: preliminary
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C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 01-Mar-2002
C;Accession: H90725
                                                                                                                                                                                                                                                                                                                                                                                                       peptidoglycan-associated lipoprotein precursor [imported] - Salmonella enter C; Species: Salmonella enterica subsp. enterica serovar Typhi A; Note: this species has also been called Salmonella typhi C; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 01-Mar-2002 C; Accession: AI0592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and A;Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Hayashi, T.
gasawara, N.;
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A;Experimental source: strain O157:H7, substrain EDL933
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A; Residues: 1-173 <STO>
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A; Residues: 1-173 <HAY>
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                                                                                                                                                                                         th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Faff, S.; Moule, S.; O'Gadra, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se A;Reference number: AB0502; PMID:11677608
A;Accession: AI0592
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A;Gene: STY0/95
C;Superfamily: outer membrane protein A
                                                                          A;Cross-references: GB:AL513382; PIDN:CAD05211.1; PID:g16501981;
                                                                                                            A; Molecule type: DNA
A; Residues: 1-174 < PAR>
                                                                                                                                                                                                                                                                                                                                                   R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr
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                                                      C; Genetics:
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N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
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omp16 protein [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C; Species: Agrobacterium tumefaciens
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A; Residues: 1-176 <HAT>
A; Cross-references: EMBI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cysteine synthase (EC 4.2.99.8), mitochondrial [imported] - Arabidopsis thaliana (fragme C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 03-Nov-2000 C;Accession: T52661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: 226167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Hatzfeld, Y.; Maruyama, A.; Schmidt, A.; Noji, M.; Ishizawa, K.; Saito, K. Plant Physiol. 123, 1163-1171, 2000
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C;Superfamily: Aeropyrum pernix hypothetical protein APE1690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: strain K1
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A; Residues: 1-174 <KAW>
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A;Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  K;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Konaka, Res. 6, 83-101, 1999
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C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
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Local Similarity 100.0%; Pred. No. 48;
hes 7; Conservative 0; Mismatches
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                                                                                                                                   127 AAAAAAL 133
Agrobacterium tumefaciens
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                                                                                                                                                                                                                                               Similarity 100.0%;
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Mismatches
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R; White, O.; Eisen, J.A.; Heidelberg, J.F.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; S.; Smith, H.O.; Venter, J.C.; Fraser, C.M. Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1. A;Reference number: A75250; MUID:20036896; PMID:10567266 A;Accession: D75351
                                                                                                                                                                                                          C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
                                                                                                                                                                                                  C; Accession: D75351
                                                                                                                                                                                                                                                                probable acetyltransferase - Deinococcus radiodurans (strain R1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldm A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, Science 294, 2333-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium
                                                                                                                                                                                                                                                                                                                                      RESULT 37
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C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 01-Mar-2002
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A; Residues: 1-177 < KUR>
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A;Accession: AE3013
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                                                                                                                           J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J athevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;
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100.08; Pr
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R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Abriones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H.; Bas-Neto, E.; Docena, C.; El-Ocrry, H.; Facincani, A.P.; Ferreira, A.J.S.; Submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajıma, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigu, J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajıma, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigu, C.A.; Martios, M.A.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A.; Martins, E.M.; Marcoa, E.C.; Miyaki, C.Y.; Althors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.M.; F.G.; Nunes, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A; Althors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira, M.T.; Suhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; 2
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C;Superfamily: Escherichia coli ribosomal-protein-alanine N-acetyltransferase rimJ
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A; Residues: 1-179 <WHI>
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A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein XF0883 [imported] - Xylella fastidiosa (strain 9a5c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: strain 9a5c R; Simpson, A.J.G.; Reinach, F.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-185 <SIM>
A; Cross-references: GB:AE003927; GB:AE003849; NID:g9105783; PIDN:AAF83693.1; GSPDB:GN001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
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A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trac
A;Reference number: A71570; MUID:99000809; PMID:9784136
A;Accession: E71495
                                                                                                                                                                          probable peptidoglycan-associated lipoprotein - Chlamydia trachomatis (serotype D, C;Species: Chlamydia trachomatis C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 17-Mar-2000 C;Accession: E71495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: XF0883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Contents: annotation
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                                                                                                     R;Stephens, R.S.;
Science 282, 754-7
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                                                                                                                                                                                                                                                                                                                                                         RESULT 39
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                                                                                                             754-759, 1998
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                                                                                                                                          Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-188 <ARN>
A;Cross-references: GB:AE001330; GB:AE001273; NID:g3329034; PIDN:AAC68202.1; PID:g332
A;Experimental source: serotype D, strain UW-3/Cx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptidoglycan-associated lipoprotein CP1091 [imported] - Chlamydophila pneumoniae (st C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 19-May-2000
C;Accession: H72036; CB1504
C;Accession: H72036; CB1504
R;Kalman, S; Mitchell W; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, R;Kalman, S; Mitchell W; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Nature Genet 21, 385-389, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Genetics:
A;Gene: pal
C;Superfamily: outer membrane protein
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R; Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke R; Read, T.D.; Brunham, R.C.; Shen, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzbe Nucleic Acids Res. 28, 1397-1406, 2000
Nucleic Acids Res. 28, 1397-1406, 2000
A; Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis. A,Reference number: A72000; MUID:99206606; PMID:10192388 A;Accession: H72036
                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AE002265; GB:AE002161; NID:g7189999; PIDN:AAF38862.1; PID:g719
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A; Accession: C81504
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                                                                                                                                                                                                                                                       A;Gene:
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A; Residues: 1-192 < REA>
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123 GHTDERG 129
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Maximum Match 100%
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AAB59181
AAB59182
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AAX3434362
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AAX96097
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AAB84122
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AAB08317
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AAB18804
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AAR85450
AAB59180
AAR99625
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H. pylori outer me Expressed antigen H. pylori Netari me Expressed antigen H. pylori outer me Protein encoded by H. pylori omp22 ou H. pylori recombin Chlamydia pneumoni Chlamydia pneumoni Chlamydia pneumoni Chlamydia pneumoni Expressed antigen Chlamydia trachoma Moraxella catarrha Momp P5. Haemophi P. aeruginosa oppr P. aeruginosa op

Escherichia

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RESULT 1
AAY55089
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components of arrays which are useful for diagnostic and prognostic purposes. The polypeptides can be used to produce antibodies, and as a target for the screening of antimicrobial drugs. The polypeptides can also be used in vaccine formulations, and to identify agonists and antagonists. The polypeptides, antibodies, agonists and antagonists which are bacteristatic) are used for the treatment and prevention of diseases including bacterial infection, otitis media in infants and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M. catarrhalis BASB019 protein sequence #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY55089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY55089 standard; Protein; 172 AA
                                                                                                 This sequence is a Moraxella catarrhalis BASB019 protein of the invention. The sequences can be used for diagnosis of disease, staging of disease, or determining response of an infectious organism to drugs. The polynucleotides may be used as a source for hybridisation probes, and for
                                                                                                                                                                                                                 WPI; 2000-062148/05.
N-PSDB; AAZ40351.
                                                                                                                                                                                                                                                                                              06-MAY-1998;
                                                                                                                                                                                                                                                                                                                    03-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                     Moraxella catarrhalis.
                                                                                                                                                                                Novel BASB019 polynucleotides and polypeptides from Moraxella catarrhalis used to prepare vaccines against bacterial infections
                                                                                                                                                          Claim 3; Fig 3; 101pp; English.
                                                                                                                                                                                                                                                    Ruelle J
                                                                                                                                                                                                                                                                        (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS:
                                                                            screening of genetic mutations, serotype, organism or strain identification, identification of mutation in BASB013 sequences, and as
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AAB09475
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Soluble Porphyromo
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AAY55090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         children, pneumonia in the elderly, sinusitis, nosocomial infections and invasive diseases, chronic otitis media with hearing loss, fluid accumulation in the middle ear, auditive nerve damage, delayed speech learning, infection of the upper respiratory tract and middle ear infection. They are also used in the prevention of adhesion of bacteria to eukaryotic matrix proteins on in-dwelling devices, or to extracellular proteins on wounds, and to thus prevent tissue damage and/or block the normal progression of pathogenesis in infections initiated other than by the implantation of in-dwelling devices or by other surgical techniques. The frequency of Moraxella catarrhalis infections has risen dramatically, and it is no longer common to isolate M. catarrhalis strains that are resistant to standard antibiotics. The BASB019 products of the invention can be used screen for new antibacterial compounds that may target these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                      BASB019 protein; diagnosis; infectious organism; auditive nerve damage; genetic mutation screening; antibody production; vaccine; otitis media; bacterial infection; pneumonia; sinusitis; nosocomial infection; invasive disease; delayed speech learning; bacteria adhesion prevention; upper respiratory tract infection; middle ear infection; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY55090 standard; Protein; 172 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              resistant bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M. catarrhalis BASB019 protein sequence #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY55090;
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                                                                                                                                                                                                                                                06-MAY-1998;
                                                                                                                                                                                                                                                                                   03-MAY-1999;
                                                                                                                                                                                                                                                                                                                     11-NOV-1999
                                                                                                                                                                                                                                                                                                                                                      W09957277-A2
                                                                                                                                                                                                                                                                                                                                                                                        Moraxella catarrhalis.
                                   Claim 3; Fig 3; 101pp; English.
                                                                 Novel BASB019 polynucleotides and polypeptides from Moraxella catarrhalis used to prepare vaccines against bacterial infections
                                                                                                                       WPI; 2000-062148/05
N-PSDB; AAZ40352.
                                                                                                                                                                                                           (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 GERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELSY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 ALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ALASKLPSLVYFDFDSDETKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNNSL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MMLHIQIAAAAAALSVLTFMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 AA;
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                                                                                                                                                                                                                                                                                     99WO-EP03038
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Pred. No. 8.7e-86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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This sequence is a Moraxella catarrhalis BASB019 protein of the

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RESULT 3
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AC AAX5
XX AX5
XX O1-M
XX O1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASB019 protein; diagnosis; infectious organism; auditive nerve damage; genetic mutation screening; antibody production; vaccine; otitis media; bacterial infection; pneumonia; sinusitis; nosocomial infection; invasive disease; delayed speech learning; bacteria adhesion prevention; upper respiratory tract infection; middle ear infection; therapy.
                                                                                                                                                                                                                          03-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M. catarrhalis BASB019 protein sequence #3.
                                                                                                                                                                                                                                                                                                                                             11-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Moraxella catarrhalis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 GERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELSY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 ALASTLPSLYYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MMLHIQIAAAAAALSVLTFMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    {\tt MMLHIQIAAAAAALSVLTFMTGCANKSTSQVMVAPNAPTGYTGYTTGVAPLVDNDETVK}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     172 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                98GB-0009683.
                                                                                                                                                                                                             99WO-EP03038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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This sequence is a Moraxella catarrhalis BASB019 protein of the CC invention. The sequences can be used for diagnosis of disease, staging of components of or determining response of an infectious organism to drugs. The CC polynucleotides may be used as a source for hybridisation probes, and for cidentification, identification of mutation in BASB013 sequences, and as components of arrays which are useful for diagnostic and prognostic components of arrays which are useful for diagnostic and prognostic components of recening of antimicrobial drugs. The polypeptides can be used to produce antibodies, and as a cc also be used in vaccine formulations, and to identify agonists and catagonists. The polypeptides, antibodies, agonists and antagonists and components. The polypeptides, antibodies, agonists and arrayonists and contagonists. The polypeptides, antibodies, agonists and arrayonists and contagonists. The polypeptides, antibodies, agonists and arrayonists and contagonists. The polypeptides, antibodies, agonists and prevention of diseases including bacterial infection, otitis media in infacts and contagonists and contagonists. The polypeptides used for the treatment and prevention of contagonists and contagonists and contagonists and contagonists and contagonists and contagonists. The polypeptides and the infections and diseases, chronic otitis media with hearing loss, fluid accumulation in the middle ear, suditive nerve damage, delayed speech contagonists and contagonists and accumulation of the upper respiratory tract and middle ear to eukaryotic matrix proteins on in-dwelling devices, or to extracellular contagonists and to thus prevent tissue damage and/or block the contagonist and to the proteins on infections initiated other than by the infection of in-dwelling devices or by other surgical techniques. The frequency of Moraxella catarrhalis infections has risen dramatically can be used screen for new antibacterial compounds that may threet these
Sequence
                                                                   can be used screen for new antibacterial compounds that may target
                                                             resistant bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Fig 3; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      catarrhalis used to prepare vaccines against bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel BASB019 polynucleotides and polypeptides from Moraxella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ruelle J;
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172 AA;
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            121
                    121 GERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELSY 172
                                                                        61 TLASTLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSL
                                                                                                          61 ALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSL 120
                                                                                                                                                   1 MMLHIQIAAAAAALSVLTFMTGCANKSTSQVMVAAANAATGYTGVIYTGVAALVDNDETIK
                                                                                                                                                                       1 MMLHIQIAAAAAALSVLTFMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVK 60
GERRAVAVRNYLLGKGINQASVETISFGEERPIAFGTNEEAWSQNRRAELSY 172
                                                                                                                                                                                                                                        Conservative
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Matches Query Match Best Local :

169;

Local

Similarity

98.3%;

Score 850; DB 21; Pred. No. 1.4e-84;

DB 21;

Length 172;

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AAY55092
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BASB019 protein; diagnosis; infectious organism; auditive nerve damage; genetic mutation screening; antibody production; vaccine; otitis media; bacterial infection; pneumonia; sinusitis; nosocomial infection; invasive disease; delayed speech learning; bacteria adhesion prevention; upper respiratory tract infection; middle ear infection; therapy.
                                                                                                                      M. catarrhalis BASB019 protein sequence #4.
                                                                                                                                                                       01-MAR-2000
                                                                                                                                                                                                                                         AAY55092 standard; Protein; 172 AA
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(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS

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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              components of arrays which are useful for diagnostic and prognostic purposes. The polypeptides can be used to produce antibodies, and as a target for the screening of antimicrobial drugs. The polypeptides can also be used in vaccine formulations, and to identify agonists and antagonists. The polypeptides, antibodies, agonists and antagonists and antagonists are used for the treatment and prevention of (which are bacteristatic) are used for the treatment and prevention of diseases including bacterial infection, otitis media in infants and children, pneumonia in the elderly, sinusitis, nosocomial infections and invasive diseases, chronic otitis media with hearing loss, fluid annually accompanies of the children of the children
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                accumulation in the middle ear, auditive nerve damage, delayed speech learning, infection of the upper respiratory tract and middle ear infection. They are also used in the prevention of adhesion of bacteria to eukaryotic matrix proteins on in-dwelling devices, or to extracellular proteins on wounds, and to thus prevent tissue damage and/or block the normal progression of pathogenesis in infections initiated other than by the implantation of in-dwelling devices or by other surgical techniques. The frequency of Moraxella catarrhalis infections has risen dramatically, and it is no longer common to isolate M. catarrhalis strains that are resistant to standard antibiotics. The BASBO19 products of the invention can be used screen for new antibacterial compounds that may target these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ruelle J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence is a Moraxella catarrhalis BASB019 protein of the invention. The sequences can be used for diagnosis of disease, staging of disease, or determining response of an infectious organism to drugs. The polynucleotides may be used as a source for hybridisation probes, and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel BASB019 polynucleotides and polypeptides from Moraxella catarrhalis used to prepare vaccines against bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAZ40354.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   screening of genetic mutations, serotype, organism or strain identification, identification of mutation in BASB013 sequences, and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-062148/05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
   AAR07145 standard; protein; 153 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                              121
                                                                                                                                                                                         121 GERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELSY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      169; Conservative
                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MMLHIQIAAAAAALSVLTFMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                  ALASTLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSL 120
                                                                                                                                                        GERRAVAVRNYLLSKGINOASVEIISFGEERPIAFGTNEEAWSQNRRAELSY 172
                                                                                                                                                                                                                                                                                                                                                 ALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSL 120
                                                                                                                                                                                                                                                                                                                                                                                                               MMLHIQIAAAAAALSVLTFMTGCANKSTSQVMVAPNAPTGYAGVIYTGVAPLVDNDETVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98GB-0009683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 844; DB 21; Length 172; pred. No. 6.3e-84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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PR XX PA XX PI DR DR DR PT PT PT XX
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AAP82947
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PD XXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.6kD outer membrane protein (OMP) of H.influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR07145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Purification of outer membrane protein of haemophilus influenzae - by separation from an insoluble fraction using detergent-contg., then detergent-free buffers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 8; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murphy TF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-OCT-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-MAR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-MAR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H.influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Method claimed produces large quantities of the purified OMP, useful in raising antibodies for detection, and as a vaccine against
                                                                                                                     16600 dalton outer membrane protein of non-typable H influenzae.
                                                                                                                                                                              AAP82947;
                                                                                                                                                                                                       AAP82947 standard; protein; 153 AA
                           EP281673-A.
                                                     Haemophilus influenzae
                                                                               pneumonia; meningitis; ss.
                                                                                           Haemophilus influenzae; 16600 dalton outer membrane protein (OMP);
                                                                                                                                                   10-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                        105 RADAVKGYLAGKGVDAGKLGTVSYGEEKPAVLGHDEAAYSKNRRAVLAY 153
                                                                                                                                                                                                                                                                                                    124 RAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELSY 172
                                                                                                                                                                                                                                                                                                                               51 -----VYFGFDKYDITGEYVQILDAHAAYLNATPAAKVLVEGNTDERGTPEYNIALGQR
                                                                                                                                                                                                                                                                                                                                                         64 SKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGER 123
                                                                                                                                                                                                                                                                                                                                                                                                                25 NKSTSQVMVAPNAPT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                          62;
                                                                                                                                                                                                                                                                                                                                                                                   2 NKFVKSLLVAGSVPALAACSSSNNDAAGNGAAQSFGGYS-----VADLQQRYNT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ07145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Apicella MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               153 AA;
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RESULT 7

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     Plasmids, E.coli, hybridomas and antibodies from H.influenzae protein for use as vaccine and detection of Haemophilus influenzae
                                                                                                  N-PSDB; AAN81194.
                                                                                                                                                                              Murphy TF,
                                                                                                                                                                                                                                                                                    08-OCT-1987;
08-NOV-1986;
                                                                                                                                                                                                                                                                                                                                                                   12-NOV-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16600 dalton outer membrane protein of non-typable H influenzae.
                                                                                                                                                                                                                                  (UYNY-) RES UNIV NEW YORK.
                                                                                                                                                                                                                                                                                                                                                                                                                    14-SEP-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pneumonia; meningitis; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haemophilus influenzae; 16600 dalton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAP80593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAP80593 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            such as radiolabelled probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmids, E.coli, hybridomas and antibodies from H.influenzae protein for use as vaccine and detection of Haemophilus influenzae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; ; ; English.
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08-NOV-1986;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                           1988-258472/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 GYLAGKGVDAGKLGTVSYGEEKPAVLGHDEAAYSKNRRAVLAY 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 VYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVR 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 51; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAN81194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          153 AA;
                                                                                                                                                                              Apicella MA
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86US-0932872
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 264; DB 9;
Pred. No. 1.1e-20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     outer membrane protein (OMP);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32;
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RESULT 8
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                  The PBOMP proteins were isolated from a PBOMP-enriched insoluble cell wall fraction from physically disrupted cells of H. influenze and then solubilising the PBOMP from the cell wall fraction by heating in the presence of a detergent or digesting the cell wall fraction with lysozyme, opt. in the presence of a detergent. The genes encoding the PBOMP proteins were isolated by screening a DNA library with an oligonucleotide probe based on the amino acid sequence of the PBOMP protein, or using antibodies to PBOMP.
Sequence
                                                                                                                                                                                       Outer membrane protein epitopes of Haemophilus influenzae- used in the prodn. of antibodies, in vaccines and for prodn. of reagents for
                                                                                                                                                 Disclosure; Fig 11; 164pp; English.
                                                                                                                                                                               diagnosis
                                                                                                                                                                                                                                    N-PSDB; AAQ03869
                                                                                                                                                                                                                                                                            Anilionis A,
                                                                                                                                                                                                                                                                                                                                   01-SEP-1988;
21-AUG-1989;
                                                                                                                                                                                                                                                                                                                                                                            31-AUG-1989;
                                                                                                                                                                                                                                                                                                      (PRAX-) PRAXIS BIOLOGICS IN.
                                                                                                                                                                                                                                                                                                                                                                                                      22-MAR-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Outer membrane proteins; PBOMP-1; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         An epitope of this protein is recognised by the 7F3 antibody in a number of isolates. Monoclonal antibodies to the 16600 D OMP are produced by hybridomas and used to detect H.influenzae. A suspect sample is contacted with the MAb in the presence of an indicator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PBOMP-1 gene product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR05797;
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                                                                                                                                                                                                                                               1990-115815/15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111 GYLAGKGVDAGKLGTVSYGEEKPAVLGHDEAAYSKNRRAVLAY 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 VYFGFDKYDITGEYVQILDAHAAYLNATPAAKVLVEGNTDERGTPEYNIALGQRRADAVK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 VYEDEDSDEIKPQAAAILDEQAQELTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVR 129
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153 AA;
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                                                                                                                                                                                                                                                                            Seid RC,
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89US-0396572
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                                                                                                                                                                                                                                                                            Deich RA,
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Pred. No. 1.1e-20;
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                                                                                                                                                                                         reagents for
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Query Match Best Local Similarity

30.7%;

Score 264; DB 11; Pred. No. 1.1e-20;

Length 153;

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Best Local :
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08-OCT-1987;
29-MAR-1989;
12-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 identification; pneumonia; bacteraemia; meningitis; postpartum sepsis; acute febrile tracheobronchitis; neonatal sepsis; acute otitis media; Haemophilus influenzae; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Outer membrane protein; vaccine; antibody; treatment; identification; pneumonia; bacteraemia; meningitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                The P6 outer membrane protein (OMP) is conserved among strains of Haemophilus influenzas and so antibodies to the OMP can be used to identify H. influenzas in clinical samples. The OMP can also be used in the development of vaccines against H. influenzas which causes pneumonia, bacteraemia, meningitis, postpartum sepsis and acute febrile tracheobronchitis in adults and neonatal sepsis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-APR-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Purifying outer membrane protein of Haemophilus influenzae extn. with detergent buffer, treatment with RNase and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1994-109467/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apicella MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-NOV-1986;
                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; Figure 11b; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                solubilising by heat-treating in detergent-free buffer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYNY ) UNIV NEW YORK STATE RES
                                                                                                                                                                                                                                                                                                                                                                                                        acute otitis media in infants and children
                                                                                                                                                                                                                                                                Local Similarity
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                                                         130 NYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELSY 172
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GYLAGKGVDAGKLGTVSYGEEKPAVLGHDEAAYSKNRRAVLAY 153
                                                                                                                  VYFGFDKYDITGEYVQILDAHAAYLNATPAAKVLVEGNTDERGTPEYNIALGQRRADAVK 110
                                                                                                                                                   VYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVR 129
                                                                                                                                                                                                                                                                                                                                                    153 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              influenzae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murphy TF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86US-0932872.
87US-0092948.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91US-0807049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89US-0330229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86US-0932872
                                                                                                                                                                                                                                                             30.7%;
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                                                                                                                                                                                                                                                          Score 264; DB 15;
Pred. No. 1.1e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ₹
                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32;
                                                                                                                                                                                                                                                                                        Length 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                     0;
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                                                                                                                                                                                                                                     Gaps
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RESULT 11
AAW20394
ID AAW20

AAW20394 standard;

Protein;

AAW20394;

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RESULT 10
AAP80665
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                                            Вр
                                                                  Qy
                                                                                          Matches
                                                                                                    Query Match
Best Local (
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02-MAR-1987;
31-DEC-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAP80665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAP80665 standard; protein; 153 AA.
                                                                                                                                                                     A pure antigenic peptide or protein related to an epitope of Haemophili influenzae is claimed. Also claimed is a recombinant vector comprising DNA sequence coding for an antigenic determinant of an Haemophilus influenzae outer membrane protein, the transformed cell, a subunit vaccine in a pharmaceutical carrier, a method of immunising humans and
                                                                                                                                                                                                                                                                 Pure peptide related to epitope of Haemophilus influenzae - used as immunogens in vaccines and for producing antibodies passive immunisation and assays
                                                                                                                                                                                                                                                                                                              N-PSDB; AAN80226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vaccine; diagnosis; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein-1
                                                                                                                                       Sequence
                                                                                                                                                            an assay for Haemophilus influenzae
                                                                                                                                                                                                                                           Disclosure; Fig 11; 129pp; English.
                                                                                                                                                                                                                                                                                                                                                 Deich RA,
                                                                                                                                                                                                                                                                                                                                                                      (PRAX-) PRAXIS BIOLOGICS IN.
                                                                                                                                                                                                                                                                                                                                                                                                                                           23-DEC-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO8804932-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                           1988-205305/29
                     130 NYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELSY 172
                                               51
                                                           70 VYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVR 129
                                                                                           50;
                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encoded
VYLGFDKYDITGEYVQILDAHAAYLNATPAAKVLVEGNTDERGTPEYNIALGQRRADAVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PBOMP-1)
                                                                                                                                         153 AA;
                                                                                                                                                                                                                                                                                                                                                 Zlotnick G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                             87US-0132073.
87US-0020849.
86US-0948364.
                                                                                                                                                                                                                                                                                                                                                                                                                                           87WO-US03423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Claimed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene.
                                                                                                     30.1%;
                                                                                                                                                                                                                                                                                                                                                   Green
                                                                                           20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            passive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             influenzae Praxis Biolgics Outer Membrane
                                                                                                       Score 259; DB 9;
Pred. No. 3.8e-20;
                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunisation
                                                                                                                 Length 153;
                                                                                                                                                                                                                                                                                   for
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                                                                                                                                                                                                             Haemophilus
comprising a
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The protein may be used in a vaccine to prevent or treat H. pylori
infection or to identify H. pylori polypeptide binding compounds,
useful as potential H. pylori life cycle activators or inhibitors.

The genomic sequence of H. pylori (ATCC 55679) was determined from
coverlapping contigs generated by mechanically shearing the bacterial
and the predicted coding regions defined by computer evaluation. To
dentify likely H. pylori antigens for vaccine development, the amino
daid sequences predicted from various ORF were analysed for significant
and determined the sequences of interest, particular regions can be
isolated from H. pylori by PCR amplification for recombinant polypeptide
production, e.g. in E. coli hosts.
                                                                                                                                                                                                                                                                                                                              Query Match
Best Local (
AAW24651;
                    AAW24651 standard; Protein; 179 AA
                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 56; Page 577; 1481pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-052306/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1996;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Berglindh OT, Smith D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Outer membrane; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ASTR ) ASTRA AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W09640893-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H. pylori outer membrane protein 31262.aa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUL-1997 (first entry)
                                                                                                                               117 NMSLGERRAYAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAEL 170
                                                                                                 122 NOALGYKRTLSVKNALVIKGVEKDMIKTISFGESKPKCVOKTRECYRENRRVDV 175
                                                                                                                                                                65 PAIE--SCTIIASIYFDFDKYEIKESDQETLDEIVQKAKENH-MQVLLEGNTDEFGSSEY
                                                                                                                                                                                               57 ETVKALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREY 116
                                                                                                                                                                                                                                                               15 SVLIFM-----TGCANK------STSQVMVAP--NAPTGYTGVIYTGVAPLVDND 56
                                                                                                                                                                                                                                5 SVFSFLVAFLLVVGCSHKMDNKTVAGDVSTKAVQTAPVTTEPAPEKEEPKQEPAPVVEEK 64
                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                             179 AA;
                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96US-0630405
95US-0487032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96WO-US09122
                                                                                                                                                                                                                                                                                                                       25.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mellgaerd BL;
                                                                                                                                                                                                                                                                                                         30;
                                                                                                                                                                                                                                                                                                                     Score 215.5; DB : Pred. No. 2.6e-15
                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                  DB 18; Length 179;
                                                                                                                                                                                                                                                                                                      66;
                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                          also useful for generating vaccines for immunising subjects against H. pylori or for use in detecting the presence of Helicobacter species in a sample. Antisense nucleic acid sequences of these sequences are used to inhibit expression of a gene from Helicobacter species. H. pylori whole genomic DNA was isolated and nebulised to a median size of BstXI-linker adapters in 100-1000 fold molar excess. These linkers are complementary to the BstXI-cut pMPX vectors, while the overhang is not self-complementary. Therefore the linkers will not concatemerise nor were ligated to each of the 20 pMPX vectors to construct a series of shotgum subclone libraries. The purified DNA samples were then
                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bacterial life cycle, for the ability to bind an H. pylori nucleic acid sequence. The nucleic acid sequences, and corresponding proteins, are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Helicobacter pylori has been strongly linked to chronic gastritis and duodenal ulcer disease. The nucleic acid sequences of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       are used to evaluate compounds, especially activators or inhibitors of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 18; Page 171; 235pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents an H. pylori outer membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Helicobacter pylori nucleic acid sequences and related proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAT77469.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-298052/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane; cytoplasmic; cell envelope; flagella; transport; secreted; periplasmic; chronic gastritis; duodenal ulcer disease; activator; inhibitor; bacterial life cycle; vaccine; immunise;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ASTR ) ASTRA AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-MAY-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            detection; antisense; inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9719098-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H. pylori outer membrane protein 31262.aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-AUG-1997 (first entry)
                                                                                                                                                                                                                                               Local
122 NQALGVKRTLSVKNALVIKGVEKDMIKTISFGESKPKCVQKTRECYRENRRVDV 175
                                117 NMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAEL 170
                                                                                                                                                                                                                                                                                                                                     the related specification, W09640893.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for diagnostics and therapeutics
                                                                     65 PAIE--SGTIIASIYFDFDKYEIKESDQETLDEIVQKAKENH-MQVLLEGNTDEFGSSEY
                                                                                                        57 ETVKALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREY
                                                                                                                                                                             15 SVLTFM-----TGCANK------STSQVMVAP--NAPTGYTGVIYTGVAPLVDND 56
                                                                                                                                                                                                                                                                                                                                           The ORF/protein reference number for this sequence was obtained
                                                                                                                                          5 SVFSFLVAFLLVVGCSHKMDNKTVAGDVSTKAVQTAPVTTEPAPEKEEPKQEPAPVVEEK 64
                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                   179 AA;
                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95US-0561469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96WO-US18542.
                                                                                                                                                                                                                                   25.0%; Score 215.5; DB 18; Length 179; 32.8%; Pred. No. 2.6e-15;
                                                                                                                                                                                                                           30;
                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gastritis and
                                                                                                                                                                                                                      21;
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RESULT 13

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RESULT 14
AAB46316
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                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a Helicobacter pylori antigenic protein that is characterised by immunoreactivity with H. pylori-positive antisera. The proteins are highly immunogenic and induce a long-lasting immune response that persists even after antimicriobial treatment. In antibody-detection assays, on sera, plasma, urine, saliva etc., they are highly sensitive and specific. The specification also describes 69 previously unrecognised immunogenic cluster families. H. pylori antigens are used to detect H. pylori-specific antibodies, for diagnosing infection or to confirm eradication of infection, and in vaccines to protect against H. pylori infection and related diseases (gastritis, peptic ulcer, gastric adenocarcinoma/lymphoma).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antigen; immunogenic cluster family; vaccine; gastritis; diagnosis; peptic ulcer; gastric adenocarcinoma; gastric lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9849314-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Expressed antigen for clone Y175A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW89982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW89982 standard; Protein; 179 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Helicobacter pylori antigens and related nucleic acid sequences - useful in serological diagnosis and protective vaccines, providing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-OCT-1997;
25-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-NOV-1998
05-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 16; Page 321; 402pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        long-lasting immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-009433/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GENE-) GENELABS TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-APR-1998;
                                                                 AAB46316 standard; Protein; 179 AA
                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                    117 NMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAEL 170
                                                                                                                                                                                                                    65 PAVE---SGTIIASIYFDFDKYEIKESDQETLDEIVQKAKENH-MQVLLEGNTDEFGSSEY
                                                                                                                                                                                                                                                                                                                     15 SYLTEM-----TGCANKSTSQVMVAP-NAPTGYTGVIYT------GVAPLVDND 56
                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                  ETVKALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREY 116
                                                                                                                                                                                                                                                                                     SVFSFLVAFLLVAGCSHKMDNKTVAGDVSAKTVQTAPVTTEPAPEKEEPKQEPAPVVEEK 64
                                                                                                                                                  179 AA;
                                                                                                                                                                                                                                                                                                                                                     Conservative
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-0061958.
97US-0045107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-US08487
                                                                                                                                                                                                                                                                                                                                               25.0%; Score 215.5; DB 20; Lewy...
32.2%; Pred. No. 2.6e-15;
32.2%; wismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                      Length 179;
                                                                                                                                                                                                                                                                                                                                                          21;
                                                                                                                                                                                                                                                                                                                                                          Gaps
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QΥ
                                                                                                                                                                              Db
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                                           δõ
                                                                                        Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes a novel preparation of an agent (A) for detection, prevention and/or treatment of microbial infection by:

(I) identifying essential genes (I) and corresponding polypeptides (II); (II) identifying compounds that are directed against (II) and (II); (II) formulating selected (A). Identifying essential genes (I) comprises (IV) formulating selected (A). Identifying essential genes (I) comprises (IV) formulating selected (A). Identifying essential genes (I) comprises (IV) formulating selected (A). Identifying essential genes (I) comprises (IV) formulating selected (A). Identifying essential genes (I) comprises (IV) formulating selected (A) and/or subtractive recombination mutagenesis (SRM). (C) inhibition (CAI) and/or subtractive recombination mutagenesis (SRM). (C) inhibition for the invention have annibacterial activity. (A) (which may comprise the products of the invention have annibacterial activity. (A) (which may compressed in III) in the products of the invention of note cell containing (IA), derived (C) comprise or an inhibitor of (IIA) are particularly used for diagnosis, (IIA) are used in DNA, subunit or live vaccines. The method (IIA) and (IIA) are used in DNA, subunit or live vaccines in other (IIA) containing the sectivity. Many containing the broad spectrum of activity. Many
                                                                                                                                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H. pylori HPS144 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Preparing an agent for diagnosis or control of microbial infection, useful particularly against Helicobacter, based on identification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAY-2000; 2000WO-EP05024.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200073502-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vaccine; screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Microbial infection; antibacterial; Helicobacter pylori infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 37; Page 253; 366pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAF25593.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apfel H, Fuchs TM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         essential genes in defective mutants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-049948/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
                                                                                                                                                                                                                                                                                                                                                                                                          identifies essential genes, including those that have homologs in other species, so identified (A) should have a broad spectrum of activity. Many gene-deficient cells can be screened quickly, in an automated process, and the identified genes can be used for screening without purification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                  Sequence
122 NQALGVKRTLSVKNALVIKGVEKDMIKTISFGETKPKCAQKTRECYKENRRVDV 175
                                             117 NMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAEL 170
                                                                                                                                                                                                                            15 SVLTFM-----TGCANKSTSQVMVAP-NAPTGYTGVIYT------GVAPLVDND 56
                                                                                        65 PAVE--SGTIIASIYFDFDKYEIKESDQETLDEIVQKAKENH-MQVLLEGNTDEFGSSEY
                                                                                                                                   57 ETVKALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREY 116
                                                                                                                                                                                 5 SYFSFLVAFLLVAGCSHKMDNKTVAGDVSAKTVQTAPVTTEPAPEKEEPKQEPAPVVEEK 64
                                                                                                                                                                                                                                                                                               h 25.0%; score 215.5; DB 22; Length 179; similarity 32.2%; Pred. No. 2.6e-15;
                                                                                                                                                                                                                                                                                                                                                                      179 AA;
                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99DE-1027740
99DE-1034029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99DE-1024965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gibbs CP,
                                                                                                                                                                                                                                                                                34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hueck CJ,
                                                                                                                                                                                                                                                                                63;
                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                     21; Gaps
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RESULT 15 AAW20795

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                                                                                                                                                                                                                                                                                                                           This sequence is a H. pylori outer membrane protein.

C The protein may be used in a vaccine to prevent or treat H. pylori confection or to identify H. pylori polypeptide binding compounds, and in the protential H. pylori life cycle activators or inhibitors. The sequence of H. pylori (ATCC 55679) was determined from CC ONA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To conditify likely H. pylori antigens for vaccine development, the amino can determined the sequences of interest, particular regions can be considered from H. pylori by PCR amplification for recombinant polypeptide yrv
                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                     Query Match
Best Local
AAW89813 standard; Protein; 179 AA
                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 56; Page 1203; 1481pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polypeptide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Helicobacter pylori nucleic acid sequences and related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAT68048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-052306/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Berglindh OT, Smith D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; envelope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infection, and to detect Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ASTR ) ASTRA AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9640893-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H. pylori outer membrane protein 07gp31516orf4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW20795 standard; Protein; 187 AA.
                                                                                                                                                                                                                                                                    Local Similarity
                                                                130 NQALGVKRTLSVKNALVIKGVEKDMIKTISFGESKPKCVQKTRECYRENRRVDV 183
                                                                                          117 NMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAEL 170
                                                                                                                        73 PAIE--SGTIIASIYFDFDKYEIKESDQETLDEIVQKAKENH-MQVLLEGNTDEFGSSEY
                                                                                                                                                  57 ETVKALASKLPSLVYFDFDSDETKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREY 116
                                                                                                                                                                               13 SVFSFLVAFLLVVGCSHKMDNKTVAGDVSTKAVQTAPVTTEPAPEKEEPKQEPAPVVEEK 72
                                                                                                                                                                                                           15 SVLIFM-----TGCANK------STSQVMVAP--NAPTGYTGVIYTGVAPLVDND 56
                                                                                                                                                                                                                                                        57;
                                                                                                                                                                                                                                                                                                            187 AA;
                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95US-0487032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96US-0630405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96WO-US09122.
                                                                                                                                                                                                                                                            25.0%; Score 215.5; DB 1 32.8%; Pred. No. 2.8e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mellgaerd BL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for vaccines to treat or prevent H. pylori
                                                                                                                                                                                                                                                 30;
                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                          DB 18;
                                                                                                                                                                                                                                             66; Indels
                                                                                                                                                                                                                                                                       Length 187;
                                                                                                                                                                                                                                           21;
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XAXEX
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                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                     Best Local
           23-JAN-1998
                                                             AAW23592 standard; Protein; 179 AA.
                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a Helicobacter pylori antigenic protein that is characterised by immunoreactivity with H. pylori-positive antisera. The proteins are highly immunogenic and induce a long-lasting antisedy-detection assays, on sera, plasma, urine, saliva etc., they are previously unrecognised immunogenic cluster families. H. pylori antigens infection or to confirm eradication of infection, and in vaccines to protect against H. pylori infection and related diseases (gastritis, peptic ulcer, gastric adenocarcinoma/lymphoma).
                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 10; Page 96-97; 402pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                long-lasting immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Hellcobacter pylori antigens and related nucleic acid sequences useful in serological diagnosis and protective vaccines, providing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAV90545.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-009433/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-OCT-1997;
25-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GENE-) GENELABS TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09849314-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antigen; immunogenic cluster family: vaccine; gastritis; diagnosis; peptic ulcer; gastric adenocarcinoma; gastric lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein encoded by clone Gla ORF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW89813;
                                                                                                                                                           118 MSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAEL 170
                                                                                                                             123 QALGVKRTLSVKNALVIKGVEKDMIKTISFGETKPKCAQKTRECYKENRRVDV 175
                                                                                                                                                                                       64 KPAIESGTIIASIYFDFDKYEIKESDQETLDEIVQKAKENH-MQVLLEANTDEFGSSEYN
                                                                                                                                                                                                                    66 LPSL-----VYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYN 117
                                                                                                                                                                                                                                                4 SSAFSFLVAFILLVAGCSHKMDNKTVAGDVSAKTVQTAPVTTEPAPEKEEPKQEPAPVVEE 63
                                                                                                                                                                                                                                                                            8 AAAAAALSVLTFMTGCANKSTSQVMVAP-NAPTGYTGVIYTGVAPLVDNDETVKA-LASK 65
                                                                                                                                                                                                                                                                                                                     54; Conservative
                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fry KE, Lim MY, McAtee CP;
                                                                                                                                                                                                                                                                                                                                                                              179 AA;
      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0045107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98WO-US08487.
                                                                                                                                                                                                                                                                                                                           24.6%; Score 211.5; DB 20; Length 179; 31.2%; Pred. No. 7.2e-15;
                                                                                                                                                                                                                                                                                                               36; Mismatches
                                                                                                                                                                                                                                                                                                            /.2e-15;
hes 72;
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                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H. pylori Omp22 outer membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Omp22 gene; outer membrane protein; antigen; immunogen; stomach;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gastritis; peptic ulcers; gastric cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09728264-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents Omp22, an outer membrane protein which exhibits antigenicity and immunogenicity against Helicobacter pylori. This bacterium is associated with inflammation of the stomach and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Helicobacter pylori outer membrane protein, Omp22 - used in a vaccine for treatment or prevention of H. pylori infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-AUG-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               gastritis related diseases e.g. peptic ulcers and gastric cancer. Omp22 could be used in immunological therapy as a H. Pylori-specific antigen for the treatment and prevention of diseases associated with this microorganism e.g. as the active ingredient in a diagnostic kit or a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAT74195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-402617/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kim J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MOGA-) MOGAM BIOTECHNOLOGY RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Fig 5; 38pp; English.
Omp22 gene; outer membrane protein; antigen; immunogen; stomach;
                             H. pylori recombinant Omp22 recombinant outer membrane protein.
                                                          23-JAN-1998
                                                                                       AAW23591;
                                                                                                                    AAW23591 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                    122 ERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAEL 170
                                                                                                                                                                                                                                                                          62 LASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLG 121
                                                                                                                                                                                                                                                                                                                                   14 LSVLTFMTGCANKSTSQVMVAP-NAPTGYTGVIYTGV-----APLVDNDETVKA 61
                                                                                                                                                                                                                                              69 -SGTIIASIYFDFDKYEIKESDQETLDEIVQKAKENH-MQVLLEGNTDEFGSSEYNQALG 126
                                                                                                                                                                                                                                                                                                         10 LVAFLFIAGCKHNMDKETVAGDVSAKAVQSAPVSTEIAQEKQEPKQEPAPVVEEKPAVE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Moon H, Park Y, Seo W,
                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                         VKRTLSVKNALVIKGVEKDMIKTISFGETKPKCTQKTRECYKENRRVDV 175
                                                                                                                                                                                                                                                                                                                                                                                                                          179 AA;
                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96KR-0002105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96WO-KR00154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Omp22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= mature_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= leader_sequence
                                                                                                                                                                                                                                                                                                                                                                              24.2%; Score 208.5; DB 1 30.8%; Pred. No. 1.5e-14;
                                                                                                                                                                                                                                                                                                                                                                   33;
                                                                                                                     144 AA
                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yu G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnostic; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                              DB 18; Length 179;
                                                                                                                                                                                                                                                                                                                                                                      69; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                       Gaps
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sinusitis;

purulent otitis media; erythema nodosum;

pharyngitis;

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RESULT 19
AAY35412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This amino acid sequence of Omp22, is a recombinant outer membrane protein which is identical to the mature protein of its native form (see AAW23592). It retains antigenicity and immunogenicity against Helicobacter pylori. This recombinant Omp22 protein can be mass produced in via expression in E.coli DH5-Alpha cells. H. pylori is associated with inflammation of the stomach and gastritis related diseases e.g. with inflammation of the stomach and gastritis related diseases e.g. peptic ulcers and gastric cancer. The native and the recombinant form of Omp22 could be used in immunological therapy as a H. Pylori-specific antigen for the treatment and prevention of diseases associated with this microorganism e.g. as the active ingredient in a diagnostic kit or a prophylactic/therapeutic vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gastritis; peptic ulcers; gastric cancer; diagnostic; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             recombinant protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-AUG-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Helicobacter pylori outer membrane protein, Omp22 - used in a vaccine for treatment or prevention of H. pylori infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kim J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MOGA-) MOGAM BIOTECHNOLOGY RES INST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                              Chlamydia pneumoniae transmembrane protein sequence
                                                                                                                                                                                                  AAY35412 standard; Protein; 192 AA
Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
                                                                                                                                                   AAY35412;
                                                                                                    13-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 ERGSREYNMSLGERRAVAVRNYLLGKGINQASVEIISEGEERPIAFGTNEEAWSQNRRAE 169
                                                                                                                                                                                                                                                                                                                           140 V 140
                                                                                                                                                                                                                                                                                                                                                                            170 L 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50 APLVDNDETVKALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTD 109
                                                                                                                                                                                                                                                                                                                                                                                                                        23 APVVEEKPAVE--SGTIIASIYFDFDKYEIKESDQETLDEIVQKAKENH-MQVLLEGNTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Moon H, Park Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity
46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Recombinant outer membrane protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 205.5; DB 1
Pred. No. 2.4e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yu G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yum J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 18; Length 144;
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AAE04322
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Best Local
                      20-DEC-2000; 2000WO-CA01534.
                                                                                         Chlamydia pneumoniae
                                                                                                               acute respiratory disease; cough; sore throat; atherosclerosis; asthma;
                                                                                                                             Omp P6 precursor; outer membrane protein; Chlamydia infection; pneumonia; upper respiratory tract disease; bronchitis; sinusitis;
                                                                                                                                                               Chlamydia pneumoniae omp p6 precursor protein.
                                                                   WO200146224-A2
                                                                                                              vaccine; antibiotic.
                                                                                                                                                                                       04-SEP-2001 (first entry)
                                                                                                                                                                                                                    AAE04322
                                                                                                                                                                                                                                    AAE04322 standard; Protein; 192 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see AAX91990) of Chlamydia pneumoniae. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in nucleotides sequences can also be used as immunogenic compositions as vaccines. Vectors containing C. pneumoniae especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 1196-1197; Disclosure; 1912pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome sequence of Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-357842/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-NOV-1998;
21-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vaccine; neutralising epitope.
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                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                     128 RGAASYNLALGARRÂNAIKEHLRKQGISADRLSTISYGKEHPLNSGHNELAWQQNRRTE 186
                                                                                                                                                                                                                                                                                                         111 RGSREYNMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAE 169
                                                                                                                                                                                                                                                                                                                                68 DSKEEKQYKSSQVAAFRNITFATDSYTIKGEENLAILINLVHYMKKNPKATLYIEGHTDE 127
                                                                                                                                                                                                                                                                                                                                                     54 DNDETVKALASKLPSL--VYFDFDSDEIK-PQAAAILDEQAQFLTTNQTARVLVAGHTDE 110
                                                                                                                                                                                                                                                                                                                                                                                      46;
                                                                                                                                                                                                                                                                                                                                                                                                                                192 AA;
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97FR-0014673.
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                                                                                                                                                                                                                                                                                                                                                                                                   DB 20; Length 192;
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   RESULT 21
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Best Local :
03-JUL-2001; 2001WO-IB01445
                       10-JAN-2002.
                                                                              Protein
                                                                                                    Peptide
                                                                                                                                                         strain CWL029
                                                                                                                                                                                                                                                                         ABB90544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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Chlamydial infection; antigen; immunogen; vaccine; diagnosis; human respiratory disease; cardiovascular disease; atherosclerosis; coronary artery disease; carotid artery stenosis; myocardial infarction; cerebrovascular disease; aortic aneurysm; claudication; stroke;
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W0200202606-A2
                                                                                                                                                                                                                                      Chlamydia pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chlamydia pneumoniae cp7090 protein, SEQ ID NO:37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JUL-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 16; Fig 1; 74pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128 RGAASYNLALGARRANAIKEHLRKQGISADRLSTISYGKEHPLNSGHNELAWQQNRRTE 186
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                                                                                                                                                                            Location/Qualifiers
                                                   /note= "Mature protein"
                                                                                                           /label= Signal_peptide
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                                                                                              .192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24; Mismatches
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Best Local 9
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18-AUG-2000;
14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     also involved in the development of cardiovascular diseases such as atherosclerosis, coronary artery disease, carotid artery stenosis, anyocardial infarction, cerebrovascular disease, carotid artery stenosis, envolved in the invention claudication and stroke. The proteins and nucleic acids of the invention was the used in vaccines and pharmaceutical compositions for the prevention or treatment of chlamydial infections, particularly Chlamydia pneumoniae infections. The proteins may also be used in the detection of chamydia pneumoniae, and the nucleic acids may be used in PCR, branched DNA probe assay or blotting techniques for determining Chlamydia pneumoniae gene expression. The present sequence represents a specifically claimed Chlamydia pneumoniae protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequences ABB90526-ABB90715 represent novel proteins from Chlamydia pneumoniae (strain CWL029), and ABL91184-ABL91373 represent DNA encoding them. The proteins are predicted to be immunogenic and may therefore be useful in vaccine production and for diagnostic purposes. Chlamydia pneumoniae is a common cause of respiratory disease in humans, and is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel Chlamydia pneumoniae protein useful in the manufacture of a medicament for treatment or prevention of infection due to Chlamydia, preferably Chlamydia pneumoniae, and for diagnostic purposes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CHIR-) CHIRON SPA.
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 05-NOV-1998
                                 WO9849314-A2
                                                                  Helicobacter pylori
                                                                                                 Antigen; immunogenic cluster family; vaccine; gastritis; diagnosis; peptic ulcer; gastric adenocarcinoma; gastric lymphoma.
                                                                                                                                                       Expressed antigen for clone Y89A
                                                                                                                                                                                             18-FEB-1999
                                                                                                                                                                                                                               AAW89983;
                                                                                                                                                                                                                                                              AAW89983 standard; Protein; 104 AA
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                                                                                                                                                                                                                                                                                                                                                                                  111 RGSREYNMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAE 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                    54 DNDETVKALASKLPSL--VYFDFDSDEIK-PQAAAILDEQAQFLTTNQTARVLVAGHTDE 110
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2000GB-0017047.
2000GB-0017983.
2000GB-0019368.
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2000GB-0022583.
2000GB-0027549.
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a Helicobacter pylori antigenic protein that is characterised by immunoreactivity with H. pylori-positive antisera. The proteins are highly immunogenic and induce a long-lasting immune response that persists even after antimicriobial treatment. In antibody detection assays, on sera, plasma, urine, saliva etc., they are highly sensitive and specific. The specification also describes 69 previously unrecognised immunogenic cluster families. H. pylori antigens are used to detect H. pylori-specific antibodies, for diagnosing infection or to confirm eradication of infection, and in vaccines to protect against H. pylori infection and related diseases (gastritis, peptic ulcer, gastric adenocarcinoma/lymphoma).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-OCT-1997;
25-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 16; Page 322; 402pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Helicobacter pylori antigens and related nucleic acid sequences useful in serological diagnosis and protective vaccines, providing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chow TP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GENE-) GENELABS TECHNOLOGIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                long-lasting immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                        04-NOV-1998;
28-NOV-1997;
17-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                     paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; bartholinitis; pneumopathy; venereal lymphogranulomatosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vaccine; eye disease; conventional trachoma; nonendemic trachoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chlamydia trachomatis surface exposed protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-OCT-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY37603;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY37603 standard; Protein; 214 AA
                                                                                                                                                                                                                                                                                                    W09928475-A2
                                                                                                                                                                                                                                                                                                                                                            Chlamydia trachomatis.
                                                                                                                                                                                                                                              10-JUN-1999
(GEST ) GENSET
                                                                                                                                                                                   27-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 NYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAEL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 VYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVR 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 NALVIKGVEKDMIKTISFGETKPKCAQKTRECYKENRRVDV 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 IYFDFDKYEIKESDQETLDEIVQKAKENH-MQVLLEGNTDEFGSSEYNQALGVKRTLSVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fry KE, Lim MY, McAtee CP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-0061958
97US-0045107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98WO-US08487
                                                                                           98US-0107077.
97FR-0015041.
                                                                                                                                                                                         98WO-IB01939
                                                                     97FR-0016034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 197.5; DB 2
Pred. No. 1.1e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 104;
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RESULT 24
AAB20105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local
New BASB113 polypeptide isolated from Moraxella catarrhalis bacterium, useful for diagnosing and producing vaccines against bacterial infections such as otitis media and pneumonia
                                                                                                              Thonnard J;
                                                                    N-PSDB; AAF30043.
                                                                                                                                   (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                    25-JUN-1999;
                                                                                                                                                                                          23-JUN-2000; 2000WO-EP05851.
                                                                                                                                                                                                                                                      WO200100836-A1.
                                                                                                                                                                                                                                                                              Moraxella catarrhalis.
                                                                                                                                                                                                                                                                                                          BASB311; infection; otitis media; pneumonia; therapy; diagnosis;
                                                                                                                                                                                                                                                                                                                                              Moraxella catarrhalis BASB113 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                             AAB20105 standard; Protein; 224 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY36754-Y37949 are encoded by open reading frames (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). The polypeptides can be used as can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye paratrachoma, and inclusion conjunctivitis; genital diseases such as conventional trachoma, nonendemic trachoma, nongonococcal uretritis, epidymitis, cervicitis, salpingitis, perihepatitis, bartholinitis; pneumopathy in breast feeding infants; and venereal lymphogranulomatosis. The polypeptides of the invention may be of use in treating these diseases.
                                                                                                                                                                                                                                                                                                       antibacterial; antimicrobial.
                                                                                                                                                                                                                                                                                                                                                                            23-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 1248-1249; 1755pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome sequence of Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-371125/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Griffais R;
                                                                               2001-112458/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 HPVHPGHNELAWQQNRRTE 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 RPIAFGTNEEAWSQNRRAE 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 VRHLHKSPKATLYIEGHTDERGAAAYNLALGARRANAVKQYLIKQGIAADRLFTISYGKE 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91 AQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGKGINQASVEIISFGEE 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 GFVPFYSDEEIQQAFVEDFDSKEEQLYKTSAQSTSFRNITFATDSYSIKGEDNLTILASL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   214 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                              99GB-0015044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22.8%; Score 196.5; DB 20; 35.3%; Pred. No. 4e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 214;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASBILI polypeptides, and polynucleotides encoding them, as well as cexpression vectors, host cells and methods for producing BASBILI accomposition comprising a BASBILI polypeptides using recombinant methods. Also claimed is a vaccine composition comprising a BASBILI polypeptide, an immunogenic composition comprising a BASBILI polypeptide, or a polypeptide having at least composition oxid sequence identity to BASBILI, or comprising a polypeptide encoding such a polypeptide. A claimed method of composition and a diagnosing a woraxella infection involves identifying a BASBILI composition useful composition with M. catarrhalis infection composition useful contracted against a BASBILI polypeptide. BASBILI composition comprises at least polypeptides also have utility in raising specific antibodies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
23-AUG-2001
                                                                      WO200161013-A1
                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          surface exposed loop; major outer membrane protein P5; MOMP P5; non-typeable H. influenzae; ntHi; LB1(f) peptide; B cell epitope; otitis media; sinusitis; conjunctivitis;
                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lower respiratory tract infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOMP P5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB47447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB47447 standard; Protein; 353 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and in screening for antibacterial drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is that of BASB113 protein from Moraxella catarrhalis strain Mc2931 (ATCC 43617), a causative agent of citits media in children and pneumonia in adults. The invention provides BASB113 polypeptides, and polynucleotides encoding them, as well as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 67; 86pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       159 QAAYNQELSERRADSVRYYLINQGVDPYRIQTVGYGMRQPIASNATEAGRAQNRRVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 SREYNMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSONRRAEL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99 VTHDTDTGNINLTMPGNITFAHDDDTLNSAFLGRLNQLANTMNQYHETTIVIVGHTDSTG 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53 VDNDETVKALASKLPSLVYFDFDSDETKPQAAAILDEQAQFLTTNQTARVLVAGHTDERG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42 IGAVAGALGGTAISKATGGEKTGRDAIL-GAAVGAAAGAYMERQAKQIEQQMQGTGVT-- 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 IAAAAAALSVLTEMTGCANKSTSQVMVAPNAPTGYTGVIY------TGVAPL 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the state of th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                       181..204
                                                                                                                                                                                                                                                                                     136..150
                                                                                                                                                                                                                                                                                                                                                                               89..100
                                                                                                                                                                                                        /label= Loop 3
/note= "Extracellular domain"
                                                                                                                                                                                                                                                                                                  /note= "Extracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                   /label= Loop 1
/note= "Extracellular domain"
                                                                                                                    /note= "Extracellular domain"
                                                                                                                                                      /label= Loop 4
                                                                                                                                                                                                                                                                                                                                          /label= Loop 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22; Length 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17; Gaps
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RESULT 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   non-typeable H. influenzae. One or more surface exposed loops of this protein may be replaced with a modified peptide of the invention. Each of these peptides contain an LBI(f) peptide which is a 19 amino acid peptide derived from the sequence of MOMP P5 from strain ntHill28, representing amino acids Argl17 to G1y135. This peptide represents the third exposed loop of P5 and is a potential B cell epitope. The loops of the invention are modified in terms of being in a non-native
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant bacterial outer membrane protein where one or more surface-exposed loops are modified is useful as a vaccine to prevent or treat Haemophilus influenzae infection or associated disease, e.g.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                environment in the recombinant outer membrane protein. The modi MOMP P5 may be used to induce an immune response in a mammal to prevent or treat Haemophilus influenzae infection or associated disease, e.g., otitis media, sinusitis, conjunctivitis, or lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents the major outer membrane protein P5 of non-typeable H. influenzae. One or more surface exposed loops of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 1; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   otitis media and conjunctivitis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-522599/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-FEB-2000; 2000GB-0003502.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   respiratory tract infection.
                                   Protein
                                                                                                                                        Pseudomonas aeruginosa serotype 6 (ATCC 33354).
                                                                                                                                                                          antibody; glutathione-S-transferase; GST
                                                                                                                                                                                             Vaccine; fusion protein; OprF; OprI; outer membrane protein;
                                                                                                                                                                                                                               P. aeruginosa orpF-oprI fusion protein.
                                                                                                                                                                                                                                                                      01-OCT-1996
                                                                                                                                                                                                                                                                                                                                         AAR99626 standard; Protein;
                                                                                        Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 252 QATIDSIYGEMSQVKSAKVAVAGYTDRIGSDAFNVKLSQERADSVANYFVAKGVAADAIS 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     193 PNTALNYNPWIGSINAGISYRFGQGAAPVVAAPEVVSKTFS-LNSDVTFAFGKANLKPQA 251
                                                                                                                                                                                                                                                                                                                                                                                                                              312 ATGYGKANPVTGATCDQVKGRKALIACFAPDRRVEIA 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                               144 IISFGEERPIAFGTNEE-----AWSQNRRAELS 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35 PNAPTGY-----TGVIY---TGVAPLVDNDETVKALASKLPSLVYFDFDSDEIKPQA 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 AAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGKGINQASVE 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   353 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Denoel P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001WO-EP01556.
                                                                                                                                                                                                                                                                    (first entry)
                                   /note= "oprF amino acids 192-342"
152..214
/note= "oprI amino acids 21-83"
                  /label= oprI
                                                                     /label= oprf
                                                                                                       location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20.5%; Score 176.5; 30.6%; Pred. No. 1.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Poolman J, Thonnard J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 1.2e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The modified
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RESULT 27
AAR85450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 13-14; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein was expressed in Escherichia coli and Saccharomyces cerevisiae transformants. The oprF-oprI hybrid protein, and antibodies raised against it, conferred protection against P. aeruginosa infection in laboratory animals. The hybrid protein was significantly more immunogenic than an oprI-oprF fusion (AAR99627).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A cDNA sequence (AAT32600) codes for a fusion (AAR99626) between amino acids 192-342 of the outer membrane protein F (oprF) and amino acids 21-83 of outer membrane protein I (oprI) of Pseudomonas aeruginosa ATCC 33354. A glutathione-S-transferase fusion with the hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fusion proteins for Pseudomonas aeruginosa vaccines - contgragments of outer membrane proteins I and {\bf F}.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAT32600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-279559/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Von Specht BU;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Broeker M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BEHW ) BEHRINGWERKE AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP717106-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fragments of outer membrane proteins I and
                                                                                                                                                                                                                                                                                              AAR85450;
                                                                                                                                                                                                                                                                                                                         AAR85450 standard; Protein; 338
                                                                                                                                                                                                                                         Nontypable H. influenzae P5 protein
                            EP680765-A1
                                                                                 Misc-difference 311
                                                                                                                           Misc-difference 195
                                                                                                                                                                   Haemophilus influenzae
                                                                                                                                                                                              chronic pulmonary obstructive disease
                                                                                                                                                                                                           P5 outer membrane protein; vaccine; otitis media; sinusitis;
                                                                                                                                                                                                                                                                     15-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                       130 NYLLGK-GINOASYEIISFGEERPIAFGTNEEAWSQNRRAELSY 172
                                                                                                                                                                                                                                                                                                                                                                                             111 DVLVNEYGVEGGRVNAVGYGESRPVADNATAEGRAINRRVESSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 VKFDFDKSKVKENSYADIKNLADFMKQYPSTSTTVEGHTDSVGTDAVNQKLSERRANAVR 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 VYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVR 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Domdey H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94EP-0120023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95EP-0118098
                                                                                               /note= "amino acid at identified in
                                                      /note= "amino acid at position 311 is not
   identified in the specification"
                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20.4%; Score 175.5; DB 1 37.5%; Pred. No. 7.8e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hungerer K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Knapp B,
                                                                                                  position 195 is no
the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 17; Length 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ulrich B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Novel isolated polynucleotide useful for producing fibronectin binding proteins which are useful in production of vaccine, in diagnostic assays and for prophylactic and therapeutic purposes
                                                                 WPI; 2001-079546/09.
                                                                                           Garvis SG,
                                                                                                              (UNIW ) UNIV WASHINGTON STATE RES FOUND.
                                                                                                                                             16-MAY-1997;
                                                                                                                                                                                                   05-DEC-2000
                                                                                                                                                                                                                           US6156546-A.
                                                                                                                                                                         15-MAY-1998;
                                                                                                                                                                                                                                                   Pseudomonas fluorescens
                                                                                                                                                                                                                                                                                               Protein associated with C.coli and C.jejuni CadF.
                                                                                                                                                                                                                                                                        Fibronectin binding protein;
                                                                                                                                                                                                                                                                                                                                  22-MAR-2001
                                                                                                                                                                                                                                                                                                                                                              AAB59180;
                                                                                                                                                                                                                                                                                                                                                                              AAB59180 standard; protein; 326 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nontypable H. influenzae HI outer membrane protein P5 was isolated by extraction of the outer membrane with detergents and cation-exchange chromatography. P5 (or its peptide fragments) are used in vaccines for prevention of H. influenzae infections implicated in otitis media, sinusitis and chronic pulmonary obstructive disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 7-8; 16pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Purified H.influenzae P5 outer membrane protein - used for preventing reducing susceptibility to or treating H.influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1995-375029/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AMCY ) AMERICAN CYANAMID CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                            295 ISATGYGKANPVTGATXDQVWGRWALIATLAPDRRVEIA 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 VEIISFGEERPIAFGTNEEAWSQ-----NRRAELS 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              235 QAQATLDSIYGEMSQVKSAKVAVAGYTDRIGSDAFNVKLSQERADSVANYFVAKGVAADA 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 INPNTAIHYNPXIGSINAGISYRFGQGAAP-----VKTFSLNLD--VTFAFGKANLKP 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 QAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGKGINQAS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33 VAPNAPTGY-----TGVIY---TGVAPLVDNDETVKALASKLPSLVYFDFDSDEIKP 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46;
                                                                                         Konkel ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     338 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                            97US-0046763
                                                                                                                                                                     98US-0080025.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20.3%; Score 174.5; DB 16; Length 338; 28.9%; Pred. No. 1.9e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27; Mismatches
                                                                                                                                                                                                                                                                  CadF; vaccine; diagnostic assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                           A cDNA sequence (AAT32599) codes for the C-terminal region, amino acids 190-350 (AAR99625), of the Pseudomonas acruginosa ATCC 33354 outer membrane protein F (oprF). A hybrid protein between glutathione-5-transferase and the OprF moiety was expressed in Escherichia coli. OprF-OprI (AAR99626) and OprI-OprF (AAR99627) fusion proteins were also prepd. and tested for their efficacy as vaccines
 Sequence
                       proteins were also prepd. and te against P. aeruginosa infection.
                                                                                                                                         Disclosure; Page 11-12; 23pp; English.
                                                                                                                                                                                  Fusion proteins for Pseudomonas aeruginosa vaccines - contg
                                                                                                                                                                                                                                     WPI; 1996-279559/29
                                                                                                                                                                                                                                                                                    Broeker M,
                                                                                                                                                                    fragments of outer membrane proteins I and {	t F.}
                                                                                                                                                                                                                          N-PSDB; AAT32599
                                                                                                                                                                                                                                                                       Von Specht BU;
                                                                                                                                                                                                                                                                                                               (BEHW ) BEHRINGWERKE AG
                                                                                                                                                                                                                                                                                                                                             16-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                           17-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                      19-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas aeruginosa serotype 6 (ATCC 33354).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vaccine; fusion protein; OprF; OprI; outer membrane protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                     EP717106-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibody; glutathione-s-transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P. aeruginosa oprf C-terminal region (aa190-350).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR99625;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a Campylobacter jejuni or Campylobacter coli fibronectin binding protein (CadF). A recombinant expression vector with cadF is useful in an assay for determining the presence of C.jejuni or C.coli in a test sample or for determining whether a test isolate of Campylobacter is a strain of C.coli. cadF is useful in the construction of DNA probes for identifying and quantifying the level of expression of CadF in a cell. The gene can also be used in a vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR99625 standard; Protein; 161 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Column 39-42; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 NYLLGKGINQASVETISFGEERPIAFGTNEEAWSQNRRAELS 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 279 QVLVKDGVAPSRITAVGYGESRPVADNATEAGRAVNRRVEAS 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       219 VKFDFDKSVVKPNSYGDVKNLADFMAQYPATNVEVAGHTDSIGPDAYNQKLSQRRADRVK 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 VYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVR 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
161 AA;
                                                                                                                                                                                                                                                                               Domdey H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       326 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                             94EP-0120023
                                                                                                                                                                                                                                                                                                                                                                        95EP-0118098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20.2%; Score 174; DB 22; 2013 136.3%; Pred. No. 2e-10; Indels
                                                                                                                                                                                                                                                                               Hungerer K,
                                                                                                                                                                                                                                                                             Knapp B,
                                                                                                                                                                                                                                                                             Ulrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 326;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                      Query Match
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR99627 standard; Protein; 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vaccine; fusion protein; OprF; OprI; outer membrane protein;
antibody; glutathione-S-transferase; GST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR99627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas aeruginosa serotype 6 (ATCC 33354).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P. aeruginosa orpI-oprF fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP717106-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein
                                                                                                    A cDNA sequence (AAT34419) codes for a fusion (AAR99627) between amino acids 21-83 of the outer membrane protein I (oprI) and C-terminal amino acids 190-350 of outer membrane protein F (oprF) of Pseudomonas aeruginosa ATCC 3354, the 2 moleties being joined by a linker dipeptide. A glutathione-S-transferase fusion with the hybrid protein as expressed in Escherichia coli and Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                 17-NOV-1995;
                                                                                                                                                                                                       Disclosure; Page 13-14; 23pp; English.
                                                                                                                                                                                                                                  Fusion proteins for Pseudomonas aeruginosa vaccines - contg. fragments of outer membrane proteins I and F.
                                                                                                                                                                                                                                                                                                                                                                                       16-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JUN-1996.
                                                   Sequence
                                                                                                                                                                                                                                                                                                                                  Broeker M,
                                                                                                                                                                                                                                                                                                                                                            (BEHW ) BEHRINGWERKE AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                            transformants. The oprI-oprF hybrid protein was significantly less immunogenic than an oprF-oprI fusion (AAR99627).
        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 DVLVNEYGVEGGRVNAVGYGESRPVADNATAEGRAINRRVE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 NYLLGK-GINQASVEIISFGEERPIAFGTNEEAWSQNRRAE 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53 VKFDFDKSKVKENSYADIKNLADFMKQYPSTSTTVEGHTDSVGTDAYNQKLSERRANAVR 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 VYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVR 129
                                                                                                                                                                                                                                                                                          1996-279559/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38;
                                                                                                                                                                                                                                                                            AAT34419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                     226 AA;
                                                                                                                                                                                                                                                                                                                                Domdey H,
Conservative
                                                                                                                                                                                                                                                                                                                                                                                          94EP-0120023
                                                                                                                                                                                                                                                                                                                                                                                                                    95EP-0118098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "oprI amino acids 21-83"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "oprF amino acids 190-350"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Linker_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= OprI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19.9%;
           19.9%; Score 171.5; DB 1
37.6%; Pred. No. 2.3e-10;
                                                                                                                                                                                                                                                                                                                                   Hungerer K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OprF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 171.5; DB 1
Pred. No. 1.4e-10;
15; Mismatches
                                                                                                                                                                                                                                                                                                                                      Knapp B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 17; Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47; Indels
                            DB 17; Length 226;
                                                                                                                                                                                                                                                                                                                                        Ulrich B;
    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
    1;
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     Gaps
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AAP82053
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В
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                                                                                                       QΥ
                                                                                                                                               Matches
                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Outer membrane protein F of Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAP82053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAP82053 standard; protein; 350 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Outer membrane protein F; OMPF; vaccination; antibodies.
                                                                                                                                                                                                                                                lambda EMBL 3. One positive clone includes a 15 kb insert conty. The protein gene, which can be isolated as a 2.5 kb PStI fragment. This fragment cannot be cloned int a high copy no. vector because of the toxicity of the gene prod. . so is subcloned as two fragments with an overlapping region of about 500bp. Ab's are raised by usual immunisation or cell-fusion procedures. The Ab's are useful in diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-OCT-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                        The protein is isolated from the OMP of P. aeruginosa serotype 6 ATTCC 33354) and purified by HPLC. The amino-terminal and trypsin fragments are sequenced and a series of oligonucleotide probes constructed corresponding to the established sequences. These probes used to screen a gene bank of 15-20 kb fragments of genomic DNA in used to screen a gene bank of 15-20 kb fragments of genomic DNA in the contractions of the contractions includes a 15 kb insert conty. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New outer membrane protein {\tt F} of Pseudomonas aeruginosa DNA sequences encoding it and derived antibodies, usefu vaccination and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-JUN-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-JUN-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DE3718591-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; ; p; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAN82023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1988-361619/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Domdey H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-DEC-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BEHW ) BEHRINGWERKE AG
                                                                                                                                                                                                                    Sequence
                                                                                                                                                            Match 19.9%; Score 171.5; DB 9; Local Similarity 37.6%; Pred. No. 4.2e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 VKFDFDKSKVKENSYADIKNLADFMKQYPSTSTTVEGHTDSVGTDAYNQKLSERRANAVR 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 DVLVNEYGVEGGRVNAVGYGESRPVADNATAEGRAINRRVE 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 NYLLGK-GINQASVEIISFGEERPIAFGTNEEAWSQNRRAE 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 VYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVR 129
                                  130 NYLLGK-GINQASVEIISFGEERPIAFGTNEEAWSQNRRAE 169
                                                                      242 VKFDFDKSKVKENSYADIKNLADFMKQYPSTSTTVEGHTDSVGTDAYNQKLSERRANAVR
302 DVLVNEYGVEGGRVNAVGYGESRPVADNATAEGRAINRRVE 342
                                                                                                         70 VYEDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVR 129
                                                                                                                                                 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lottspeich F,
                                                                                                                                                                                                                       350 AA;
                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87DE-3718591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     von Specht B-U,
                                                                                                                                                     15;
                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Duchene M;
                                                                                                                                                       47;
                                                                                                                                                          Indels
                                                                                                                                                                                         Length 350;
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RESULT 32

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RESULT 33
AAY96098
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                                                                                                                                                                                                                                                                                                                                                                                         Query Match
EP1035133-A2
                                                        Outer membrane protein; OmpAl; vaccine; pig; immunogen;
                                                                                     Actinobacillus pleuropneumoniae Ompa2.
                                                                                                                   19-DEC-2000 (first entry)
                   Actinobacillus pleuropneumoniae
                                          dual immune response; immunogen; pleuropneumonia.
                                                                                                                                                       AAY96098;
                                                                                                                                                                        AAY96098 standard; Protein; 369 AA
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                 determining whether a test isolate of Campylobacter is a strain of C.coli. cadf is useful in the construction of DNA probes for identifying and quantifying the level of expression of Cadf in a cell. The gene can also be used in a vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a Campylobacter jejuni or Campylobacter coli fibronectin binding protein (CadF). A recombinant expression vector with cadF is useful in an assay for determining the presence of C. Jejuni or C. coli in a test sample or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated polynucleotide useful for producing fibronectin binding proteins which are useful in production of vaccine, in diagnostic assays and for prophylactic and therapeutic purposes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Column 37-40; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Garvis SG, Konkel ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-079546/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UNIW ) UNIV WASHINGTON STATE RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fibronectin binding protein; CadF; vaccine; diagnostic assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-DEC-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US6156546-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein associated with C.coli and C.jejuni Cadf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB59179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB59179 standard; protein; 350 AA
                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                        302 DVLVNEYGVEGGRVNAVGYGESRPVADNATAEGRAINRRVE 342
                                                                                                                                                                                                                                                                   130 NYLLGK-GINQASVEIISFGEERPIAFGTNEEAWSQNRRAE 169
                                                                                                                                                                                                                                                                                           242 VKFDFDKSKVKENSYADIKNLADFMKQYPSTSTTVEGHTDSVGTDAYNQKLSERRANAVR 301
                                                                                                                                                                                                                                                                                                                                                               38;
                                                                                                                                                                                                                                                                                                                    70 VYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVR 129
                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   350 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-0046763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0080025.
                                                                                                                                                                                                                                                                                                                                                                19.9%; Score 171.5; DB 22; Length 350; 37.6%; Pred. No. 4.2e-10;
                                                                                                                                                                                                                                                                                                                                                       15; Mismatches
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SOS XXX DE XXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
  Actinobacillus pleuropneumoniae strain Pz420
                                  OmpA2; outer membrane protein; APP; pneumonic pathogen; swine; Sus scrofa; serotype; antigen; vaccine; cross-reactive immunity; cross-protection; diagnosis.
                                                                                                               Actinobacillus pleuropneumoniae outer membrane protein, OmpA2.
                                                                                                                                                             11-SEP-2000 (first entry)
                                                                                                                                                                                                                                      AAY97900 standard; Protein; 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vertebrate; and a second protein, which is an immunogen from a pathogen capable of infecting the vertebrate, and which causes the vertebrate's immune system to recognise the first protein, producing a response that inhibits the activity of the first protein, and also protecting the vertebrate from infection by the pathogen when the vertebrate is vaccinated with the fusion protein. In the present case, a fusion protein of cholecystokinin and Ompha is useful for encouraging appetite in swine while simultaneously providing a protective immune response against porcine
                                                                                                                                                                                                          AAY97900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Actinobacillus pleuropneumoniae. OmpA2 can be utilised in fusion proteins of the invention that are used as vaccines eliciting a dual immune response. Such fusion proteins comprise: a first protein that is endogenous to a vertebrate, the activity of which is to be inhibited within the vertebrate, and which is incapable by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 58-60; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             itself of eliciting an effective immunoinhibitory response in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is that of outer membrane protein OmpA2 of Actinobacillus pleuropneumoniae. OmpA2 can be utilised in fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel fusion protein for producing a dual immune response comprises a peptide analogous to an endogenous peptide which is to be inhibited, connected to a peptide analogous to an immunogen from a pathogen which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infects a vertebrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-566924/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PFIZ ) PFIZER PROD INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-FEB-2000; 2000EP-0301103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                   327 YGEANPVTGATCDKV--KGRKA 346
                                                                                                                                                                                                                                                                                                                                                                      147 FGEERPIAFGTNEEAWSONRRA 168
                                                                                                                                                                                                                                                                                                                                                                                                  267 AANTEIANLGLATPAIQVNGYTDRIGKEASNLKLSQRRAETVANYLVSKGQNPANVTAVG 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           210 APDIHSVTAGLSYRFGQGAVAPVVEPEVVTKNFA--FSSDVLFDFGKSSLKPAAATALD-
                                                                                                                                                                                                                                                                                                                                                                                                                                    90 QAQFLTTN----OTARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGKGINQASVEIIS 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34 APNAPTGYTGVIYT----GVAPLVDNDETVKALASKLPSLVYFDFDSDEIKPQAAAILDE 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 369 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Martinod SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0120454.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19.7%; Score 170; DB 21; Length 369; 34.5%; Pred. No. 6.6e-10; rative 20; Mismatches 61; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Durtschi BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yule TD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 12;
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This sequence represents a low molecular weight outer membrane CC protein, OmpAA, from Actinobacillus pleuropneumoniae (APP) strain CC pz420 (ATCC 98930). The invention relates to the novel APP outer CC pz420 (ATCC 98930). The invention relates to the novel APP outer CC membrane proteins omp20, OmpM, Omp27, OmpA1 and OmpA2 (AAV979986-Y97900) CC membrane proteins omp20, OmpM, Omp27, OmpA1 and OmpA2 (AAV979986-Y97900) CC and to nucleic acids encoding them (AAA38554-A38558). APP is a Gram CC engative coccobacillus which is one of the most important swine CC which vary in geographic distribution. Prior art attempts at vaccinating CC against APP have produced mainly serotype-specific immune responses. In CC contrast, natural immunity to any one serotype seems to confer CC significant protection from disease caused by other serotypes, suggesting CC that natural exposure induces cross-reactive immunity to shared antigens. CC The novel outer membrane proteins of the invention are present in all 12 cc serotypes, and may provide a target for cross-protective immunisation. CC used as a vaccine against APP in swine. They can also be used as CC used as a vaccine against APP in swine. They can also be used as
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                                                                                                                                                                                                   Db
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 EXE
                                                                                                                          AAB44589
                                                                                                                                              RESULT 35
                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Fig 5; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Low molecular weight Actinobacillus pleuropneumoniae proteins and DNA encoding them, for use as vaccines against the bacteria in swine -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Warren-Stewart LM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PFIZ ) PFIZER PROD INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
Virulence gene protein #69
                                     08-FEB-2001 (first entry)
                                                                        AAB44589
                                                                                                           AAB44589 standard; Protein; 369 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000-320438/28.
                                                                                                                                                                                                                                                                         267 AANTEIANLGLATPAIQVNGYTDRIGKEASNLKLSQRRAETVANYLVSKGQNPANVTAVG 326
                                                                                                                                                                                                                                                                                                                                                 210 APDIHSYTAGLSYRFGOGAVAPVVEPEVVTKNFA--FSSDVLFDFGKSSLKPAAATALD- 266
                                                                                                                                                                                                     327 YGEANPYTGATCDKV--KGRKA 346
                                                                                                                                                                                                                                                                                                                                                                                    34 APNAPTGYTGVIYT----GVAPLVDNDETVKALASKLPSLVYFDFDSDEIKPQAAAILDE 89
                                                                                                                                                                                                                                                                                                            90 QAQFLTTN---QTARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGKGINQASVEIIS 146
                                                                                                                                                                                                                                        FGEERPIAFGTNEEAWSQNRRA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    369 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0105285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Signal peptide"
20..369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baarsch MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Suiter BT;
                                                                                                                                                                                                                                                                                                                                                                                                                                             19.7%; Score 170; DB 21; 34.5%; Pred. No. 6.6e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Mature OmpA2"
                                                                                                                                                                                                                                                                                                                                                                                                                               20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Campos M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Keich RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                   61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 369;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rosey EL;
                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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THE STATE OF THE S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR66294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Virulence gene; antibacterial; vaccine; bacterial infection; septicemia; bronchopneumonia; rhinitis; wound infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Actinobacillus pleuropneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The family Pasteurellaceae encompasses several pathogens that infect a wide variety of animals. The present invention relates to virulence genes from Pasteurellaceae. The present sequence is a protein encoded by one such virulence gene. The virulence genes of the present invention may be mutated in order to produce an inactive gene. The inactive virulence gene may in turn be used to produce a vaccine, which is useful for treating bacterial infections such as septicemias, bronchopneumonias, rhinitis and bacterial infections such as septicemias, bronchopneumonias, rhinitis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Attenuated Pasteurellaceae bacteria comprising mutations in virulence genes, useful as a live attenuated vaccine against bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-APR-2000; 2000WO-US09218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 39; Pages 308-309; 322pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAC79664.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-647422/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lowery DE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PHAA ) PHARMACIA & UPJOHN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-OCT-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  wound infections.
                   Region
                                                                                                                      Haemophilus influenza strain 1128
                                                                                                                                                                          Fimbrin protein; vaccine; otitis media.
                                                                                                                                                                                                                                     Non-typable Haemophilus influenza (NTHi) fimbrin protein
                                                                                                                                                                                                                                                                                                          09-AUG-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                         AAR66294;
                                                                                                                                                                                                                                                                                                                                                                                                                                AAR66294 standard; Protein;
                                                    Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210 APDIHSVTAGLSYRFGQGAVAPVVEPEVVTKNFA--FSSDYLFDFGKSSLKPAAATALD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147 FGEERPIAFGT 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          267 AANTEIANLGLATPAIQVNGYTDRIGKEASNLKLSQRRAETVANYLVSKGQNPANVTAVG 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       327 YGEANPVTGAT 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 APNAPTGYTGVIYT----GVAPLVDNDETVKALASKLPSLVYFDFDSDEIKPQAAAILDE 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90 QAQFLTIN----QTARVLYAGHTDERGSREYNMSLGERRAVAVRNYLLGKGINQASVEIIS 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          369 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fuller TE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9905-0153453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9905-0128689.
                                                              Location/Qualifiers
   /label= amino terminus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.6%; Score 169; DB 21; 35.9%; Pred. No. 8.5e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kennedy MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                              359 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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RESULT 37
                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                               Moraxella; vaccine; respiratory tract infection; antiinflammatory; auditory; antibacterial; otitis media; sinusitis; pneumonia.
                         07-MAR-2002
                                                                                                                     M catarrhalis MCA100854 protein SEQ ID NO:
                                              WO200218595-A2.
                                                                                                                                              19-JUL-2002 (first entry)
                                                                    Moraxella catarrhalis
                                                                                                                                                                         AAO17571;
                                                                                                                                                                                        AAO17571 standard; Protein; 228 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 influenzae 1128 strain is a particularly suitable immunogen to protect against the different non-typable HJ. influenzae that cause office the fimbrin protein is produced by culturing a transformed microbial host, pref. E.coli, Sporodoptera frugiperda or a mucosal pathogen. Fimbrin protein (FP) produced by this process is claimed. The FP protein migrates in polyacrylamide genes to a posn. equiv. to a mool. wt. of 25.5 kD or 37.5 kD.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The fimbrin proteins from 15 randomly selected type b and non-typable clinical isolates of Haemophilus influenzae share common
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  epitopes. Thus frimbrin isolated from non-typable Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 5; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vaccine comprising non-typable Haemophilus influenza fimbrin protein - useful in studying, preventing or reducing the severity of otitis media, also fimbrin protein and DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (OHIO-) OHIO STATE RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-NOV-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09426304-A
                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                               318 ATGYGEANPVTGATCDQVKGRKALIACLAPDRRVEIA 354
                                                                                                                                                                                                                                                                     144 IISFGEERPIAFGTNEE-----AWSQNRRAELS 171
                                                                                                                                                                                                                                                                                       258 QATILDSVYGEISQVKSRKVAVAGYTNRIGSDAFNVKLSQERADSVANVFVAKGVAADAIS 317
                                                                                                                                                                                                                                                                                                                                  199 PNTAINYNPWIGCINAGISYRFGQGEAPVVAAPEMVSKTES-LNSDVTFAFGKANLKPQA 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1995-006359/01.
                                                                                                                                                                                                                                                                                                           84 AAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGKGINQASVE 143
                                                                                                                                                                                                                                                                                                                                                        35 PNAPTGY------TGVIY---TGVAPLVDNDETVKALASKLPSLVYFDFDSDEIKPQA 83
                                                                                                                                                                                                                                                                                                                                                                                             47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ78916
                                                                                                                                                                                                                                                                                                                                                                                                                                       359 AA;
                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kolattukudy PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93US-0065442.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94WO-US05477.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234..249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= internal CNBr fragment
                                                                                                                                                                                                                                                                                                                                                                                               19.2%; Score 165.5; DB 29.9%; Pred. No. 2e-09;
                                                                                                                                                                                                                                                                                                                                                                                     26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sirakova T;
                                                                                                                                                                                                                                                                                                                                                                                                         DB 16; Length 359;
                                                                                                                                                                                                                                                                                                                                                                                   63; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                AAM50718
                                          RESULT 38
                                                                              Вb
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                                                                                                                                              QУ
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                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                      Query Match
AAM50718;
                                                                                                                                                                                                                                                              Sequence
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AAM50718 standard; Protein; 344 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides the protein and coding sequences of proteins from Moraxella catarrhalis. These can be used to produce vaccines which protect against M. catarrhalis infection, which can otitis media, respiratory infection, sinusitus, and pneumonia. The present sequence is a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-SEP-2000;
05-SEP-2000;
05-SEP-2000;
05-SEP-2000;
05-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 28; Fig 21; 277pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Moraxella polypeptide and polynucleotides useful as vaccine for immunizing a host e.g. humans against disease e.g. otitis media, pneumonia, caused by infection of the bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-AUG-2000;
21-SEP-2000;
01-SEP-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAL46503.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-401721/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Loosmore S, Wang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AVET ) AVENTIS PASTEUR LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                       186 VASNATEOGREONRRIE 202
                                                                                                                                               153 IAFGTNEEAWSQNRRAE 169
                                                                                                                                                                           126 KLKAVPETTLRIIGHTDTQGTHEYNQDLSESRAAAVKEYLVSKGVAAERLNTQGASFDYP
                                                                                                                                                                                                                 93 FLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGKGINQASVEIISFGEERP 152
                                                                                                                                                                                                                                                           68 VADSIETARVAIVALG--DTVEENEMDILINALNTQIINFALDSTEIPQENKEILDLAAE
                                                                                                                                                                                                                                                                                                33 VAPNAPTGYTGVIYTGVAPLVDNDETVKALASKLPSLVYFDFDSDEIKPQAAAILDEQAQ 92
                                                                                                                                                                                                                                                                                                                                                                42;
                                                                                                                                                                                                                                                                                                                                                                                                                                               228 AA;
                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US - 228296

2000US - 228438P

2000US - 228441P

2000US - 228441P

2000US - 228442P

2000US - 228442P

2000US - 228412P

2000US - 228512P

2000US - 228712P

2000US - 228773P

2000US - 228773P

2000US - 229478P

2000US - 229803P

2000US - 229803P

2000US - 229803P

2000US - 229805P

2000US - 229805P
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2000US-230214P.
                                                                                                                                                                                                                                                                                                                                              19.2%; Score 165; DB 23; 30.7%; Pred. No. 1.2e-09; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bradley B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ochs M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yang Y;
                                                                                                                                                                                                                                                                                                                                                                                        Length 228;
                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                              2;
                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cause
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The present sequence is that of the HagA haemagglutinin of C Haemophilus paragallinarum strain 2403 (serovar A), the causative agent of infectious coryza in chickens. The invention provides C recombinant haemagglutinin polypeptides (see AAM50716-27) and C encoding nucleic acids (see ABA91417-27) from 11 strains (serovars C a, B and C) of H. paragallinarum, the causative agent of infectious C coryza of chickens. The polypeptides are useful in vaccines for C coryza of chickens the polypeptides are useful in vaccines for C when expressed in attenuated bacteria, especially Salmonella or Mycoplasma (claimed). The recombinant polypeptide is preferably the mature protein, or a biologically active fragment, variant or C derivative, that is capable of eliciting an immune response, or provide of the mature protein agrainst one of the combinant polypeptide is preferably C derivative, that is capable of eliciting an immune response,
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                                                                                                                                                                       8
                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haemagglutinin; HagA; antigen; vaccine; immunisation; coryza;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haemophilus paragallinarum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New haemagglutinin polypeptide isolated from Haemophilus paragallinarum useful as a vaccine for immunising chickens against coryza caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUL-2000; 2000AU-0008652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-JUL-2001; 2001WO-AU00822.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200204485-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Fig 4; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ABA91419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Terry TD, Tseng H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYQU ) UNIV QUEENSLAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-154917/20.
                                                                                                                                                                                                                                                                                                                 diagnosis of infectious coryza in chickens
                                                                                                                                                                                                                                                                                                                                 providing protection against one or more strains of H. paragallinarum in chickens. Also claimed are methods of using the haemagglutinin polypeptides and nucleic acids for detection and
                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                 ocal
                               136 GINOASVEIISFGEERPIAFGTNE-----EAWSQNRRAELS 171
                                                                  239 RPEAQNVLDGIYGEIAQL----KSVQVDVAGYTDRIGSEAANLKLSQRRADTVANYLVSK 294
                                                                                                                                       181 GRVEKDGSRVDYTPSIGSVTAGLSYRFGQSAPVVEPKVVAKTFA--LNSDYTFAFGKANL 238
                                                                                                                                                                             22 GCANKSTSQVMVAPNAPTGYTGVIYT--GVAPLVUNDETVKALASKLPSLVYFDFDSDEI 79
                                                                                                    80 KPOAAAILD----EQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGK 135
                                                                                                                                                                                                                  51;
                                                                                                                                                                                                                                 h 18.8%; Score 161.5; DB 23; Length 344; Similarity 30.9%; Pred. No. 5.1e-09;
GVAQEVISSTGYGEANPVTGAKCDTVKGRKALIACLADDRRVEIS 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 paragallinarum strain 2403 haemagglutinin.
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239 RPEAQNVLDGIYGEIAQL----KSVQVDVAGYTDRIGSEAANLKLSQRRADTVANYLVSK 294

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RESULT 39
AAM50721
                                                                                                                                                         An The present sequence is that of the HagA haemagglutinin of CC Haemophilus paragallinarum strain 0222 (serovar B), the causative CC agent of infectious coryza in chickens. The invention provides CC recombinant haemagglutinin polypeptides (see AAM50716-27) and CC encoding nucleic acids (see ABA91417-27) from 11 strains (serovars CC A, B and C) of H. paragallinarum, the causative agent of infectious CC immunisation against infectious coryza, as are the nucleic acids cimmunisation against infectious coryza, as are the nucleic acids when expressed in attenuated bacteria, especially Salmonella or CC when expressed in attenuated bacteria, especially Salmonella or CC the mature protein, or a biologically active fragment, variant or CC derivative, that is capable of eliciting an immune response, CC paragallinarum in chickens. Also claimed are methods of using the CC paragallinarum in chickens. Also claimed are methods of infectious CC diagnosis of infectious coryza in chickens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Terry TD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-JUL-2000; 2000AU-0008652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New haemagglutinin polypeptide isolated from Haemophilus paragallinarum useful as a vaccine for immunising chickens against coryza caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-154917/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Fig 4; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the species
                                                                                                                                                         Sequence
                                                                                                               Local
                                  181 GRVEKDGSRVDYTPSIGSVTAGLSYRFGQSAPVVEPKVVAKTFA--LNSDVTFAFGKANL 238
80 KPQAAAILD----EQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGK 135
                                                               22 GCANKSTSQVMVAPNAPTGYTGYIYT--GVAPLYDNDETVKALASKLPSLYYFDFDSDEI 79
                                                                                                                 Similarity
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                                                                                                                                                             344 AA;
                                                                                                 Conservative
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                                                                                                               18.8%; Score 161.5; DB 30.9%; Pred. No. 5.1e-09
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The present sequence is that of the HagA haemagglutinin of C Haemophilus paragallinarum strain 2671 (serovar B), the causative agent of infectious coryza in chickens. The invention provides crecombinant haemagglutinin polypeptides (see AMS0716-27) and crecombinant haemagglutinin polypeptides (see AMS0716-27) and C and C) of H. paragallinarum, the causative agent of infectious coryza of chickens. The polypeptides are useful in vaccines for c immunisation against infectious coryza, as are the nucleic acids c when expressed in attenuated bacteria, especially Salmonella or CC when expressed in attenuated bacteria, especially Salmonella or CC the mature protein, or a biologically active fragment, variant or CC cervative, that is capable of eliciting an immune response, c providing protection against one or more strains of H. CC paragallinarum in chickens. Also claimed are methods of using the CC diagnosis of infectious coryza in chickens.
                                                                                         Query Match
Best Local Similarity
                                                                                 Matches
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AAM50722
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                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Fig 4; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New haemagglutinin polypeptide isolated from Haemophilus paragallinarum useful as a vaccine for immunising chickens against coryza caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Terry TD, Tseng H, Hobb RI, Jennings MP, Downes J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ABA91423.
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181 GRVEKDGSRYDYTPSIGSVTAGLSYRFGQSAPVVEPKVVAKTFA--LNSDVTFAFGKANL 238
                              22 GCANKSTSQVMVAPNAPTGYTGYIYT--GVAPLVDNDETVKALASKLPSLVYFDFDSDEI 79
                                                                        51; Conservative
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                                                                                                                                          344 AA;
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                                                              18.8%; Score 161.5; DB 23; Length 344; 30.9%; Pred. No. 5.1e-09; tive 25; Mismatches 68; Indels 21;
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                                                                                                                                  239 RPEAQNVLDGIYGEIAQL----KSVQVDVAGYTDRIGSEAANLKLSQRRADTVANYLVSK 294
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     GenCore version (c) 1993 - 2003
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COBM_MYCTU
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PYRK_METKA
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HXD8_HUMAN
PSBO_CHLRE
RBSK_BACHD
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ALIGNMENTS

FSH\_DROME
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01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
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Ludwig B., Schmid A., Marre R., Hacker J.;
"Cloning, genetic analysis, and nucleotide sequence of a determinant coding for a 19-kilodalton peptidoglycan-associated protein (Ppl) of
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01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
01-OCT-1994 (Rel. 30, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00691; OmpA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; S16631; S16631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X60543; CAA43033.1; -. PIR; A60337; A60337.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Legionella pneumophila.";
Infect. Immun. 59:2515-2521(1991).
-i- FUNCTION: VERY STRONGLY ASSOCIATED WITH THE PEPTIDOGLYCAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lipoprotein antigen.";
mol. Microbiol. 5:2021-2029(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Engleberg N.C., Howe D.C., Rogers J.E., Arroyo J., "Characterization of a Legionella pneumophila gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SIMILARITY: TO OTHER PAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=AA100 / Serogroup 1;
MEDLINE=92114778; PubMed=1766377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-AA100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Legionella pneumophila.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAL OR PPLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptidoglycan-associated lipoprotein precursor (19 kDa surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAL_LEGPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Attached to the outer membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                     105 AGHTDERGSREYN 117
                                                                                                                                                                                                                                                                                                                          l Similarity
13; Conserv
                                                                                                                                                                                                                                                   AGHTDERGSREYN 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PPL).
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176 AA;
                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Outer membrane; Antigen; Signal.
                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                               18911 MW;
                                                                                                                                                                                                                                                                                                                                       100.0%;
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                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                                                                             Score 13; DB 1;
Pred. No. 5.2e-(
                                                                                                                                                                                                                                                                                                                                                                                                                                                        OMPA-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEPTIDOGLYCAN-ASSOCIATED LIPOPROTEIN.
N-ACYL DIGLYCERIDE (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                            7D9C3EBECBE621DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      subdivision;
                                                                                    491 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              176
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                                                                                                                                                                                                                                                                                                                                                                      Length 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eisenstein B.I.; encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       by a lipid
                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                    Gaps
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        RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Mosell D., Nakai S., Noback M.,
RA Noone D., O'Railly M., Ogawa K., Ogiwara A., Oudeya B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Satot T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sorokin A., Tacconi E., Takayi T., Takahashi H., Takamaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Vassarotti A.,
RA Winters P., Wipat A., Yanamoto H., Yamane K., Yasumoto K., Yata K.,
Yoshida K., Yoshikawa H.F., Zumsteln E., Yoshikawa H., Danchin A.,
RA Winters P., Wipat A., Yanamoto H., Yamane K., Yasumoto K., Yata K.,
RA Winters P., Wipat A., Yanamoto H., Yamane R., Yasumoto K., Yata K.,
RA Winters P., Wipat A., Yanamoto H., Yamane R., Yasumoto K., Yata K.,
RA Winters P., Wipat A., Yanamoto H., Yamane R., Yasumoto K., Yata K.,
RA Winters P., Wipat A., Yanamoto H., Yamane R., Yasumoto K., Yata K.,
                                                                                                     PRINTS; PR00922; DADACBPTASE3.
TIGRFAMS; TIGR00666; PBP4; 1.
                                                                                                                                                         SubtiList; BG10969; pbp.
InterPro; IPR000667; Peptidase_S13.
Pfam; PF02113; Peptidase_S13; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                        MEROPS;
                                                                                                                                                                                                                                                                EMBL; Z34883; CAA84366.1; EMBL; Z99113; CAB13718.1;
                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
                              SIGNAL
                                                      Complete proteome.
                                                                            Peptidoglycan synthesis; Cell division; Cell wall; Hydrolase; Signal;
                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-168
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Bacteria; Firmicut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUN-2002 (Rel. 41, Last annotation update) Putative penicillin binding protein precursor PBP OR DACC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Microbiology 141:645-648(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "A putative new peptide synthase operon in Bacillus subtilis: partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tognoni A., Franchi E., Magistrelli C., Colombo E., Cosmina P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95227362; PubMed=7711903;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO PEPTIDASE FAMILY S13; ALSO KNOWN AS THE D-ALANYL-D-ALANINE CARBOXYPEPTIDASE 3 FAMILY.
                                                                                                                                                                                                                                        S13.UPW;
                                                                                                                                                                                                                                                                                                                                                                                                                       non-profit institutions as long as its content
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  PUTATIVE PENICILLIN BINDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                           Usage
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RESULT 3

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Pfam; PF00178; Ets; 1
                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FlyBase; FBqn0000567; Eip74EF.
InterPro; IPR000418; Ets.
InterPro; IPR002341; HSF_ETS.
                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. The surpease by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                           HSSP; P14921; 2STT.
TRANSFAC; T00208; -
                                                                                                                                          PIR; A34692; A34692.
                                                                                                                                                                 EMBL; M37082; AAA28493.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ecdysone responses in Drosophila.";
Development 118:613-627(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Puffs and PCR: the in vivo dynamics of early gene expression during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94038699; PubMed=8223281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Burtis K.C., Thummel C.S., Jones C.W., Karim F.D., Hogness D.S., "The Drosophila 74EF early puff contains E74, a complex ecdysone inducible gene that encodes two ets-related proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING MEDLINE-90199900; PubMed=2107982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell 61:85-99(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEVELOPMENTAL STAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ecdysone-induced protein 74EF isoform A (ETS-related protein E74A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E74A_DROME
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                                                                                                                                                                                                                                                                                                                                                                                                    REGULATED AND IS CORRELATED WITH THE 20-OH-ECDYSONE INDUCED ACTIVITY OF PUFF 74EF.
SIMILARITY: BELONGS TO THE ETS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88 AAAALSVL 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 AAAALSVL 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ruiz C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   491 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Richards G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52891 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E442E5A227B7D080 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                   Query Match
Best Local
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Best Local
                                              Antifreeze protein; Repeat; Multigene family. SEQUENCE 37 AA; 3144 MW; 46AA951A962DECA9 CRC64;
                                                                                                                                                                                                                            americanus),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei
Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
Pleuronectoidei; Pleuronectidae; Pseudopleuronectes.
                                                                         PRINTS;
                                                                                                                                       Biochim. Biophys. Acta 495:388-392(1977).
                                                                                                                                                      Devries A.L., Lin \gamma.; "Structure of a peptide antifreeze and mechanism of adsorption to
                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                      InterPro; IPR000104; Antifreeze_1.
PRINTS; PR00308; ANTIFREEZEI.
                                                                                                                                                                                                                                                                                     Pseudopleuronectes americanus (Winter flounder) (Pleuronectes
                                                                                                                                                                              MEDLINE=78060969; PubMed=588591;
Devries A.L., Lin Y.;
                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                           NCBI_TaxID=8265;
                                                                                                                                                                                                                                                                                                       Antifreeze peptide 3
                                                                                                                                                                                                                                                                                                                                                     P02733;
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PROSITE; PS00346; ETS_DOMAIN_2; 1.

PROSITE; PS50061; ETS_DOMAIN_3; 1.

Nuclear protein; Transcription regulation; DNA-binding;
PROSITE; PSDICING.
        Local Similarity les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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SMART; SM00413; ETS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                              ALANINE-RICH, AMI
; A03192; FDFL3W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  es 8; Conserv
                                                                                                                FUNCTION: ANTIFREEZE PROTEINS LOWER THE BLOOD SIMILARITY: BELONGS TO THE TYPE-I AFP FAMILY.
                                                                                                                                                                                                                                                                                                                                                               PSEAM
                                                                                                                                                                                                                                                                                                                                                                                                                      195 IAAAAAAL 202
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       Conservative
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                                                                                                      AMPHIPHILIC AND ALPHA-HELICAL.
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      100.0%; E
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                             4.18;
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100.0%; Pred. No.
              Score 7; [
Fred. No.
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POLY-GLN.
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      Mismatches
              DB 1;
o. 6.2;
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                         Length 37;
    0,
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   Indels
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Antifreeze peptide GS-8.

Myoxocephalus aenaeus (Grubby sculpin).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;

Cottoidei; Cottidae; Myoxocephalus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-MAY-1991 (Rel. 18, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chakrabartty A., Hew C.-L., Shears M., Fletcher G.;
*Primary structures of the alanine-rich antifreeze polypeptides from
grubby sculpin, Myoxocephalus aenaeus.";
Can. J. Zool. 66:403-408(1988).
-i- FUNCTION: ANTIFREEZE PROTEINS LOWER THE BLOOD FREEZING POINT.
-i- SIMILARITY: BELONGS TO THE TYPE-I AFP FAMILY. TYPE 1 AFP ARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANP8_MYOAE
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                                                                                                                                                                                                                                                                                                                                   Pseudopleuronectes americanus (Winter flounder) (Pleuronectes
                                                                                                                                                                                                                                                                                                                                                    Antifreeze protein A/B precursor
                                                                                                                                                                                                                                                                                                                                                                23-OCT-1986 (Rel. 02, Created)
23-OCT-1986 (Rel. 02, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                        ANPA_PSEAM
                                                                                                                                                                                                                                                                                                                                                                                                                                           PSEAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antifreeze protein; Repeat.
                                                                                  SEQUENCE FROM N.A. (PROTEIN A).
MEDLINE-88259236; PubMed=3133486;
Scott G.K., Davies P.L., Kao M.H.,
                                                                                                                                                                                      SEQUENCE FROM N.A. (PROTEIN A).
MEDLINE-82197490; PubMed-6952188;
Davies P.L., Roach A.H., Hew C.-L
SEQUENCE FROM N.A. (PROTEIN B).
MEDLINE-84264559; PubMed=6086629;
                                                                                                                                                                                                                                                 NCBI_TaxID=8265;
                                                                                                                                                                                                                                                               Pleuronectoidei; Pleuronectidae; Pseudopleuronectes
                                                       pleuronectinae.
                                                                       "Differential amplification of antifreeze protein
                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 79:335-339(1982)
                                                                                                                                                                        DNA sequence coding for an antifreeze protein precursor from winter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALANINE-RICH, AMPHIPHILIC AND ALPHA-HELICAL, S07046; FDF18G
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                                            Evol.
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                                            27:29-35(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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100.0%; Pred. No.
                                                                                                                                                                                            Hew C.-L.;
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                                                                                         Fletcher G.L.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                82 AA
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                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is no doi for commercial modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Energy-optimized structure of antifreeze protein and its binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L00138; AAB59964.1; JOINED. EMBL; L29178; AAB59964.1; JOINED. EMBL; M62414; AAA49469.1; -... EMBL; M62416; AAA49471.1; -.. EMBL; M62417; AAA49472.1; -.. EMBL; M62417; AAA49472.1; -..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sicheri F., Yang D.S.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95281060; PubMed=7760940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 45-81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mechanism.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92209995; PubMed=1555765.
                                                                                                                                                                                                  CHAIN
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Ice-binding structure and mechanism of an antifreeze protein from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3D-STRUCTURE MODELING OF 45-81
                                                                                                                                        CONFLICT
HELIX
                                                                                                                         SEQUENCE
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                                                                                                                                                                                   VARIANT
                                                                                                                                                                                                                                                                                                                                                 nterPro;
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                                                            Local
                                                                                                                                                                                                                                                                                                                                                                1WFB; 03-JUN-95.
                                                                                                                                                                                                                                                                                                                                                                                                                               JS0704; JS0704
8 AAAAAAL 14
                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                 IPR000104; Antifreeze_1.
                                                                                                                                                                                                                                                                                                      protein; Repeat; Multigene family; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                             15-OCT-94.
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                                         Conservative
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36
70
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                                                                                                                           7711 MW;
                                                                                                                                                                  82
36
70
24
                                                              4.1%; Score 7;
100.0%; Pred. No
                                             0;
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A -> D (IN PROTEIN B).
S -> R (IN REF. 2).
                                                                                                                             C2AE7B74C0D46CC1 CRC64;
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                                                                   Pred. No.
                                             Mismatches
                                                                                    DB 1;
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CU19_ARADI STANDARD; PRT; 120 AA.
P80515;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Adult-specific rigid cuticular protein 11.9 (ACP 11.9).
                                                                         Pfam; PF00379; Chitin_bind_4; 1.
PRINTS; PR00947; CUTICLE; 1.
PROSITE; PS00233; CUTICLE; 1.
                                                                                                      980517;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-JUN-2002 (Rel. 41, Last annotation update)
18-Jun-2002 (Rel. 41, Last annotation update)
                                               SEQUENCE
                                                          Structural protein; Cuticle. DOMAIN 73 83
                                                                                                                                                                      MEDLINE-97166616; PubMed-9014336;
Norup T., Berg T., Stenholm H., Andersen S.O.,
"Purification and characterization of five cuti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00379; Chitin_bind_4; 1.
PRINTS; PR00947; CUTICLE.
PROSITE; PS00233; CUTICLE; 1.
Structural protein; Cuticle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Araneus diadematus (Spider).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
Araneomorphae; Entelegynae; Araneoidea; Araneidae; Araneus.
                                                                                                                                                                                                            ISSUE=Cuticle;
                                                                                                                                                                                                                                                                                                                                           CU26_ARADI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Araneus diadematus (Spider).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
Araneomorphae; Entelegynae; Araneoidea; Araneidae; Araneus.
                                                                                                                                                                                                                                           NCBI_TaxID=45920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Purification and characterization of five cuticular proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-97166616; PubMed-9014336;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-45920;
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     Similarity 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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     Conservative
                                              ΑA;
                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                             12589 MW;
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  4.1%; Score 7; 100.0%; Pred. No. tive 0; Mismatc
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                                                       POLY-ALA.
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                                          9BFBFCFB2B6AA4B9 CRC64;
   Mismatches
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           DB 1;
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AZUP_PARPN
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                   METAL
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                                                                                                                                                                                                                                                                                                                                              Williams P.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochem. J.
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P80401;
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                                                                                                                                                                                                     Pfam; PF00127; copper bind; 1.
PRINTS; PR00156; COPPERBLUE.
PRODOM; PD001235; Copper blue; 1.
PROSITE; PS00196; COPPER BLUE; 1.
                                                                                                                                                      Copper; Electron transport; SIGNAL 1 22
                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z73141; CAA97485.1; -. EMBL; Z70033; CAA93848.1; -. PDB; 1ADW; 15-MAY-97.
                                                                                                                                                                                                                                                                                                                           InterPro; IPR000923; BlueCu_1.
InterPro; IPR001235; Copper_blue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBUNIT: HOMODIMER.
-!- SUBCELULAR LOCATION: Periplasmic.
-!- SIMILARITY: CONTAINS 1 PLASTOCYANIN-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (FEB-1997) to the PDB data bank.
-!- FUNCTION: THIS SOLUBLE ELECTRON TRANSFER COPPER PROTEIN IS REQUIRED FOR THE INACTIVATION OF COPPER-CONTAINING NITRITE REDUCTASE IN THE PRESENCE OF OXYGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 23-145.
STRAIN-ATCC 35512 / LMD 82.5;
MEDLINE-95289994; PubMed-7772045;
Chan C., Willis A.C., Robinson C.V., Aplin R.T., Radford S.E., Ferguson S.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The complete amino acid sequence confirms the presence of pseudoazurin in Thiosphaera pantotropha."; Blochem. J. 308:585-590(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The pseudoazurin gene from Thiosphaera pantotropha: analysis of upstream putative regulatory sequences and overexpression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97184655; PubMed=9032456; Leung Y.-C., Chan C., Reader J.S., Willis A.C., van Spanning R.J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND SEQUENCE OF 23-32 STRAIN=ATCC 35512 / LMD 82.5;
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Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli."
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15-JUL-1998 (Rel.
15-JUN-2002 (Rel.
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36, Last sequence update)
41, Last annotation update)
PSEUDOAZURIN.
PLASTOCYANUN-LIKE.
COPPER (BY SIMILARITY).
COPPER (BY SIMILARITY).
COPPER (BY SIMILARITY).
                                                                                                                                                                        Signal; Periplasmic; 3D-structure.
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RESULT 10
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01-APR-1988 (Rel. 07, Last sequence update)
01-JUN-2002 (Rel. 41, Last annotation update)
Peptidoglycan-associated lipoprotein precurso
PAL OR EXCC OR B0741 OR Z0909 OR ECS0776.
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                                                                                                                                                                                                     Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.
                                                                                                                                                                                                                                                                                                                                                            Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F. Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lazzaroni J.-C., Portalier R.;
"The excC gene of Escherichia coll K-12 required for cell envelope integrity encodes the peptidoglycan associated lipoprotein (PAL)."; Mol. Microbiol. 6:735-742(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=87133578; PubMed=3545827;
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Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
                                                                                                                          "A 718-kb DNA sequence of the Escherichia corresponding to the 12.7-28.0 min region DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Nucleotide sequence of the gene for the peptidoglycan-associated lipoprotein of Escherichia coli K12."; Eur. J. Biochem. 163:73-77(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=562, 83334;
                                                              STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
                                                                                                                                                                                        Sampei G.,
                                                                                                                                                                                                                                                                                                                              "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                     MEDLINE=97061202; PubMed=8905232;
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                                                                                                                                                                          ., Seki Y., Tagami H., Takemoto K., Wada C., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Henning U.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108
145 AA;
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15446 MW;
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; 725ECB5929EC3831 CRC64;
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OR ECS0776.
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on the linkage ma
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MEDLINE-21156231; PubMed=11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,

Hayashi T., Makino E., Nakayama K., Murata T., Tanaka M., Tobe T.,

Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,

Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli

0157:H7 and genomic comparison with a laboratory strain K-12.";

DNA Res. 8:11-22(2001).
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Nature 409:529-533(2001).
[6]
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"Crystallization and preliminary crystallographic study of the
peptidoglycan-associated lipoprotein from Escherichia coli.";
Acta Crystallogr. D 57:317-319(2001).
-i- PUNCTION: Thought to play a role in bacterial envelope integrity.
-i- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Apodaca J., Anantharaman T.S., Lin J., Yen G., Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    their products, components of a multistep translocation system Escherichia coli.";
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SEQUENCE
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"Nucleotide sequences of the tola and tolB genes and localization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=90078104; PubMed=2687247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-30 FROM N.A.
                                                                                                                                                                                                                                                                           PRINTS; PRO1021; OMPADOMAIN.
PRODOM; PD000930; Bac_OmpA; 1.
PROSITE; PS000013; PROKAR_LIFOPROTEIN; 1.
PROSITE; PS01068; OMPA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: TO OTHER PAL PROTEINS.
                                                                                                                                                                                                                                           Outer membrane; Signal; Lipoprotein; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                               EcoGene; EG10684; pal
InterPro; IPR001145;
                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00691; OmpA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteriol. 171:6600-6609(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S20547; S20547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A27534; LPECPG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M28232; -; NOT_ANNOTATED_CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 an email to license@isb-sib.ch).
Similarity 7; Conserv
                                                                                                    22
22
105
173
  Conservative
                                                                                                                A
A
                                                                                                                                       22
149
                                                                                                                18824 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                     Bac_OmpA
                         4.1%; Score 7;
100.0%; Pred. No
     0;
                                                                                                                                                                 PEPTIDOGLYCAN-ASSOCIATED LIPOPROTEIN N-ACYL DIGLYCERIDE.
                                                                                                                                          OMPA-LIKE
                                  Pred. No.
                                                                                                                449F9959C0274430 CRC64;
     Mismatches
                                                         DB
                                                            Length 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schwartz D.C.,
        Indels
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        Gaps
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120

SLGERRA 126

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                                                                  Matches
                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- FUNCTION: MAY BIND RNA.
-!- FUNCTION: MAY BIND RNA.
-!- TISSUE SPECIFICITY: EXRRESSED IN DEVELOPING HEART, PRONEPHROS,
RETINA AND EPIPHYSIS. IN ADULT, HIGH EXPRESSION IN HEARR, MODERATE
IN KIDNEY, UNDETECTABLE IN LIVER, LUNG AND SKELETAL MUSCLE.
IN KIDNEY, UNDETECTABLE IN LIVER, LUNG AND SKELETAL MUSCLE.
-!- DEVELOPMENTAL STAGE: MRNA FIRST DETECTED IN THE TAILBUD EMBRYO
(STAGE 26) IN THE PAIRED HEART PRIMORDIA AND IN THE CONDENSING
EPITHELIUM THAT WILL FORM THE PRONEPHROS; AT THE LATE TAILBUD
STAGE (STAGE 34) IN THE DEVELOPING RETINA AND EPIPHYSIS. AS
DEVELOPMENT PROCEEDS, DETECTED THROUGH THE ENTIRE LENGTH OF THE
HEART TUBE, IN THE MUSCULAR TISSUE OF THE OTTELOW TRACT, AND IN
THE DUCT EPITHELIUM OF THE PRONEPHROS. DURING LATER DEVELOPMENT,
MRNA FOUND IN ALL SUBREGIONS OF THE HEART, IN THE GLOMUS, TUBULES
AND DUCT OF THE PRONEPHROS, IN THE RETINAL GANGLION CELL LAYER
(GCL) AND IN THE EPIPHYSIS.
-!- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9YGF5;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
RNA-binding protein with multiple splicing homolog (RBP-MS) (HEart, RRM Expressed Sequence) (Hermes).
                                                                                                                                  SEQUENCE
                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                         InterPro; IPR000504; RNA_rec_mot. Pfam; PF00076; rrm; 1. SMART; SM00350; RRM; 1.
                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    XENLA
                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the developing heart.";
Mech. Dev. 80:77-86(1999).
                                                                                                                                                                                               RNA-binding.
                                                                                                                                                                                                                                                                                                  HSSP; P09012;
                                                                                                                                                                                                                                                                                                                EMBL; AF107889; AAD16971.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gerber W.V., Yatskievych T.A., Antin P.B., Correia K.M., Conlon R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99195799; PubMed=10096065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Krieg P.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The RNA-binding protein gene, hermes, is expressed at high levels in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RBMS_XENLA
167 AAAAAAL 173
                                 œ
                                                                Similarity 7; Conserv
                                                                                                                                                                                                             PS00030; RRM_RNP_1;
                               AAAAAAL 14
                                                                                                                                                                                                                                PS50102;
                                                                                                                                167
196 AA;
                                                                Conservative
                                                                                                                                                                 20
11
                                                                                                                                                                                                                                                                                                  2U1A.
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                                                                                                                                                                                                                                RRM;
                                                                                                                                                97
14
172
                                                           100.08; 1
                                                                                                                              21675 MW;
                                                                            4.1%; Score 7;
100.0%; Pred. No.
                                                                                                                           POLY-ALA.
; 7964198C1122A3D3 CRC64;
                                                                                                                                                            POLY-ASN.
                                                                                                                                                                             RNA-BINDING (RRM).
                                                                                                                                                                                                              FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                Mismatches
                                                                              DB 1;
o. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   196 AA
                                                                                             Length 196;
                                                              0;
                                                            Indels
                                                           0;
                                                         Gaps
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RBMS_CHICK
                                                                                                                                                                       RESULT 13
                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                           Query Match
Best Local :
                                                   CTFI_MOUSE STANDARD; PRT; 203 AA. 060753; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-JUL-1998 (Rel. 36, Last annotation update) cardiotrophin-1 (CT-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
    Eukaryota;
Mammalia; E
                               Mus musculus (Mouse)
                                                 CTF1.
                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                 RNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT 2001 (Rel. 40, Created)
16-OCT 2001 (Rel. 40, Last sequence update)
16-OCT 2001 (Rel. 40, Last annotation update)
RNA-binding protein with multiple splicing homolog (RBP-MS) (HEart, RRM Expressed Sequence) (Hermes).
                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00102; RRM; 1.
PROSITE; PS00030; RRM_RNP_1; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- TISSUE SPECIFICITY: EXPRESSED IN DEVELOPING HEART.
-!- DEVELOPMENTAL STAGE: MRNA ALREADY DETECTED AT STAGE 7-8 IN THE CARDIOGENIC MESODERM, AND BECOME ALMOST UNDETECTABLE IN THE OUTER CURVATURE OF THE VENTRICULAR REGION WHEREAS REMAINING HIGH IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the developing heart.";
Mech. Dev. 80:77-86(1999).
-!- FUNCTION: MAY BIND RNA.
                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF129933; AAD30273.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEVELOPING ATRIAL REGIONS.
-I- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The RNA-binding protein gene, hermes, is expressed at high levels in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99195799; PubMed=10096065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000504; RNA_rec_mot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Krieg P.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gerber W.V., Yatskievych T.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RBPMS OR HERMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9W611;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RBMS_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                          Local Similarity hes 7; Conserv
                                                                                                                                                                                                                  171 AAAAAAL 177
                                                                                                                                                                                                                                             8 AAAAAAL 14
   ; Metazoa;
Eutheria;
                                                                                                                                                                                                                                                                                                                                        200 AA;
                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                        169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                        100.0%;
   Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                     21856 MW; 4093B3C780BBC1DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                     99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi;
Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                          4.1%; Score 7; DB 1; 100.0%; Pred. No. 27;
                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                     POLY-ALA
                                                                                                                                                                                                                                                                                                                                                                RNA-BINDING (RRM).
Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antin P.B., Correia K.M., Conlon R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200 AA
                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                      Length 200;
                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                      Gaps
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q63507;

Ol-NOV-1997 (Rel. 35, Created)

Ol-NOV-1997 (Rel. 35, Last sequence update)

Ol-NOV-1997 (Rel. 35, Last annotation update)

60S_ribosomal protein L14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Expression cloning of cardiotrophin 1, a cytokine that induces cardiac myocyte hypertrophy";
Proc. Natl. Acad. Sci. U.S.A. 92:1142-1146(1995).
-i- FUNCTION: INDUCES CARDIAC MYOCYTE HYPERTROPHY IN VITRO. BIN AND ACTIVATES THE LEUKEMIA INHIBITORY FACTOR RECEPTOR (LIF
                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                             Chan Y.-L., Olvera J., Wool I.G.;
"The primary structure of rat ribosomal protein L14.";
Biochem. Biophys. Res. Commun. 222:427-431(1996).
-i- SIMILARITY: BELONGS TO THE L14E FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pennica D., King K.L., Shaw K.J., Luis E., Rullamas J., Luoh
Darbonne W.C., Knutzon D.S., Yen R., Chien K.R., Baker J.B.,
                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Sprague-Dawley; TISSUE-Liver; MEDLINE=96222520; PubMed=8670222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090
                          EMBL; X94242; CAA63926.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND SEQUENCE OF 1-40 AND 119-141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95166785; PubMed=7862649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART,
LIVER, LUNG AND KIDNEY. LOWER LEVELS IN TESTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXPRESSION IN SPLEEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RECEPTOR)/GP 130 RECEPTOR COMPLEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGI:105115; Ctf1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U18366;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 AAALSVL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC52173.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21509 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.1%;
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mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8B3D414A0B3B232F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       213 AA.
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COBM_MYCTU
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Best Local :
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DOMAIN
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REPEAT
                                                                                                                                                                                                                                                                                               Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harr. Cold S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harr. Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroy. Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Quairer S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ribosomal protein; Repeat.
INIT_MET 0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPRUU
Pfam; PF00467;
                                                                                                                                                                             STRAIN-CDC 1551 / Oshkosh;

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,

Peterson J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,

Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,

Belcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Precorrin-4 C11-methyltransferase (EC 2.1.1.133) (Precorrin-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q10672;
15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COBM_MYCTU
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REPEAT
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                                                  laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: METHYLTRANSFERASE THAT CATALYZES THE METHYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          methylase)
                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98295987; PubMed=9634230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COBM OR RV2071C OR MT2131 OR MTCY49.10C.
                                                                                                                                                       "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                      Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                      SIMILARITY: BELONGS TO A FAMILY
                       AND CBIL/COBI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bacteria; Actinobacteria (class); Actinobacteridae;
Corynebacterineae; Mycobacteriaceae; Mycobacterium
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173
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100.08;
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 Mismatches

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Pred. No
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                        THAT GROUPS
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                                         SUMT,
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through a collaboration
                                           CYSG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium
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                                           CBIF/COBM
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RESULT 16
GSHI_MOUSE
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                                          Singh G., Kaur S., Stock J.L., Jenkins N.A., Gilbert D.J.,
Copeland N.G., Potter S.S.;
"Identification of 10 murine homeobox genes.",
Proc. Natl. Acad. Sci. U.S.A. 88:10706-10710(1991).

1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR THAT BINDS TO THE DNA
SEQUENCE 5'-GC[TA][AC]ATTA[A]-3'. ACTIVATES THE TRANSCRIPTION OF
THE GHRH GENE. PLAYS AN IMPORTANT ROLE IN PITUITARY DEVELOPMENT.

1- SUNCELLULAR LOCATION: Nuclear.

1- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                     SEQUENCE OF 146-205 FROM N.A.
MEDLINE=92073356; PubMed=1683707;
                                                                                                                                                                                                                                                             development
                                                                                                                                                                                                                                                                                                        MEDLINE=96181350;
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSHI_MOUSE STANDARD; PRT; 261 AA P31315; O1-JUL-1993 (Rel. 26, Created) 01-OCT-1996 (Rel. 34, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                             "Gsh-1, an orphan Hox gene, is required for normal pituitary
                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=NIH Swiss;
MEDLINE=96172995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOUSE
                                                                                                                                                                                                                                                                                                                                                  Dev. Dyn. 203:337-351(1995)
                                                                                                                                                                                                                                                                                                                                                                      *Gsh-1: a novel murine homeobox gene expressed in the central nervous
                                                                                                                                                                                                                                                                                                                                                                                                     Valerius M.T., Li H., Stock J.L., Weinstein M., Kaur S., Singh G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSH1 OR GSH-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homeobox protein GSH-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cobalamin biosynthesis; Porphyrin biosynthesis; Transferase; Methyltransferase; Complete proteome. SEQUENCE 251 AA; 26420 MW; 8D8F213ABFC91CD3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000878; Cor/por_Metransf.
InterPro; IPR003043; Uropor_Metransf.
Pfam; PF005590; Tp_methylase; 1.
PROSITE; PS00839; SUMT_1; 1.
PROSITE; PS00840; SUMT_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TubercuList; Rv2071c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no will modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGR; MT2131;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; 273966; CAA98218.1; -
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                                                                                                                                                                                                                                                                                   ., Zeitler P.S., Valerius M.T., Small K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 AAAAAAL 120
                                                                                                                                                                                                                                          15:714-724(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 AAAAAAL 14
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                                                                                                                                                                                                                                                                                                        PubMed=8631293;
                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=8589431;
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100.08;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         261 AA.
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                                                                                                                                                                                                                                                                                 Potter S.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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A Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,
A Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
A Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
A Malykh A.G., Koonin E.V., Kozyavkin S.A.;
The complete genome of hyperthermophile Methanopyrus kandleri Av19
AT and monophyly of archaeal methanogens.",
RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
C-!- FUNCTION: Is responsible for channelling the electrons from the Oxidation of dihydroorotate from the FMN redox center in the pyrD Subunit to the ultimate electron acceptor NAD(+) (By similarity).
C-!- COPACTOR: Binds a 2Fe-2S cluster and FAD (By similarity).
C-!- SUBUNIT: Heterotetramer of 2 pyrK and 2 pyrD subunits (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PYRK_METKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                         similarity).
-!- SIMILARITY: BELONGS TO THE PYRK FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-AV19 / DSM 6324 / JCM 9639;
MEDLINE=21927647; PubMed=11930014;
                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-AV19 / DSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tb-JUN-2002 (Rel. 41, Last annotation update)
Probable dihydroorotate dehydrogenase electron transfer subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PYRK OR MK0564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=2320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Methanopyrus kandleri
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transcription regulation; Activator; Homeobox; DNA-binding; Nuclear protein; Developmental protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PYCODM; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX_1; 1
PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:95842; Gsh1.
InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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A38809; A38809.
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100.0%; Pred. No.
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RESULT 18
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Pyrimidine biosynthesis; Transport; Electron transport; Metal-binding; Iron; Iron-sulfur; Flavoprotein; FAD; Complete proteome.
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15-JUN-2002 (Rel. 41, Last annotation update)
Tetrahydromethanopterin S-methyltransferase s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   deltaH: functional analysis and comparative genomics.";

J. Bacteriol. 179:7135-7155(1997).

j. FUNCTION: THIS ENZYME COMPLEX CATALYZES AN INTERMEDIATE FUNCTION: THE FORMATION OF METHYL-COENZYME M AND MSTHANGENESIS, THE FORMATION OF METHYL-COENZYME M AND NS-METHYL-TETRAHYDROMETHANDETERIN FROM COENZYME M AND NS-METHYL-COENZYME M AND NS-METHYL-CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jiwani N., Caruso A., Busn D., Odet W., Dietrovski S., Church G.M., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; Baniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; "Complete genome sequence of Methanobacterium thermoautotrophicum "Complete genome is and comparative genomics.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J., Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McCourall C. Chimar C. Corell N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tetrahydromethanopterin S-methyltransferase subunit C (EC 2.1.1.86) (N5-methyltetrahydromethanopterin--coenzyme M methyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MTRC_METTH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Methanobacterium thermoautotrophicum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       subunit C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=187420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Methanobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L5-JUL-1999
                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98037514; PubMed=9371463;
                                                                                                                                      modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                         -i- SUBUNIT: COMPOSED OF 8 DIFFERENT SUBUNITS (BY SIMILARITY)
                          Transferase; Methyltransferase; Transmembrane; Methanogenesis;
                                                        TIGRFAMS; TIGR01148;
                                                                                   EMBL; AE000885; AAB85650.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSLOCATING STEP (BY SIMILARITY).

CATALYTIC ACTIVITY: 5-methyl-5,6,7,8-tetrahydromethanopterin + 2-mercaptoethanesulfonate = 5,6,7,8-tetrahydromethanopterin + 2-
                                                                                                                                                                                                                                                                                                                                                                                                                                     PATHWAY: Methanogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TETRAHYDROMETHANOPTERIN. THIS IS A ENERGY-CONSERVING,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AE010350; AAM01779.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (methylthio)ethanesulfonate.
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  proteome
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262 AA;
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IRON-SULFUR 1 (2FE-2S) (BY SIMILARITY).
IRON-SULFUR 2 (2FE-2S) (BY SIMILARITY).
IRON-SULFUR 2 (2FE-2S) (BY SIMILARITY).
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Best Local
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15-JUN-2002 (Rel. 41, Last annotation update)
Tetrahydromethanopterin S-methyltransferase subunit C (EC 2.1.1.86)
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01-JUL-1993 (Rel. 26,
01-NOV-1997 (Rel. 35,
15-JUN-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
Archaea: Euryarchaeota: Methanobacteria: Methanobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MTRC_METIM
                                                                                                                                                                                                                                                                 Eur.
                                                                                                                                                                                                                                                                           Gaertner P., Ecker A., Fischer R., Linder D., Fuchs G., Thauer I "Purification and properties of N5-methyl tetrahydromethanopterin:coenzyme M methyltransferase from Methanobacterium thermoautotrophicum.";
Eur. J. Biochem. 213:537-545(1993).
                                                                                                                                                                                                                                                                                                                                                                                               N5-methyltetrahydromethanopterin: coenzyme-M methyltransferase from Methanobacterium thermoautotrophicum.";
                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning, sequencing and immunological characterization of the corrinoid-containing subunit of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stupperich E., Juza A., Hoppert M., Mayer F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94039026; PubMed=8223548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=79929
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            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-30.
MEDLINE=93238732; PubMed=8477726;
                                                                                                        This
                                                                                                                                                                                                  -
                                                               the European Bioinformatics Institute. Thuse by non-profit institutions as long
                                                                                                                                                                                   TRANSLOCATING STEP.

CATALYTIC ACTIVITY: 5-methyl-5,6,7,8-tetrahydromethanopterin mercaptoethanesulfonate = 5,6,7,8-tetrahydromethanopterin + 2
                                                                                                                                                                                                                                      FUNCTION: THIS ENZYME COMPLEX CATALYZES AN INTERMEDIATE STEP METHANGENESIS, THE FORMATION OF METHYL-COENZYME M AND TETRAHYDROMETHANOPTERIN FROM COENZYME M AND N5-METHYL-
                                                                                                                                SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                           TETRAHYDROMETHANOPTERIN. THIS IS A ENERGY-CONSERVING,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 AAALSVL 146
                                                                                                                                                           PATHWAY:
                                                                                                                                                                         (methylthio)ethanesulfonate.
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                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                COMPOSED OF 8 DIFFERENT SUBUNITS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                     Linder D., Fuchs G., Thauer R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                    There are no restrictions on 
ong as its content is in no
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EMBL; X73123; CAA51554.1; -.

S30343;

S30343.

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Best Local
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                                                                               the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
EMBL; AC009336; -; NOT_ANNOTATED_CDS.
EMBL; AY014304; AAG42152.1; -.
EMBL; AY014303; AAG42152.1; JOINED.
EMBL; X15507; CAA33529.1; -.
PIR; B32830; B32830.
PIR; S05957; S05957.
                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                             Genes
                                                                                                                                                                                                                                                                                  MEDLINE=89306602; PubMed=2568311;
Oliver G., Sidell N., Fiske N., Heinzmann C., Mohandas T.,
Sparkes R.S., de Robertis E.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN 1990 (Rel. 13, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homeobox protein Hox-D8 (Hox-4E) (Hox-5.4). HOXD8 OR HOX4E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HUMAN
                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 193-287 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
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TIGRFAMs;
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P13378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                         Complementary homeo protein gradients in developing limb buds."; henes Dev. 3\!:\!641\!-\!650(1989).
                                                                                                                                                                                                                                                                                                                                                                A complete mutation
                                                                                                                                                                                                                                                                                                                                                                            Kosaki K., Kosaki R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HXD8_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                   irren
                                                                                                                                                                                          SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
                                                                                                                                                                                                        FUNCTION: SEQUENCE-SPÉCIFIC TRANSCRIPTION FACTOR WHICH IS PART OF A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS. SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140 AAALSVL 146
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                                                                                                                                                                                                                                                                                                                                               , Kosaki R., Suzuki T., Yoshihashi H., Sasaki K., te mutation analysis panel of human HOX genes."; (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                   (AUG-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGR01148;
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to the EMBL/GenBank/DDBJ databases
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Pred. No. 34;
0; Mismatches
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Y -> S (IN REF.
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29843603282D7807 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                         Matsuo N.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 21
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mayfield S.P., Schirmer-Rahire G., Frank H., Zuber H., Rochaix J.-D. "Analysis of the genes of the OEE1 and OEE3 proteins of the photosystem II complex of Chlamydomonas reinhardtii."; Plant Mol. Biol. 12:683-693(1989).

-i- FUNCTION: STABILIZES THE MANGANESE CLUSTER WHICH IS THE PRIMARY SITE OF WATER SPLITTING (BY SIMILARITY).
                                                                        PIR; S05508; S05508.
InterPro; IPR002628; PSII_MSP.
Pfam; PF01716; MSP; 1.
        Thylakoid; Membrane; TRANSIT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                             Photosynthesis; Photosystem II; Chloroplast; Transit peptide;
                                                                                                                                                        EMBL; X13826; CAA32053.1; -.
                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane; with the photosystem II complex.
-!- SIMILARITY: BELONGS TO THE PSBO FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=137c / CC-125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
01-0CT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oxygen-evolving enhancer protein 1, chloroplast precursor (OEE1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transcription regulation. DOMAIN 15 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001827; Antennapedia.
InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSFAC; T03332; -. Genew; HGNC:5139; HOXD8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homeobox; DNA-binding; Developmental protein; Nuclear protein;
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                          Manganese
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100.0%; Pred. No.
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CHLOROPLAST.
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G -> A (IN REF. 3).
; 75FF95A73E2AA85F CRC64;
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POLY-PRO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>.</u>
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o. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           update)
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TO THE DNA

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RESULT 23
GSH2_HUMAN
ID GSH2_HI
AC Q9BZM3
DT 15-JUN-
DT 15-JUN-
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RBSK_BACHD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ρ
                                                                                                                                                                                                                                                                                                                   SOUTH THE PROPERTY OF 
                                                                                                                                                           밁
                                                                                                                                                                                              Š
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic Acids Res. 28:4317-4331(2000).

- CARALYTIC ACTIVITY: ATP + D-ribose = ADP + D-ribose 5-phosphate.

- PATHWAY: Ribose metabolism; first step.

- SUBCELLULAR LOCATION: Cytoplasmic (By Similarity).

- SIMILARITY: BELONGS TO THE PFKB FAMILY OF CARBOHYDRATE KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Ribokinase (EC 2.7.1.15).
RBSK OR BH3728.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
                                      GSH2_HUMAN
Q9BZM3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-20512582; PubMed-11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9K6K1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus halodurans.
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RBSK_BACHD
  15-JUN-2002
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00583; PFKB_KINASES_1; 1. PROSITE; PS00584; PFKB_KINASES_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002139;
Pfam; PF00294; pfkB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                      Transferase; Kinase; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P05054; 1RK2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genome sequence of the alkaliphilic bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002173; PfkB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                     Local Similarity
tes 7; Conserv
                                                                                                                                                           264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 AAAAAAL 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AP001519; BAB07447.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAAAAL 14
                                                                                                                                                           AAAALSV 270
                                                                                                                                                                                                AAAALSV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53
291 AA;
                                                                                                                                                                                                                                                                                                                     294 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
  (Rel. 41, Created)
(Rel. 41, Last sequence update)
                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / JCM 9153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                 RIBOKINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 291
30522 MW;
                                                                                                                                                                                                                                                                                                                     31089 MW;
                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Ribokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.18;
                                                                                                                                                                                                                                                                              4.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 7; 1; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                          Score 7; DB 1; pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OXYGEN-EVOLVING ENHANCER PROTEIN 1.; 5DF4DFAEB1324267 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                     8C13E0FCF5E89FDE CRC64;
                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             294 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
b. 37;
                                                               304 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 291;
                                                                                                                                                                                                                                                                            Length 294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                          QУ
          GSH2_MOUSE
                                                                                                                                                                                                                                           RESULT 24
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Developmental protein
DNA_BIND 202 261
DOMAIN 124 130
DOMAIN 134 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sakai T., Sakamoto S., Nakamura K., Muraki T.; "Human homeobox protein GSH-2."; Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).

Homo sapiens (Human).

Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; cincipaca; catarrhini; Hominidae; Homo.
                                                                                                                         GSH2_MOUSE STANDARD; PRT; 305 AA. p31316; 01-JUL-1993 (Rel. 26, Created) 01-OCT-1996 (Rel. 34, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUN-2002 (Rel. 41, Last annotation update) Homeobox protein GSH-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The sequence of the human GSH2 gene
                                                                                    GSH2 OR GSH-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transcription regulation; Homeobox; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00027; HOMEOBOX_1; 1. PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000047;
InterPro; IPR001356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
        NCBI_TaxID=10090;
                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
                                                                                                      Homeobox protein GSH-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS;
                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF306344; AA
AF306343; AA
P14653; 1B72
                                                                                                                                                                                                                                                                                                         157 AAAAAAL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AB028838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                            8 AAAAAAL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PD000010; Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PR00031; HTHREPRESSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PR00024; HOMEOBOX
                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Marynen P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               147
304 AA;
                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAK00880.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BAB84822.1; -. AAK00880.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 162
32061 MW;
                                                                                                                                                                                                                                                                                                                                                                                                       4.1%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homeobox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTH_repressr
                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                       Score 7;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLY-ALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HOMEOBOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLY-HIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POLY-HIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E896D5422488E6C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                           305 AA
                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 304;
                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                         Indels
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0; Gaps

0;

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RESULT 25
GVPL_HALME
                                                                                                                                                                                                                                                                                                                                 ρ
                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                        Query Match
                                                                                               Q02237;
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence up
01-JUL-1993 (Rel. 26, Last annotation
                                          Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
                                                      Halobacterium mediterranei (Haloferax mediterranei)
                                                                                       GvpL protein.
SEQUENCE FROM N.A
                       NCBI_TaxID=2252;
                                   Halobacteriaceae; Haloferax
                                                                                                                                                         GVPL_HALME
                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                  Transcription regulation; Homeobox; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00024; HOMEOBOX.
ProDom; PD000010; Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the EUropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00027; HOMEOBOX_1; 1. PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                       DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                              Developmental protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00389; HOX; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001356; Homeobox. Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:95843; Gsh2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; B38809; B38809.
HSSP; P14653; 1B72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; B37290; B37290.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: Nuclear.
-!- TISSUE SPECIFICITY: EXPRESSED IN THE DEVELOPING BRAIN.
-!- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Singh G., Kaur S., Stock J.L., Jenkins N.A., Gilbert D.J., Copeland N.G., Potter S.S., "Identification of 10 murine homeobox genes.", Proc. Natl. Acad. Sci. U.S.A. 88:10706-10710(1991).
                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-92073356; PubMed=1683707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 203-262 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hsieh-Li H.M., Witte D.P., Szucsik J.C., Weinstein M., Li H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95344993; PubMed=7619729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Gsh-2, a murine homeobox gene expressed in the developing brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Potter S.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-NIH Swiss;
                                                                                                                                                                                                                        158 AAAAAAL 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 5'-CNAATTAG-3'.
                                                                                                                                                                                                                                                 8 AAAAAAL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dev. 50:177-186(1995).
                                                                                                                                                                                                                                                                                                                              305 AA;
                                                                                                                                                                                                                                                                                                                                           147
                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                    203
                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                        100.0%; Pative 0;
                                                                                                                                                                                                                                                                                                                             32167 MW;
                                                                                                                                                                                                                                                                                   4.1%; Score 7; 1
100.0%; Pred. No.
                                                                                                              sequence update)
                                                                                                                                                                                                                                                                                                                                                   POLY-HIS.
                                                                                                                                                                                                                                                                                                                                        POLY-ALA
                                                                                                                                                                                                                                                                                                                                                                                HOMEOBOX.
                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                         51E7F2DB76E32608 CRC64;
                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                   322 AA
                                                                                                update)
                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                   38;
                                                                                                                                                                                                                                                                                                Length 305;
                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                   Gaps
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A Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Burandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Burandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Burandon R.C., Rogers Y.-H.C., Blazej R.G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Gherry J.M., Cawley S., Dahlke C., Davengort L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Fleischmann W.,
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Best Local
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MEDLING-92275347; PubMed=1317319;
Grossniklaus U., Pearson R.K., Gehring W.J.;
"The Drosophila sloppy paired locus encodes two proteins involved in segmentation that show homology to mammalian transcription factors.";
Genes Dev. 6:1030-1051(1992).
                                                                                                                                                                                                                                                                                                           MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                    STRAIN-Berkeley;
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01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Fork head domain transcription factor slp1 (Sloppy paired locus
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapo
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein 1).
SLP1 OR FD6 OR CG16738.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    halophilic archaea.";
J. Mol. Biol. 227:586-592(1992).
-!- FUNCTION: MAY PLAY A STRUCTURAL OR REGULATORY ROLE IN GAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gas vesicle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-DSM 1411;
MEDLINE=93021102; PubMed=1404376;
MEDLINE=93021102; PubMed=1404376;
Three different but related gene clusters encoding gas vesicles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Syliskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Williams S.M., Woodage T., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Thong W., Zhou S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E W., Rubin G.M., Venter J.C.;
RI Science 287:2185-2195(2000).
R. L., TRANSCRIPTION FACTOR INVOLVED IN SEGMENTATION. REQUIRED C., STRONTINE TRANSCRIPTION FACTOR INVOLVED IN SEGMENTATION. REQUIRED C., CITCORTITIA BY CORMATION OF THE MANDIBULAR LOBE. DIFFERENT LEVELS OF SLP
C. CITCORTITIA BY CORMATION OF THE MANDIBULAR LOBE. DIFFERENT SEGMENTS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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EMBL; X66096; CAA46890.1; -.
EMBL; AE003578; AAAF51058.1; -.
PIR; $23053; $23053.
PIR; $23054; $23054.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSFAC;
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DNA-binding; Developmental protein; Nuclear protein;
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                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                    Transcription regulation; Pair-rule protein; Polymorphism.
DNA_BIND 119 210 FORK-HEAD.
                                                                                                                                                                                                                                                                      VARIANT
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TISSUE SPECIFICITY: EXPRESSED IN THE POSTERIOR HALF OF EACH
PARASEGMENT JUST ANTERIOR TO THE PARASEGMENTAL BOUNDARY.
DEVELOPMENTAL STAGE: PRESENT AT 0-3 HRS OF EMBRYOGENESIS, MAXIMAL
EXPRESSION AT 3-6 HRS. STRONG RE-EXPRESSION IN FIRST-INSTAR
                                                                                                                                               Local Similarity
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PF00250; Fork_head; 1.
257 AAAAAAL 263
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                                                                                                                36202 MW;
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RESULT 27
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  GDC_BOVIN
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Infect. Immun. 58:550-556(1990).
Infect. Immun. 58:50-556(1990).
Infect. Immun. 58:50-556
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01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
01-CCT-2001 (Rel. 40, Last annotation update)
16-CCT-2001 (Rel. 40, Last annotation update)
Antigen 85-B precursor (85B) (Extracellular alpha-antigen) (Antigen 85
Antigen 85-B (Ag85B) (Mycolyl transferase 85B) (EC 2.3.1.-)
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Yamada T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=90129315; PubMed=2404875;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1768;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transferase; Acyltransferase; Antigen; Signal.
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                       Grave's disease carrier protein (GDC) (Mitochondrial solute carrier
                                                       Q01888;

Q1-APR-1993 (Rel. 25, Created)

Q1-APR-1993 (Rel. 25, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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protein homolog).
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100.0%; Pred. No. 40;
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5F2281BCC48AE30D CRC64;
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                                                                                                                                                                                330 AA
                                                               update)
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Qy
                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                    P54049;
01-OCT-1996 (Rel. 34, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
MEDLINE=96337999; PubMed=8688087
             STRAIN-JAL-1 / DSM 2661 / ATCC 43067
                                                                Archaea; Euryarchaeota; Methanococci; Meth
Methanocaldococcaceae; Methanocaldococcus.
                                                                                               Methanococcus jannaschii.
                                                                                                                 RPLPO OR MJ0509
                                                                                                                                                                                                              METJA
                             SEQUENCE FROM N.A
                                                       NCBI_TaxID=2190;
                                                                                                                                                                                               RLAO_METJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way enditied and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
TRANSMEM 132 152 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; S26596; S26596.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X66035; CAA46834.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mitochondrial transport protein associated with Grave's disease. DNA Seq. 3:71-78(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Sequence and pattern of expression of a bovine homologue of a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93091248; PubMed=1457817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLC25A16 OR GDA OR GDC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inner membrane (By similarity).
TISSUE SPECIFICITY: MOSTLY IN THYROID, LIVER, LUNG, KIDNEY AND
TO A LESSER EXTENT IN HEART AND SKELETAL MUSCLE.
DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Required for the accumulation of coenzyme A in the mitochondrial matrix (By similarity).
SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                            8 AAAAAAL 14
                                                                                                                                                                                                                                                                 2 AAAAAAL 8
                                                                                                                                                                                                                                                                                                                         Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                             218
330 AA;
                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   132
189
232
                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                     100.0%; Preu. ...
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     152
209
252
121
                                                                                                                                                                                                                                                                                                                                                                          36085 MW;
                                                                                                                                                                                                                                                                                                                                  4.1%; Score 7;
100.0%; Pred. N
                                                                            Methanococci; Methanococcales;
                                                                                                                                                                                                                                                                                                                                                                                         ω
                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                       4C614701D2B8DEA9 CRC64;
                                                                                                                                                                                           338 AA
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                                                                                                                                                                                                                                                                                                                  0; Indels
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GUB_FIBSU
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                                                                                                                                                                                        beta-glucanase (1,3-1,4-beta-D-glucan 4-glucanohydrolase) gene.",
J. Bacteriol. 172:3837-3841(1990).
-!- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glycosidic linkages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GUB_FIBSU
P17989;
                                                                                                                                                       in beta-D-glucans containing 1,3- and 1,4-bonds.
                                                                                                                                                                                                                                                      MEDIINE=90299807; PubMed=2193918;
Teather R.M., Erfle J.D.;
"DNA sequence of a Fibrobacter succinogenes mixed-linkage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Beta-glucanase precursor (EC 3.2.1.73) (Endo-beta-1,3-1,4 glucanase)
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND SEQUENCE OF 28-57. STRAIN-Isolate S85;
                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Fibrobacter/Acidobacteria group; Fibrobacter group
                                                                                                                                                                                                                                                                                                                                                                                                                                  Fibrobacter succinogenes (Bacteroides succinogenes)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             glucanase) (Lichenase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (1,3-1,4-beta-D-glucan 4-glucanohydrolase) (Mixed linkage beta-
                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ribosomal protein; Complete proteome. SEQUENCE 338 AA; 36751 MW; 63A6AF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D., Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I., Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kalne B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00466; Ribosomal_L10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001790; Ribosomal_L10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- FUNCTION: RIBOSOMÁL PRÓTEIN PO IS THE FUNCTIONAL EQUIVALENT OF E.COLI PROTEIN L10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rigr; MJ0509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               282 ALASKLP 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ALASKLP 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             U67500; AAB98499.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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DKK3_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local 9
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PIR; A44507; A44507.
HSSP; P23904; LAJK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09UBP4; 09UBP7;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [nterPro; IPR000757; Glyco_hydro_16.
                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dickkopf related protein-3 precursor (Dkk-3) (Dickkopf-3) (hDkk-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DKK3 OR REIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DKK3_HUMAN
                                                                                                                                                                                                                                                                                                Krupnik V.E., Sharp J.D., Jlang C., Robison K., Chickering T.W., Krupnik V.E., Sharp J.D., Jlang C., Robison K., Chang B., Amaravadi L., Brown D.E., Guyot D., Mays G., Leiby K., Chang B., Duong T., Goodearl A.D.J., Gearing D.P., Sokol S.Y., McCarthy S.A.; "Functional and structural diversity of the human Dickkopf gene
                                                                                                                                                 Tsuji T., Miyazaki M., Sakaguchi M., 1
"A REIC gene shows down-regulation in
human tumor-derived cell lines.";
                                                                                                                                                                                                                         Tanaka S., Sugimachi K., Sugimachi K.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20035735; PubMed=10570958;
                                                                                                                                                                                                                                                                                                                                                                rissum=Fetal brain;
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
Kobayashi K., Ouchida M., Tsuji T., Hanafusa H., Miyazaki M., Namba M., Shimizu N., Shimizu K.; "Reduced expression of the REIC/Dkk-3 gene by promoter-hypermethylation in human tumor cells.";
                                                                                                 Tate G.,
                                                                                                                                   Biochem. Biophys. Res. Commun. 268:20-24(2000)
                                                                                                                                                                                     MEDLINE=20119095; PubMed=10652205;
                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                       family
                                                                                     Submitted (NOV-1999) to the
                                                                                                              SEQUENCE FROM N.A
                                                  oubMed=11814687;
                                                               SEQUENCE FROM N.A.
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PS01034; GLYCOSYL H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAAAAAL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAAAAL 21
                                                                                                    Mitsuya T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycosidase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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NUCLEOPHILE (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY)
                                                                                        EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA TANDEM REPEATS OF P-X-S-S-S-X
                                                                                                                                                                               Inoue Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              update)
                                                                                                                                                                  human immortalized cells and
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                                                                                                                                                                                Namba M.;
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                                                                                                                                                          RESULT 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene 282:151-158(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                            Developmental protein;
                                                                                                                                                  MOUSE
                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                          Q60843;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Kruppel-like factor 2 (Lung kruppel-like factor).
                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                KLF2 OR LKLF.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                   KLF2_MOUSE
 SEQUENCE FROM N.A
                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTM: N-GLYCOSYLATED.
SIMILARITY: BELONGS TO THE DICKKOPF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF177396; AAF02676.1; --
AB033421; BAA85488.1; --
AB034203; BAA80548.1; --
AB035182; BAA87044.2; JOIN
AB045205; BAA87044.2; JOIN
AB045206; BAA87044.2; JOIN
AB045207; BAA87044.2; JOIN
AB045208; BAA87044.2; JOIN
AB045209; BAA87044.2; JOIN
                                                                                                                                                                                             338 AAAAAAL 344
                                                                                                                                                                                                                                                                                                                                                                                                                                               BC007660; AAH07660.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AB057804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AB057591; BAB84360.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AB045210; BAA87044.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                    HGNC:2893; DKK3.
                                                                                                                                                                                                                   8 AAAAAAL 14
                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                     350 AA;
                                                                                                                                                                                                                                          Conservative
                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            BAB84361.1;
                                                                                                                                                                                                                                                                                                           350
195
284
343
36
106
121
204
                                                                                                                                                                                                                                                                                        38291 MW;
                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                 4.1%;
                                                                                                                                                                                                                                                                                                                                                                                                               signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOINED.
JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOINED
                                                                                                                                                                                                                                                      Score 7; pred. No.
                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC · · ·)
N-LINKED (GLCNAC · · ·)
G -> R (IN REF · 4) · ·
                                                                                                                                                                                                                                                                                                                                   N-LINKED
                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. .
                                                                                                                                                                                                                                                                                                                                                                     DKK-TYPE CYS-2.
                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
DICKKOPF RELATED PROTEIN-3.
                                                                                                                                                                                                                                                                                                                                                                                 DKK-TYPE CYS-
                                   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein.
                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                        72F504122B40AFFE CRC64;
                                                                                                                                                                                                                                             Mismatches
                                                                                                                                          354 AA
                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                  Length 350;
                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                             . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
(POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a collaboration
                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                 0;
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RESULT
LIP2_HU
LIP2_HU
LIP2_HU
LIP2_HU
LIP2_HU
AC QS
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                 KLF2_HUMAN STANDARD; PRT; 355 AA. 09Y5W3; Q9UKR6; Q9UJS5; 30-MAY-2000 (Rel. 49. Created) 15-JUN-2002 (Rel. 41. Last sequence update) 15-JUN-2002 (Rel. 41. Last annotation update) Kruppel-like factor 2 (Lung kruppel-like factor).
Kozyrev S.V., Hansen L.L., Poltaraus A.B., Domninsky D.A.,
                                                                                                                                                                                                                                        Homo Sapiens (Human).

Homo Sapiens (Human).

Finkarvota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HUMAN
                                                                   MEDLINE=99231781; PubMed=10217429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
Transcription regulation; Activator; Zinc-finger; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO0048; ZINCFINGER.
ProDom; PD000003; Znf_C2H2; 2.
SMART; SM00355; ZnF_C2H2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBI outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is so long as its content is in no way entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:1342772; K1f2.
InterPro; IPR000822; Znf_C2H2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00096; zf-C2H2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSFAC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U25096; AAA86728.1; -. HSSP; P08047; 1SP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           multigene family.";
Mol. Cell. Biol. 15:5957-5965(1995).
-!- FUNCTION: BINDS TO THE CACCC BOX IN THE BETA-GLOBIN GENE PROMOTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *Anderson K.P., Kern C.B., Crable S.C., Lingrel J.B.,
"Isolation of a gene encoding a functional zinc finger protein
homologous to erythroid Kruppel-like factor: identification of a new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=96025976; PubMed=7565748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6 X CBA; TISSUE=Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AND ACTIVATES TRANSCRIPTION. Similarity). SUBCELLULAR LOCATION: Nuclear (By similarity). TISSUE SPECIFICITY: PREDOMINANT EXPRESSION IN THE LUNGS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                225 AAAAAAL 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 AAAAAAL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 354 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.1%; Score 7;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37700 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ? protein; Repeat
70 POLY-pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C2H2-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZINC FINGERS
C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLY-ALA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C4A99D018AC5BAF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 354;
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                                                                                                                                                                                             RESULT 34
                                                                                                             Best
                                                                                                 Matches
                                                                                                                        Query Match
                                                                                                                                                                  CONFLICT
CONFLICT
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ProDom; pD000003; znf_C2H2; 2.

SMART; SM00355; znF_C2H2; 3.

PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.

PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                    DOMAIN
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Lee H.J., Kim M.K., Kim Y.H., Seo J.M., Lee H.M., Chung H.J.,

Lee H.J., Kim M.K., Kim Y.H., Seo J.M., Lee H.M., Chung H.J.,

Sohn M.Y., Hwang S.Y., Im S.U., Jung E.J., Kim J.C.,

"A catalogue of genes in the human dermal papilla cells as identified by expressed sequence tags.",

"A catalogue of genes in the human dermal papilla cells as identified by expressed sequence tags.",

Submitted (NOY-1999) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: BINDS TO THE CACCC BOX IN THE BETA-GLOBIN GENE PROMOTER AND ACTIVATES TRANSCRIPTION (BY SIMILARITY).

-!- SUBGELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

-!- SUBGELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                   Transcription regulat
                                                                                                                                                                                                                          LN_FING
                                                                                                                                                                                                                                        ZN_FING
                                                                                                                                                                                                                                                                                   NIAMOC
                                                                                                                                                                                                                                                                                               DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/orsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000822; Znf_C2H2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSFAC; T04958;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-99389728; PubMed=10458913; Wani M.A., Conkright M.D., Jeffries S., Hughes M.J., Lingrel J.B.; "CDNA isolation, genomic structure, regulation, and chromosomal localization of human lung kruppel-like factor."; Genomics 60:78-86(1999).
                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEBS Lett. 448:149-152(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Structure of the human CpG-island-containing lung Kruppel-like factor (LKLF) gene and its location in chromosome 19p13.11-13 locus.";
                                    226 AAAAAAL 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                    602016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF123344; AAD25076.1; -. AF134053; AAD55891.1; -. AF205849; AAF13295.1; -.
                                                               8 AAAAAAL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P08047;
                                                                                              Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                              HGNC:6347; KLF2.
                                                                                                                                                 355 AA;
                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                        regulation; Activator; Zinc-finger; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1SP2.
                                                                                     100.08; ++
                                                                                                                                                 37419 MW;
                                                                                                                                                                                                                                                                                                                                     protein;
                                                                                                                        4.18;
                                                                                                    Score 7; ; Pred. No.
                                                                                                                                                           C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
S -> N (IN REF.
L -> P (IN REF.
P -> S (IN REF.
L -> M (IN REF.
                                                                                                                                                                                                                                                                                                                   POLY-PRO.
                                                                                                                                                                                                                                                                         POLY-ALA.
                                                                                                                                                                                                                                                             ZINC FINGERS.
                                                                                                                                                                                                                                                                                       POLY-PRO.
                                                                                                                                                                                                                                                                                                      POLY-GLY.
                                                                                                                                           D5849C831D676AE1 CRC64;
                                                                                        Mismatches
                                                                                                     DB 1;
o. 44;
                                                                                      0;
                                                                                                                Length 355;
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BET3\_MESAU

BET3\_MESAU

STANDARD;

367 AA

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GN DT DT AC
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                                                                                                              RESULT
                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                          Query Match
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Bukaryota; Metazoa; Chordata; Craniata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BETA3 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         009029;
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                regulator of BETA2 and MyoD responsive genes.";

Mol. Cell. Biol. 16:626-633(1996).

-i- FUNCTION: INHIBITS DNA BINDING OF TCF3 (E47) HOMODIMERS AND TCF3

-i- FUNCTION: INHIBITS DNA BINDING OF TCF3 (E47) HOMODIMERS AND TCF3

(E47) / NEUROD1 HETERODIMERS AND ACTS AS A STRONG REPRESSOR OF NEUROD1 AND MYOD-RESPONSIVE GENES, PROBABLY BY HETERODIMERIZATION WITH CLASS A BASIC HELIX-LOOP-HELIX FACTORS. DESPITE THE PRESENCE OF AN INTACT BASIC DOMAIN, DOES NOT BIND TO DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peyton M., Stellrecht C.M.M., Naya F.J., Huang H.-P., Samora P.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96140430; PubMed=8552091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isai M.-J.; ^{\prime}BETA3, a novel helix-loop-helix protein, can act as a negative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSFAC; T01674;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; S80870; AAB50691.1; -.
                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00353; HLH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00010; HLH; 1
                                                                                                 BACSU
                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                      Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50888;
                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001092; HLH_basic.
                           P42253; 034388;
01.NOV-1995 (Rel. 32, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                   DNA_BIND
Hypothetical protein ycbU precursor. YCBU.
                                                                                    CBU_BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE SPECIFICITY: KIDNEY, LUNG, BRAIN AND PANCREAS (INSULINOMA). SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF TRANSCRIPTION FACTORS. "ATONAL" SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCULULAR LOCATION: Nuclear (Potential).
                                                                                                                                                          314 AAAAAAL 320
                                                                                                                                                                                      8 AAAAAAL 14
                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 39, Rel. 39, Rel. 39, Rel. 40, Rel. 40,
                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                           A.
                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                      Transcription
                                                                                                                                                                                                                                                                                                                                                                                                                     HLH_1; 1.
HLH_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                              35905 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                    Score 7; I
; Pred. No.
                                                                                                                                                                                                                                                                                                                      BASIC DOMAIN
                                                                                                                                                                                                                                                                                           POLY-ALA
                                                                                                                                                                                                                                                                                                        HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                      POLY-GLY
                                                                                                                                                                                                                                                                                                                                                                                                         regulation; Repressor.
                                                                                        PRT;
                                                                                                                                                                                                                                                                             6CAB9AFF96E85F77 CRC64;
                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                    Length 367;
                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                             0;
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RA MEDLLINE YOU 44 U.D.; FULL PROPERTY.;

RA AZEVEDO V. BERTEYO M.G.; BESSIEVES P., BOLOTIN A., BOTCHERT S.,

RA AZEVEDO V., BERTEYO M.G.; BESSIEVES P., BOLOTIN A., BOTCHERT S.,

RA BOTILES R., BOURSIEY L., BYANG A., BYANDANO V., CATTEY N.M.,

RA BOTILES R., BOURSIEY L., BYANG A., BYANDANO V., CATTEY N.M.,

RA BOTILES R., BOURSIEY L., BYANG A., BYANDANO V., CATTEY N.M.,

RA Choi S.K., COdani J.J., CONNETTON I.F., Cummings N.J., Daniel R.A.,

RA Choi S.K., COdani J.J., CONNETTON I.F., Cummings N.J., Daniel R.A.,

RA Choi S.K., COdani J.J., CATTEY N.M.,

RA Choi S.K., COdani J.J., FADYET C., FERTATI E., FOLIGY D.,

RA CHILAR Y., Devine K.M., DUSTETHOFT A., GALIZZI A., GALIETON N.,

RA FILZ C., FUJITA M., FUJITA Y., FUMBE S., GALIZZI A., GALIETON N.,

RA GLISEPPI G., GUY B.J., HAGA K., HAICCH J., HARWOOD C.R., HENAUT A.,

RA HILDERT H., HOISAPPEI S., HOSONO S., HULLO M.F., ITAYA M., JONES L.,

RA KURITA K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,

RA KURITA K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,

RA KURITA K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,

RA NOONE D., O'Reilly M., Ogawa K., O'GYWATA A., Oudega B., Park S.H.,

RA NOONE D., O'Reilly M., O'GAWA K., O'GYWATA A., O'DAYATA A.,

RA PATRO V., POHI T.M., POTTETELLE B., RAPOPOTT G., Reyn M., Reynolds S.,

RA RIEGER M., RIVOLTA C., Rocha E., Roche B., Rose M., Sadale Y.,

RA SATO T., SCANIAN E., SCHOETER J., SCOTFONE F.,

SCANIAN S., SCHOETER J., SCHOETER P., SONGONE F.,

RA SATORIAN S., VANGENDA M., VANNEET F., TORSEN M.,

RA TAKEUCH M., TAMAKOSHI A., TANAKA T., TENSKA T., TENSKATU K.,

RA TAKEUCH M., TAMAKOSHI A., TANAKA T., TENSKA T., TENSKA T., TAKABASHI H., TAKABATU K.,

RA VIATI A., WAIDAT A., YAMAMOTO H., VANNEET F., VASSAROTTI A.,

RA VIATI A., WAIDAT A., YAMAMOTO H., YAMANDE K., YASAMOTO K., YATA K.,

RA YOSHIGA K., YOSHIKAWA H.F., ZUMSTEIN E., YOSHIKAWA H., DANCHIN A.;

THE COMPLETE P., WAIDAN S., WANGENDO M., VANNEET F., VASHAROTTI A.,

THE COMPLETE P., WAIDANO M., MOSTILVE BACCETIUM BACILLUS BACCETIUM BACILLUS BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "A 32 kb nucleotide sequence from the region of the lincomycin-
resistance gene (22-25 degree) of the Bacillus subtilis chromosome and
identification of the site of the lin-2 mutation.";
submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus subtilis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kumano M., Tamakoshi A., Yamane K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ogawa K.-I., Akagawa E., Nakamura K., Yamane K.; "Determination of a 21548 bp nucleotide sequence around the degrees region of the Bacillus subtilis chromosome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95219079; PubMed=7704254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-319 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 390:249-256(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Microbiology 141:269-275(1995).
                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-168
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-147 FROM N.A.
                                                                                                                                                                                                 -!- CAUTION: Ref.3 sequence differs from that shown due to two
                                                                                                                                                                                                                                                                                                  peptidase of Bacillus subtilis.";
                                                                                                                                                                                                                                                                                                                                                      Awade A., Cleuziat
                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=92339527; PubMed=1353026;
                                                                                                                                                                                                                                                                                                                              wade A., Cleuziat P., Gonzales T., Robert-Baudouy J.; Characterization of the pop gene encoding the pyrrolidone carboxyl
                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO CLASS-V OF PYRIDOXAL-PHOSPHATE-DEPENDENT
                                                                                                                                                                                 frameshifts.
                                                                                                                                                                                                                                   AMINOTRANSFERASES.
                                                                                                                                                                                                                                                                               305:67-73(1992)
                                                                                                                                                                                                                                                                                                                                                              Gonzales T., Robert-Baudouy J.;
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FL_ORYSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local
                                                                                                                                                                                                              MEDLINE=98151445; PubMed=9482818;

Kyozuka J., Konishi S., Nemoto K., Izawa T., Shimamoto K.;

Town regulation of RFL, the FLO/LFY homolog of rice, accompanied proc. Natl. Acad. Sci. U.S.A. 95:1979-1982(1998).

1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR (BY SIMILARITY).

1- SUBCELLULAR LOCATION: Nuclear (Probable).

1- TISSUE SPECIFICITY: In very young panicle but not in mature florets, mature leaves, roots or apical meristems.

1- SIMILARITY: BELONGS TO THE FLO / LFY FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
           DOMAIN
                                 Nuclear protein;
DOMAIN 22
                                              Pfam; PF01698; FLO_LFY; I.
Transcription regulation; Activator; DNA-binding;
                                                                                EMBL; AB005620; BAA21547.1; -. InterPro; IPR002910; FLO_LFY.
                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridipiantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FL_ORYSA
024175;
                                                                                                                                                                                                                                                                                                                                                                             STRAIN-CV.
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Putative transcription factor FL (RFL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein; Signal; Transferase; Aminotransferase; Pyridoxal phosphate; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AB000617; BAA22227.1; -- EMBL; 299105; CAB12060.1; -- CDS. EMBL; D30808; -; NOT_ANNOTATED_CDS. EMBL; X66034; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00266; aminotran_5; 1.
PROSITE; PS00595; AA_TRANSFER_CLASS_5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SubtiList; BG11176; ycbU.
InterPro; IPR000192; AminotransfV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               265 AAAAALS 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 AAAAALS 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                Toride; TISSUE=Panicle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       370 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31
207
92
133
319
Developmental protein.
37 POLY-PRO.
204 POLY-GLY.
217 POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30
370
207
92
133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40809 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.1%; Score 7; DB 1
100.0%; Pred. No. 45;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Y -> S (IN REF.
L -> V (IN REF.
D -> I (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PYRIDOXAL PHOSPHATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL PROTEIN YCBU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38C91AF0FC27DF53 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       389 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
o. 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,:
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Qy
           Query Match
Best Local Similarity
7; Conserve
                                                                                               RESULT 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SQ
                                                                                                                                 DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                       SEQUENCE
                                                                                    DOMAIN
                                                                                             DNA_BIND
                                                                                                          DOMAIN
                                                                                                                     DOMAIN
                                                                                                                                                            PROSITE; PS00027; HOMEOBOX_1; 1. PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                            TRANSFAC; T03420; --
Genew; HGNC:4979; HLXB9.
MIM; 142994; --
                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                               Homeobox; DNA-binding; Nuclear protein; Transcription regulation DOMAIN 39 48 POLY-GLY.
                                                                                                                                                                                      SMART; SM00389;
                                                                                                                                                                                                 PRINTS; PR00024; HOMEOBOX
ProDom; PD000010; Homeobox
                                                                                                                                                                                                                                                                                                                                                                                                           Harrison K.A., Druey K.M., Deguchi Y., Tuscano J.M., Kehrl J.H.;

"A novel human homeobox gene distantly related to proboscipedia is
expressed in lymphoid and pancreatic tissues.";

J. Biol. Chem. 269:19968-19975 (1994)

-!- FUNCTION: PUTATIVE TRANSCRIPTION FACTOR.

-!- SUBCELLULAR LOCATION: Nuclear.

-!- TISSUE SPECIFICITY: EXPRESSED IN LYMPHOID AND PANCREATIC TISSUES.

-!- SIMILARITY: CONTAINS 1 HOMEOBOX DOMAIN.
                                                                                                                                                                                                                     InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                EMBL; U07663; AAB60647.1;
HSSP; P14653; 1B72.
                                                                                                                                                                                                                                                                                                      EMBL; U07664; AAB60647.1;
                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-94327547; PubMed-7914194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Placenta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eucese
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HB9_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Loca1
8 AAAAAAL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             378 AAAAAAL 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 AAAAAAL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
                                                                     401 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                     Conservative
                                                                                                        120
169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          389 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                      HOX; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                               Homeobox; 1.
                              100.0%;
                                                                 40932 MW;
                        4.1%; Score 7; DB 1; 100.0%; Pred. No. 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.08; F1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42530 MW;
                                                                                                                                                                                                                                                                                        JOINED.
                    0;
                                                                            HOMEOBOX.
                                                                                                  POLY-ALA.
POLY-ALA.
                                                                                                                      POLY-GLY.
                                                            0006AEAD71D594FE CRC64;
               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 7;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLY-ALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5132AA6A34B0868A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                   Length 401;
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        0;
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170 AAAAAAL 176

RESULT 38 NU4M\_ASCSU

NU4M\_ASCSU

STANDARD;

PRT;

409 AA.

01-MAR-1992 (Rel. 21, Created)
01-NOY-1995 (Rel. 32, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
NADH-ubiquinone oxidoreductase chain 4 (EC 1.6.5.3).

Ascaris suum (Pig roundworm) (Ascaris lumbricoides).

Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;

Ascaris

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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            TUD4_AGRVI
                           RESULT 40
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REVISIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The human ribosomal protein genes: sequencing and comparative analysis of 73 genes.";
Genome Res. 12:379-390(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yoshihama M., Uechi T., Asakawa S., Kawasaki K., Kato S., Higa S., Waeda N., Minoshima S., Tanaka T., Shimizu N., Kenmochi N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Lymphoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21864036; PubMed=11875025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Colon, Eye, Muscle, Pancreas, and Skin;
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                                                                                                                                                                                             CONFLICT
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                                                                                                                                                                                                                                          CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                   SWISS-2DPAGE; P36578; HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
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                                                                                                                                                                                                                                                                                    Ribosomal
                                                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                               PROSITE; PS00939; RIBOSOMAL_L1E; 1.
                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                       Genew;
                                                                                                                                                                                 SEQUENCE
TUD4_AGRVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
SIMILARITY: BELONGS TO THE L4E FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                      L; BC001365; AAH01365.1; BC005817; AAH05817.1; BC007259; AAH07259.1; BC007248; AAH07748.1; BC007996; AAH07996.1; BC009888; AAH09888.1; BC010151; AAH10151.1;
                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                 S37197; S37197
S39803; S39803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X73974; CAA52154.1; .
                                                                                                                                                                                                                                                                                                                                           180479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L20868; AAA60281.1; ALT_SEQ. D23660; BAA04887.1; -
                                                                                                                                                                                                                                                                                                                                                                                                               AB061820; BAB79458.1;
                                                                     355 AAAAAAL 361
                                                                                                                                                                                                                                                                                                                                                         HGNC:10353; RPL4.
                                                                                                 8 AAAAAAL 14
                                                                                                                                                                                                                                                                                      protein.
                                                                                                                                                                                                                                                                                                                             IPR002136; Ribosomal_L4/LlE
                                                                                                                                                                                                                            364
36
63
                                                                                                                                                                                      427 AA;
                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                               Ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                AAH14653.1;
       STANDARD;
                                                                                                                                                                                          47697 MW;
                                                                                                                                              100.0%;
                                                                                                                                                              4.18;
                                                                                                                                                                              S -> M (IN REF. 1).
S -> R (IN REF. 1).
V -> F (IN REF. 1).
V -> F (IN REF. 1).
MISSING (IN REF. 1).
W; 4785ED31600777
                                                                                                                                    0; Mismatches
                                                                                                                                                              Score 7;
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                                                                                                                                                   Pred. No.
                                                                                                                                                                                         4785ED31699CD792 CRC64;
            PRT;
            438 AA
                                                                                                                                                    DB 1;
b. 51;
                                                                                                                                                                    Length 427;
                                                                                                                                              0;
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SON DE L'ALLE L'

Genetics 130:471-498(1992) and Ascaris suum.

- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol

Okimoto R., Macfarlane J.L., Clary D.O., Wolstenholme D.R.; "The mitochondrial genomes of two nematodes, Caenorhabditis elegans

TISSUE-Body wall muscle, and Egg; MEDLINE-92201635; PubMed=1551572;

SEQUENCE FROM N.A. NCBI\_TaxID=6253;

SEQUENCE FROM N.A. NCBI\_TaxID=9606;

Eukaryota; Metazoa; Chordata; Craniata; Vercebraca; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;

Craniata; Vertebrata; Euteleostomi;

Homo sapiens (Human).

OR RPL1.

MEDLINE-94092742; PubMed-8268230; Bagni C., Mariottini P., Annesi F., Amaldi F.; Bagni C., Mariottini P., Annesi F., amaldi F.; Human ribosomal protein L4: cloning and sequencing of the cDNA and primary structure of the protein.

Biochim. Biophys. Acta 1216:475-478(1993).

밁 Qy

147 SLVYFDF 153

68 SLVYFDF 74

Query Match Matches

Local Similarity es 7; Conserv

Conservative

100.0%; tive 0; 4.1%;

Mismatches

0;

0;

Score 7; ; Pred. No.

DB 1;

Length 409;

SEQUENCE Oxidoreductase;

409 AA;

NAD; Ubiquinone; Mitochondrion. AA; 47064 MW; A4B135C1CA5587B6 CRC64;

EMBL; X54253; CAA38170.1; -.

PIR; S26021; S26021. InterPro; IPR001750; Oxidored\_q1.

Pfam; PF00361; oxidored\_q1;

RESULT 39

RL4\_HUMAN

STANDARD;

PRT;

427 AA.

p36578; p39029; Q969Z9; 01-JUN-1994 (Rel. 29, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) 60s ribosomal protein L4 (L1).

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Search completed: July 6, 2003, 14:20:46 Job time: 20 secs
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                                                                                                                                                                                            Ouery Match
Best Local Similarity 100.0%; p
Matches 7; Conservative 0;
                                                                                                                                                                     EMBL; U25634; AAA68699.1; ... InterPro; IPR005346; UPF0125. Pfam; P803658; UPF0125; 1. Plasmid; Oxidoreductase; NADP. SEQUENCE 438 AA; 44730 MW; 38C75BAFFFB0636B CRC64;
                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensee(isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                  Crouzet P., Otten L.;

"Sequence and mutational analysis of a tartrate utilization operon from Agrobacterium vitis.";

J. Bacteriol. 177:6518-6526(1995).

-i. FUNCTION: DEGRADES AN UNIDENTIFIED TOXIC PRODUCT FROM THE FIRST STEP OF TARTRATE DEGRADATION.

-i. CATALYTIC ACTIVITY: D-glycerate + NAD(P)(+) = hydroxypyruvate +
                                                                                                                                                                                                                                                                                                                                                                                                        NAD(P)H.
-i- PATHWAY: Tartrate degradation; second step.
                                                                                                                                                                                                                                                                                                                                                                                         -!- INDUCTION: BY TARTRATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Rhizobiaceae; Rhizobium. NCBI_TaxID-373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q44472;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Putative hydroxypyruvate reductase (EC 1.1.1.81).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96062236; PubMed=7592429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Agrobacterium vitis (Rhizobium vitis). Plasmid pTrAB4.
                                                                276 AAAAAAL 282
                                                                                            8 AAAAAAL 14
                                                                                                                            4.1%; Score 7; DB 1; Length 438; 100.0%; Pred. No. 52;
                                                                                                                  Mismatches
                                                                                                             0; Indels
                                                                                                             0;
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Title:
Perfect score:
Sequence:
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                               Score
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Match
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Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                Q9x0g9 thermotoga Q8sIr2 oryza sativ Q9b1j7 drosophila Q93np5 escherichia Q93nc4 rhizobium m Q9vv18 drosophila Q996t0 rhizobium 1
                                                                                                                                                                                             Q9pc85 xylella fas
Q94ea6 oryza sativ
Q9vqm0 drosophila
Q46112 drosophila
                                     Q9ngi9
Q9ngi8
Q9ngi7
                                                                                                                                                                                                                                                                            Description
    9 drosophila
8 drosophila
7 drosophila
4 drosophila
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5 Q926C3
5 Q8U9L5
5 Q9RTG4
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2 Q919S1
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08X1XZ
08X1XZ
08JSZ1
09JSZ1
09STV5
09STV5
09SYV1
09SYV2
09M7S3
08VQP7
002Z1
09W2T0
09W2T0
09WE6
08T6B6
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08T6B6
08T6B6
09FRV2
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09FRV2

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Q99013
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Q94239
Q94239
Q94102
Q94102
Q95260
Q9
Q51489 pseudomonas
Q91424 pseudomonas
Q91424 pseudomonas
Q914662 prucella ab
Q89mx7 anabaena sp
Q9vpl1 drosophila
Q91414 ralstonia s
Q922f9 mus musculu
Q91412 oryza sativ
Q8xfh6 salmonella
Q9yba7 aeropyrum p
Q9smy4 arabidopsis
Q926G3 rhizobium m
Q8u915 agrobacteri
Q9rty4 deinococcus
Q9nmr9 leishmania
Q91931 white spott
Q9pez5 xylella fas
Q91783 chlamydophi
                                                                                                                                                                                                                                                                                                                Q94102 oryza sativ
Q94792 mus musculu
Q9842 arabidopsis
Q9v195 drosophila
Q9v195 drosophila
Q9ct43 mus musculu
Q94gr5 oryza sativ
Q9kzf6 streptomyce
Q07218 mycobacteri
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09l111 white spot

09bmp6 culicoides

09yh51 pseudopleur

09y9013 pseudopleur

09y327 oryza sativ

09430 oryza sativ

094291 oryza sativ

094291 oryza sativ

094293 oryza sativ

094293 oryza sativ

094295 oryza sativ

094639 oryza sativ

094639 oryza sativ

09474 human immun

053557 salmonella

09sew0 lilium long
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0960rl drosophila
09bmz8 drosophila
09bmz8 drosophila
09c2d2 drosophila
09c2d1 drosophila
09c2d1 drosophila
09c2d1 drosophila
09c2d1 drosophila
09c2d1 drosophila
09bmz9 drosophila
09wkj1 drosophila
09wkj1 drosophila
09wkj8 bacillus sp
09w2t1 drosophila
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Q9firv3 oryza sativ
Q9firv2 oryza sativ
Q9hkb4 thermoplasm
Q9v9f7 drosophila
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Q8x1x2 aspergillus
Q9x1x2 nelsseria m
Q991x5 rhizobium 1
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Q957s1 drosophila
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002427 ciona intes
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Q9w0e6 drosophila
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Database :

Word size Searched:

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DR PRIMTS; PRO1021; OMPA; 1.

DR PRIMTS; PRO1021; Ompa; 1.
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                                                                              Query Match
Best Local Similarity
                                                Matches
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01-OCT-2000 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20365717; PubMed=10910347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xylella fastidiosa.
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                                                                                                                                                                                                                        Complete proteome.
                                                                                                                                                                                                                                                             ProDom; PD000930; Bac_OmpA; 1.
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
                                                Conservative
                                                                                                                                                                                                                                                                                                       OMPADOMAIN.
                                                                                                                                                                                          20431 MW; C8DD2F6233DB0C92 CRC64;
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                                                                              5.8%; Score 10; DB 16; Length 186; 100.0%; Pred. No. 0.095;
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0927C5
09N7X4
09X6J7
09FTW8
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Q02667
Q02667
Q9LN12
Q9PJE0
Q946V3
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                                                    Mismatches
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0927c5 chlamydia p
0917x4 leishmania
09x6j7 vibrio chol
09ftw8 oryza sativ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QU2667 podospora a
Q91n12 arabidopsis
Q9pje0 chlamydia m
Q946v3 zea mavs /m
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Q8vqt4 vibrio chol
Q02667 podospora a
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RX MEDLINE-20165006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Appayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Abril J.F., Apbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local
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01-DEC-2001 (TremBLre
01-JUN 2002 (TremBLre
p0435H01.25 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9VQMO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases EMBL; AP003142; BAB63529.1; -. InterPro; IPR000862; RFCdomain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=CV. NIPPONBARE; Sasaki T., Matsumoto T., Yamamoto K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOC protein.
TOC OR CG9660.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4530;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P0435H01.25.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q94EA6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           170 AAAAAALSV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108 TDERGSREYN 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 AAAAAALSV 16
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9; Conser
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(TrEMBLrel. 19,
(TrEMBLrel. 21,
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Last sequence update)
Last annotation update)
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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RESULT 4
046112
ID 0461
AC 0461
DT 01-J
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DT 01-W
OS Dros
OC Euka
OC Pter
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RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lii Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Nelson K.A., Nixon K., Nusskern D.R., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K.S., Singson M., Stupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Spratling A.C., Turner R., Venter E., Wang A.H., Wang X.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R., F., Zaveri J.S., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Glbbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RA Glbbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RB EMBL, AE003581, AAF51145.1;
DR EMBL, AE00369; THIOL_PROTEASE_HIS; UNKNOWN 1.
SEQUENCE 2168 AA; 234786 MW; F26344DB2ElCAFD4 CRC64;
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                                                                                                                                                                                                            Grammont M., Dastuque B., Couderc J.L.;
"The Drosophila toucan (toc) gene is required in germline cells for the somatic cell patterning during cogenesis.";
Development 124:4917-4926(1997).
EMBL; Y14157; CAA74574.1;
FlyBase; FBgn0015600; toc.
InterPro; IPR000199; SHprot_acsite.
PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
SEQUENCE 2176 AA; 235405 MW; 35ABBDE00B49EFC7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1998 (TrEMBLrel.
01-JUN-1998 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOUCAN protein. TOC OR CG9660.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-98090047; PubMed-9362455;
                                                                                                                                                     ocal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity es 9; Conserv
973 AAAAAALSV 981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               979 AAAAAALSV 987
                                                       8 AAAAAALSV 16
                                                                                                                      Similarity 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAAAALSV 16
                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                     100.0%;
                                                                                                                                                                          5.2%;
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100.0%; Pred. No
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06, Last sequence update)
20, Last annotation update)
                                                                                                   %; Score 9; DB 5
%; Pred. No. 7.8
0; Mismatches
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                                                                                                                                  DB 5;
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                                                                                                         0;
                                                                                                                                                              Length 2176;
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Q9X0G9
                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local :
                                                                                                             Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                           "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, clone:P0506B12.";
                                                                                          SEQUENCE
                                                                                                                                                               STRAIN=CV. NIPPONBARE;
Sasaki T., Matsumoto T.,
                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                               Oryza sativa (japonica cultivar-group).
                                                                                                                                                                                                                                                                                                         01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative UDP-glucuronic acid decarboxylase.
                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                       P0506B12.31.
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Welson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

Heidelberg J., Sutton G.G., Fletschmann R.D., Eisen J.A., White O.,

Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

"Evidence for lateral gene transfer between Archaea and Bacteria from

Nature 393-323-329(1999).

EMBL; AE001768; AAD36157.1; -.

TIGR; TM1080; -. LED003500, Eib. (2-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003500; Rib/Gal_isomrase.
Pfam; PF02502; LacAB_rpiB; 1.
TIGREPAMS; TIGR00689; rpiB_lacA_lacB; 1.
Isomerase; Complete proteome.
SEQUENCE 143 AA; 15867 MW; 3E17D72A10FFCCBD CRC64;
                                                                                                                                                                                                                            NCBI_TaxID=39947
                                                                                                                                                                                                                                                                                                                                                                                 Q8S1R2;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                           Local Similarity hes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-MSB8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermotoga maritima.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sugar-phosphate isomerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity les 8; Conserv
                                                                                   AP003271; BAB89759.1; -
NCE 249 AA; 26592 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 NYLLGKGI 137
64 SKLPSLVY 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 NYLLGKGI 27
                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                        4.7%; Score 8;
100.0%; Pred. No.
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100.0%; Pred. N
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                                                                                                                                                               Yamamoto K.;
                         0;
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                                                                                7954F613B241E81F CRC64;
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                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               No.
                                                                                                                                                                                                                                                                                                                                                                                         249 AA.
                                                   DB 10; Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 16;
o. 7.5;
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                        0;
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                      0;
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                    Gaps
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                    0,
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SKLPSLVY 32

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ACCOMPAGNATION OF THE PROPERTY OF THE PROPERTY
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Best Local :
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                                                                                                          Matches
                                                                                                                                 Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DNA-binding transcriptional repressor giant (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thomas J., Arnosti D.N.; submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases EMBL; AF356543; AAK28631.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila hydei (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q93NP5 PRELIMINARY;
Q93NP5;
01-DEC-2001 (TremBLrel. 19,
01-DEC-2001 (TremBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FlyBase; FBgn0044278; Dhyd\gt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=7224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WBWC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wbwc
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                                                                                                                                                                                                                Interpro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
SEQUENCE 268 AA; 31176 MW; ClEF30
                                                                                                                                                                                                                                                                                                               of 0104 specific genes.";
Gene 270:231-236(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                             Wang L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21297197; PubMed=11404020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia
                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                         EMBL; AF361371; AAK64375.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                   Reeves P.R.
                                                                                                                                                                                                                                                                                                                                                                     Sequence of the E. coli 0104 antigen gene cluster and identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31
239 TGVIYTGV 246
                                                     42 TGVIYTGV 49
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8; Conserv
                                                                                                          8
                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAAAAALS 38
                                                                                                                                                                                                                                                                                                                                                                                                                          Briggs C.E., Rothemund D., Fratamico P., Luchansky J.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   258 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26948 MW; 09C0CA545CE455EA CRC64;
                                                                                                  4./,,
100.0%; P1
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100.0%; Pred. No.
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Last annotation update)
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                                                                                                                                                             Score 8; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                         Pred. No.
                                                                                                                                                                                                                        C1EF30C136A668F7 CRC64;
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                                                                                                             Mismatches
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lo. 12;
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RESULT 9

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В
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F., RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards G.C., Champe M., Pfeiffer B.D., RA George R.A., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Holl J., Ashraktaroglu L., Beasley E.M., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Ballew R.M., Basu A., Baxndale J., Bayraktaroglu L., Beasley E.M., RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolthakov S., RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Dev I., Dietz S.M., de pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.,
"Nucleotide sequence and predicted functions of the entire
sinorhizobium meliloti pSymA megaplasmid.",
Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
EMBL, AE007220; AAK64932.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Hypothetical protein RA0274. RA0274 OR SMA0520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plasmid pSymA (megaplasmid 1).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q930C4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rhizobium meliloti (Sinorhizobium meliloti)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21396509; PubMed=11481432;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmid; Hypothetical protein; Complete proteome. SEQUENCE 280 AA; 30615 MW; FF533F65700FC352 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9VVI8;
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                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CG6273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CG6273 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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100.0%; Pred. No.
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RESULT 11

O986T0

ID O986T0

AC O986T1

D1 O1-OCT

DT O1-OCT

DT O1-OCT

DT Hizol

GN MLR72:

OS Rhizol

OC Phyll(
OX NCBI.'

RN (II)

RP SEQUE!

RA Kanek(
RA Watan

RA Kanek

RA Mochi.

RA Mochi.

RA Mochi.

RA Mochi.

RA ITakeu

RT Mesor

RI DNA R

DR Interl

DR Interl

DR PROSI

KW Hypot.

SO SEQUE:
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RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McIeod M.P., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McIeod M.P., McPherson D.
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Massarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang X.-Y., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RT "The genome sequence of Drosophila melanogaster.";
DR RIJBASE, FB9003523 AAR49323.1;
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REMBL, AE003523 AAR49323.1;
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DR Flybase, FB90036739; CG6273.
SO SEQUENCE 306 AA; 30932 MW; 8C26CEOBEEDDADA3 CRC64;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=MAFF303099;
MEDLINE=21082930; PubMed=11214968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q986T0 PRELIMINARY; PRT; 316 AA. Q986T0; Created) Q1-OCT-2001 (TrEMBLrel. 18, Created) Q1-OCT-2001 (TrEMBLrel. 18, Last sequence update) Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=381;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein mlr7223.
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269 AAAAAALS 276
                                                            8 AAAAAALS 15
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                                                                                                                              8;
                                                                                                                                                      Similarity
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                                                                                                                        Conservative
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100.0%; Pred. No.
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Q9NGIB
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                                                                     Query Match
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Q9NGI9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                           Begun D.J., Whitley P.; "Reduced X-linked nucleotide polymorphism in Drosophila simulans."; Proc. Natl. Acad. Sci. U.S.A. 97:5960-5965(2000).
EMBL; AF252667; AAF68049.1.; -.
                                                                                               SEQUENCE
                                                                                                         NON_TER
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                                                                                                                                                                                                     STRAIN-SIM4;
                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                             Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                  Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                               Drosophila simulans (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                       NCBI_TaxID=7240;
                                                                                                                                                                                                                                                                                                            Eyelid (Fragment).
                                                                                                                                                                                                                                                                                                                                                               Q9NGI8;
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EMBL; AF255666; AAFE8048.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila simulans (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscc
Ephydroidea; Drosophilidae; Drosophila.
                                                           Local
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
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269 AAAAAALS 276
                     8 AAAAAALS 15
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                                          Similarity 100.0%; 18; Conservative 0;
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                                                                                            324 AA;
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                                                                                    32373 MW; 5ECC6A8C4546A230 CRC64;
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                                                    4.7%; Score 8;
100.0%; Pred. No.
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100.0%; Pred. No
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                                                                DB 5;
                                                                                                                                                                                                                                                                                                                                                                   324 AA.
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RESULT 14
Q9NGI7
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Q9NGB
ID Q9NGB
AC Q9NGB
AC Q9NGB
DT 01-OC
DT 01-JU
DT 01
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Best Local S
                                                                                         Matches
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Reduced X-linked nucleotide polymorphism in Drosophila simulans."; Proc. Natl. Acad. Sci. U.S.A. 97:5960-5965(2000).
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                        NON_TER
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-20283933; PubMed-10823947;
Begun D.J., Whitley P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila yakuba (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eyelid (Fragment).
                                                                                                                                                                                                                                                                           "Réduced X-linked nucleotide polymorphism in Drosophila simulans."; proc. Natl. Acad. Sci. U.S.A. 97:5960-5965(2000).
EMBL; AF255314; AAF68611.1; -
                                                                                                                                                                                                                                                     FlyBase; FBgn0041640; Dyak\osa.
                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=7245;
                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 269 AAAAAALS 276
  269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 AAAAAALS 15
                                               œ
                                                                                         l Similarity
8; Conserv
                                               AAAAAALS 15
  AAAAAALS 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      324 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                            Conservative 0; Misman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               324
                                                                                                                                                                                       324 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32399 MW; 5ECC6A8C4556B331 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                            32644 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dsim\osa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 8; pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                            65BA271ED4DDE03D CRC64;
                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               324 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 5;
                                                                                                                                             DB 5;
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                                                                                                                                                  Length 324;
                                                                                                        0;
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Best Local S
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                                               Matches
                                                                      Query Match
                                                             Best
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9N6K3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9N6K3;
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Begun D.J., Whitley P.; reduced x-linked nucleotide polymorphism in Drosophila simulans."; proc. Natl. Acad. Sci. U.S.A. 97:5960-5965(2000). EMBL; AF252670; AAF66052.1; EMBL; AF252665; AAF68047.1; EMBL; AF252665; AAF68047.1; ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eyelid (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER
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MEDLINE=20283933; PubMed=10823947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=7240;
                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FlyBase; FBgn0041660; Dsim\osa.
                                                                                                                                                                                                                                                                      Drosophila simulans (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Musciephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                      Eyelid (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                    Q9N6K2;
                                                                                                                                                                                                                                                                                                                                                                                                Q9N6K2
                                                                                                           NON_TER
                                                                                                                                                                       Begun D.J., Whitley P.; "Reduced X-linked nucleotide polymorphism in Drosophila simulans."; proc. Natl. Acad. Sci. U.S.A. 97:5960-5965(2000).
                                                                                                                                                                                                           STRAIN=SIM8, AND SIM6;
MEDLINE=20283933; PubMed=10823947;
                                                                                                                                                  EMBL;
                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                               SEQUENCE
                                                                                                                                     FlyBase;
                                                                                                                                                                                                                                                             WCBI_TaxID=7240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                              269 AAAAAALS 276
                                                                                                                                                   Natl. Acad. Sci. U.S.A.
AF252671; AAF68053.1; -.
AF252669; AAF68051.1; -.
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269 AAAAAALS 276
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                         8 AAAAAALS 15
                                                             Similarity
                                                  8
                                                                                                                                     FBgn0041660; Dsim\osa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               324 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            324
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                                                                                                   324 AA;
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                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.7%; Score 8;
100.0%; Pred. No.
                                                                 100.0%;
                                                                                                  32407 MW; 44676F22EA5071F0 CRC64;
                                                                           4.7%; Score 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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                                                      0,
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                                                               Pred.
                                                     red. No. 15
Mismatches
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                                                                                                                                                                                                                                                                                            Brachycera; Muscomorpha;
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                                                                              Length 324;
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                                                             Gaps
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RESULT 18
QBX1X2
ID QBX1X
AC QBX1X
DT 01-MA
DT 01-MA
DT 01-MA
DT 01-JU
DE Pecti
GN PELA.
OS Asper
CC Eurot
OX NCBI.
CX NCBI.
CX NCBI.
RN [1]
RP SEQUE
RC STRAI
RA Kitam
RT KBNGI
DR KSHOM
DR KSHOM
DR CHAR
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  Query Match
Best Local Similarity
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OBX1X2;
O1-MAR-2002 (TIEMBLICAL 20, C
01-MAR-2002 (TIEMBLICAL 20, I
01-JUN-2002 (TIEMBLICAL 21, I
                                                                                                                         Pfam; PF01225; Mur_ligase; ī.
Pfam; PF02875; Mur_ligase_C; 1.
TIGRFAMS; TIGR01143; murF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                       Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C., Klee S.R., Morelli G.; Basham D., Brown D., Chillingworth T., Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9JSZ1;
01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                               HSSP; P11880; 1GG4.
InterPro; IPR000713; Mur_ligase.
InterPro; IPR004101; Mur_ligase_C.
                                                                                                                                                                                                                                                                                                                                               Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G., Whitehead S., Sequence of a serogroup A strain of Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
UDP-MurNAc-pentapeptide synthetase (EC 6.3.2.15).
MURF OR NMA2068.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Z2491 / SEROGROUP A / SEROTYPE 4A;
MEDLINE=20222556; PubMed=10761919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neisseria meningitidis (serogroup A).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae;
                                                                                                                                                                                                                                                                                                                                         meningitidis Z2491."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Two pectin lyase genes (pelA and pelB) from Aspergillus oryzae KBN616: their sequence analyses and overexpression, and characterization of the gene products."; Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.

EMBL: AB029322; BAB82467.1; ...
                                                                                                                                                                                                                                                                                                                    Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=65699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aspergillus oryzae.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Asperg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00544; pec_lyase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-KBN616;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kitamoto N.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002022; Amb_allergen.
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                                                                                                                                                                                                                                                                                AL162758; CAB85286.1; -.
                                                                                                                                                                                                                                                                                                         404:502-506(2000).
                                                                        Complete proteome.
E 452 AA; 48112 MW;
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100.0%; Pred. N
  100.0%;
                             4.78;
Score 8; 1; Pred. No.
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Last annotation update)
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                                                                           9903D4DD1B64C4A9 CRC64;
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                  DB 16; Length 452;
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Q98IK5
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AP002999; BAB49511.1; -.
InterPro; IPR001145; Bac_OmpA.
Pfam; PF00691; OmpA; 1.
ProDom; PD000930; Bac_OmpA; 1.
ProDomi; PD000930; Bac_Omplete pr
SEQUENCE 504 AA; 53754 MW; AF
SEQUENCE FROM N.A.

STRAIN=ATCC 15992 / PAO1;

MEDLINE=20437337; pubMed=10984043;

Stover C.K., Pham X. Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Safter R.L., Collter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Safter M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Fseudomonas aeruginosa PAO1, an opportunistic pathogen.";
                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Probable binding protein component of ABC dipeptide
                                                                                                                                                                                                             Bacteria; Proteobacteria;
                                                                                                                                                                                                                           Pseudomonas aeruginosa.
                                                                                                                                                                                                                                              PA5317
                                                                                                                                                                                                                                                                                                                                   Q9HTN7
                                                                                                                                                                                   NCBI_TaxID=287;
                                                                                                                                                                                                   Pseudomonas
                                                                                                                                                                                                                                                                                                                   Q9HTN7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamot Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T. Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M. Takeuchi C., Yamada M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mesorhizobium loti.";
DNA Res. 7:331-338(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=MAFF303099;
MEDLINE=21082930; PubMed=11214968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhizobium loti (Mesorhizobium loti)
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01-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; alpha
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(TrembLrel. 18, Last sequence (TrembLrel. 20, Last annual)
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                                                                                                                                                                                                                                                    protein component of ABC dipeptide transporter
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100.0%; Pred. N
                                                                                                                                                                                                         gamma subdivision; Pseudomonadaceae;
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A8DC1D5759D0D0FB CRC64;
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                                                                                             Query Match
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01-MAY 2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
T16011.4 protein (AT3G09000/T16011_4).
T16011.4 OR MZB10.3.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids II; Brassicales; Brassicaceae; Arabidopsis.
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EMBL; AE004944; AAG08702.1; -..
HSSP; P23847; 1DPE.
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Pfam; PF00496; SBP_bac_5; 1.
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,

Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,

Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,

Bowser L., Carninci P., Jones T., Kamiya A., Karlin Neumann G.,

Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin Neumann G.,

Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka

Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka

Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai

Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,

Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                       Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.; "Arabidopsis thaliana chromosome III pl MZB10 genomic sequence."; submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=CV. COLUMBIA;
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
Lin X., Kaul S., Town C.D., Utterback T.R., Barnstead M.E.,
Ronning.C., White O., Nierman W.C., Fraser C.M.;
Bowman C.L., White O., Nierman W.C., Fraser C.M.;
"Arabidopsis thaliana chromosome III BAC T16011 genomic sequence.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
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01-MAY-2000
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                                                                                                                                               "Arabidopsis cDNA clones.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AC010871; AAF07827.1; ...
EMBL; AC09326; AAD56316.1; ...
EMBL; AF428276; AAL16108.1; ...
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Pred. No.
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EMBL, AY061006; ARL28554 1; T.

ElyBase; FBgn0028577; pUbsf.

InterPro; IPR000504; RNA_rec_mot.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Pfam; PF00076; rrm; 3,

PROSITE; PS50102; RRM; 3,

PROSITE; PS00030; RRM_RNP_1; UNKNOWN_2,

PROSITE; PS00030; RRM_RNP_1; E75E3781
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01-DEC-2001
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                                                                                                                                                 "A novel aromatic-ring-hydroxylating dioxygenase from the diterpenoid-degrading bacterium Pseudomonas abietaniphila BKME-9.";
J. Bacteriol. 181:2675-2682(1999).
EMBL; AF119621; AAD21067.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Syst. Appl. Microbiol. 0:0-0(1999).
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                                                                                                                                                                                                                                                                                                                                                MEDLINE=99235742; PubMed=10217753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Acids.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mohn W.W., Wilson A.E., Bicho P., Moore E.R.B.;
"Physiological and Phylogenetic Diversity of Bacteria Growing on Resin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria;
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                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                           Martin V.J., Mohn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 (TrEMBLrel. 12, (9) (TrEMBLrel. 12, 11) (TrEMBLrel. 19, 11)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                            547 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                            58500 MW; 49A627265D7C1A74 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.7%; Score 8;
100.0%; Pred. No.
        100.0%;
                                             4.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                 Score 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E75E378F7D07F24E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      545
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            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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A CONTROL OF THE CONT
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                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                         Tomich M., Herfst C.A., Golden J.W., Mohr C.D.;

"Role of Flagella in Burkholderia cepacia Host Cell Invasion.";

Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.

EMBL: AP453480; AAL65160.1;

InterPro: IPR000067; FlgMring_FLIF.

InterPro: IPR002920; YscJ_FliF.

Pfam; PF01514; YscJ_FliF.

Pfam; PF01504; PfGMRINGFLIF.
                                                                                                                                                                                                                                                                                                                                                          STRAIN=J231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-JUN-2002 (TrEMBLrel. 21, Flagellar MS ring protein.
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Burkholderia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Burkholderia cepacia (Pseudomonas cepacia)
                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8VQP7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9M7S3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8VQP7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOlium perenne.";
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AF055221; AAF37732.1;
HSSP; P08659; 1LCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT 2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
4-coumarate--CoA_ligase_4CL1 (EC 6.2.1.12).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00455; AMP_BINDING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000873; AMP-bind.
Pfam; PF00501; AMP-binding; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heath R.L., Huxley H., Spangenberg G.;
"Isolation of three 4-coumarate--CoA ligase cDNA homologues from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CV. ELLET;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 QIAAAAAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 AAAALSVL 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 QIAAAAAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10
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8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                           TIGR00206; flif; 1.
587 AA; 62991 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAAALSVL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             570 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60293 MW; 8194EE1B939D2925 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                100.0%;
                                         4.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.7%; Score 8;
100.0%; Pred. N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         beta
           Score 8;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                                     4B142D53E065CB91 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        subdivision; Burkholderia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No.
             DB 2;
o. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              587 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        570 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
ACCOMPAND ACCOMP
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002427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                             STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                           NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9W2T0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9W2T0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-1997
01-JUL-1997
01-JUN-2002
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Pfam; PF00250; Fork_head; 1.

PRINTS; PR00053; FORKHEAD.

PRODOm; PD000425; TF_Fork_head; 1.

SMART; SM00339; FH; 1.

PROSITE; PS00657; FORK_HEAD_1; 1.

PROSITE; PS00658; FORK_HEAD_2; 1.

PROSITE; PS0039; FORK_HEAD_3; 1.

SEQUENCE 587 AA; 64092 MW; 08051
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.M., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Beallew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel 13, 01-MAY-2000 (TrEMBLrel 13, 01-MAY-2000 (TrEMBLrel 13,
                                                                                                                                                                           MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                  Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                      CG15295 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ciona intestinalis.
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Dorsoventral patterning of the vertebrate neural tube is conserved in a protochordate.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001766; TF_Fork_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF002988; AAB61227.1; -. HSSP; Q63245; 2HFH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Development 0:0-0(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Forkhead homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 QIAAAAAA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             491 IAAAAAAL 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 QIAAAAAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IAAAAAAL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Erives A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 04,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                        Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               624 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                                                                  Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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RA HOSTIN D., HOUSTON KA., HOWLAND T.J., Wei M.-H., IDSGWAM C.J.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lisko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C.J., Morris J., Moshrefi A.,
RA Merkulov G., Mishina N.V., Mobarry C.J., Morris J., Moshrefi A.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
DR EMBL, AE003451; AAF46609.1; -.
DR ENBL; AE003451; AAF46609.1; -.
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     RESULT 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burttier P., Burttier R., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O9WDE; Q9W0E7; Q9U096; 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAY-2000 (TrEMBLrel. 21, Last annotation update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Poly-U-binding-splicing-factor protein (CG12085 protein). PUBSF OR POLY-U-BINDING-SPLICING-FACTOR OR CG12085.
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MEDITINE 20196006; PubMed=10731132;

MEDITINE 20196006; PubMed=10731132;

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

George R.A., Lawis S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        624 AA; 65843 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.7%; Score 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8960D41374AFD6C1 CRC64;
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Mismatches
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RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferraz S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Genbart W.M., Classer K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Lasko P., Lei Y., Levitsky AA, Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky AA, Li J., Li Z., Liang Y., Lin X.,
RA McLiu X., Mattei B., WcIntosh T.C., McLeod M.P., McPherson D.L.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Murny D.M., Nelson D.L.,
RA Mount S.M., Nelson K.A., Nison K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Sylirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Walliams S.M., Woodage T., Weinsteok G.M., Weissenbach J.,
RA Williams S.M., Wassarman D.A., Weinsteok G.M., D., Yang S., Yao Q.A.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhong L.,
RA Zhensher S.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Zhensher S.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Johbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL J. [2]
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Q8T6B9
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Matches
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O1-JUN-2002 (TrEMBLrel. O1-JUN-2002 (TrEMBLrel. O1-JUN-2002 (TrEMBLrel. Half pint.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE003471; AAF47501.1; -. EMBL; AE003471; AAF47502.1; -. EMBL; AF190745; AAF04132.1; -.
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PROSITE; PS00030; RRM_RNP_1; 2.
SEQUENCE 637 AA; 67939 MW;
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SMART; SM0,0360; RRM; 3
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FlyBase; FBgn0028577; pUbsf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (LONG ISOFORM).

Page-McCaw P.S., Amonlirdviman K., Sharp P.A.;

"PUF60: A pyrimidine-tract binding splicing factor and U2AF65 homolog.";
                           Van Buskirk C., Schupbach T.;
"Half pint regulates alternative splice site selection in Drosophila.";
                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNA 0:0-0(1999).
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EMBL; AF479079; AAL86452.1;
                 Dev. Cell 0:0-0(2002)
                                                                                                                          NCBI_TaxID=7227;
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                                                                                                                                                                                                                                        (TrEMBLrel. 21, (TrEMBLrel. 21, (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.7%; Score 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                              Last annotation update)
                                                                                                                                                                                                                                                           Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F0AD184D9EEF145F CRC64;
                                                                                                                                                                                                                                                                                                                    637 AA.
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Q9FRV2
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Q9FRV3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPP.

RINTERPRO; IPR004497; ACCHAC_1g.

R InterPro; IPR004497; ACCHAC_1g.

R InterPro; IPR004497; PPP_enzyme.

Pfam; PF00205; TPP_enzymes; 1.

R Pfam; PF002775; TPP_enzymes_C; 1.

R Pfam; PF02776; TPP_enzymes_C; 1.

R F1GRFAMs; TIGR00118; accolac_1g; 1.

W F1GRFAMs; TIGR00118; accolac_1g; 1.

W F1GRFAMs; TIGR00118; accolac_1g; 1.

SEQUENCE 644 AA; 69392 MW; ED626E55F8B89EC9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9FRV2;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence of the control of the co
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases
                                                                       STRAIN-CV. KINMAZE;
Shimizu T., Rato Y., Nakayama I., Nakayama K., Fukuda A., Tanaka Y.,
"Isolation and Expression of acetolactate synthase genes from Oryza
sativa.";
                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa (Rice).
                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Acetolactate synthase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sativa."
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Shimizu T., Kato Y., Nakayama I., Nakayama K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridipiantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9FRV3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9FRV3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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b; Pred. No. 27;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fukuda A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 637;
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                                                                                                           Tanaka Y.;
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Q9V9F7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC DR DR DR DR DR DR DR DR CKW
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MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
CG10417 protein (LD27655P).
                                                                                                                                                                                                                                                                                                                                               Q9V9F7
Q9V9F7;
                              STRAIN-BERKELEY
                                                   SEQUENCE FROM N.A.
                                                                                                                                  CG10417.
Drosophila melanogaster (Fruit fly).
ביר ארים: Arthropoda; Tracheata; Hexapoda; Insecta; אונה ארים: ארים
                                                                                                 NCBI_TaxID=7227;
                                                                                                                               Ephydroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 407:508-513(2000).
EMBL; AL445065; CAC11825.1; -
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InterPro; IPR000399; TPP_enzyme.
Pfam; PF00205; TPP_enzymes; 1.
Pfam; PF02775; TPP_enzymes_C; 1.
Pfam; PF02776; TPP_enzymes_N; 1.
TIGREAMS; TIGR00118; accolac_lg; 1.
Flavoprotein; Lyase; Thiamine pyrophosphate.
SEQUENCE 644 AA; 69345 MW; F873F121A9FD9F99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
"The genome sequence of the thermoacidophilic scavenger Thermoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C., Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20479972; PubMed=11029001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Hypothetical protein Ta0687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thermoplasmataceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thermoplasma acidophilum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9HKB4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                   Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein; Complete proteome.
51 AA; 74410 MW; 5F9E9F1711E7B733 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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100.0%; Pred. No
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100.0%; Pred. No
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o. 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards C., Champ Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., An H.-J., Andrews-pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktarojlu L., Beasley E.M.,
RA Borkova D., Betchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Ghorty J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N. I., Harvay R. Heiman W. I. Harvay R. Harris N. I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibogwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibogwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.Y., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.Y., Mobarry C., Morris J., Moshrefi A.,
RA Metson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Siden-Kiamos I., Singson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Sylrskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang S., Yao Q.A.,
RA Kilms S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang S., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong W., Raw, Raw Kallan G.M., Venter J.C.;
Raw Science 287:2185-2195(2000).
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   S A B
                                                                                                       RESULT 35
                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AE003787; AAF57333.1; -.

EMBL; AY051748; AAK93172.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FlyBase; FBgn0033021; CG10417.
InterPro; IPR000222; PP2C.
InterPro; IPR001932; PP2C-like.
Pfam; PF00481; PP2C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00332; PP2CC; 1.
SMART; SM00331; PP2C_SIG; 1.
PROSITE; PS01032; PP2C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P35813; 1A6Q.
Q9QY56;
01-MAY-2000 (TrEMBLrel. 13, Created)
                                                         Q9QY56
                                                                                                                                                                                                                                                                                                                                          ocal
                                                                                                                                                                                                 210
                                                                                                                                                                                                                                                     8 AAAAAALS 15
                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                Similarity 100.0%;
                                                                                                                                                                                                 AAAAAALS 217
                                                                                                                                                                                                                                                                                                                                                                                                                                     662 AA;
                                                                                                                                                                                                                                                                                                               Conservative
                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                  72369 MW; C34171B9B030996E CRC64;
                                                                                                                                                                                                                                                                                                                                                                           4.78;
                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                Score 8;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                 DB 5;
                                                                                                                                                                                                                                                                                                                                                                              Length 662;
                                                                                                                                                                                                                                                                                                                                 Indels
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В
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Best Local :
                                                              Matches
                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Transcription factor phi AP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001092; HLH_basic.
InterPro; IPR001092; Znf_CZH2.
pfam; PF00096; Zf-CZH2. 10.
SMART; SM00355; Znf_CZH2; 9.
SMART; SM00355; Znf_CZH2; 9.
PROSITE; PS00028; HELIX_LOOP_HELIX; UNKNOWN_1.
PROSITE; PS00028; ZINC_FINGER_CZH2_1; 6.
PROSITE; PS00028; ZINC_FINGER_CZH2_2; 9.
PROSITE; PS00028; ZINC_FINGER_CZH2_2; 9.
PROSITE; PS00028; ZINC_FINGER_CZH2_2; 9.
PROSITE; PS00028; ZINC_FINGER_CZH2_3; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF126967; AAF22563.1; HSSP; P15822; 3ZNF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                        Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AY051905; AAK93329.l. -

EMBL; AY051905; AAK93329.l. -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD; MGI:109530; E4f1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lebedeva T.V., Singh A.K.; repression by the murine analog repression of the murine Il-1 beta expression by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seq
01-MAR-2002 (TrEMBLrel. 20, Last anno
                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q960R1
                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q960R1;
                                                                                                                                                                                                                                                                                                                                                                                                              ALHAMBRÁ OR CG1070.
                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ocal Similarity
                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transcription factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 AAAAAALS 38
600 AAAAAALS 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 AAAAAALS 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                               8 AAAAAALS 15
                                                                                  Similarity
                                                                α,.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            783 AA; 84222 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                  824 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.7%; Score 8;
100.0%; Pred. N
                                                                                                                                  84327 MW;
                                                                                   100.0%;
                                                                                   4.7%; Score 8;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41FE2E09072813FD CRC64;
                                                                                                                                    8313513FFB2F6F94 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     824 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 11; Length 783;
                                                                                                     DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                     Length 824;
                                                                         Indels
                                                                         0;
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                                                                           Gaps
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RESULT 37

Q9BMZ8

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RESULT 38
Q962D2
ID Q962D
AC Q962D
DT Q1-DE
DT Q1-DE
DT Q1-MA
DE Zinc
GN ALHAM
OS DIOSO,
OC ELWART
OC PTERTY
OC PTER
                                                                                          Q8SZW9
                                                                                                              RESULT 39
                                                                                                                                                                                 В
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                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                             Query Match
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0962D2;

01-DEC-2001 (TrembLrel 19, C1

01-DEC-2001 (TrembLrel 19, L4

01-MAR-2002 (TrembLrel 20, L4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Q8SZW9;
01-JUN-2002 (TrEMBLrel. 21, Created)
                                                                6MZS8ð
                                                                                                                                                                                                                                                                                                                                            Mech. Dev. 100:291-301(2001).
EMBL; AX036104; AAK63170.1; -
F1yBase; FBgn0037471; Alhambra.
SEQUENCE 975 AA; 98713 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Babri S.M., Chia W., Yang X.;
"The Drosophila homolog of human AF10/AF17 leukemia fusion genes (Dalf) encodes a zinc finger/Leucine zipper nuclear protein required in the nervous system for maintaining EVE expression and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21095180; PubMed=11165485; Bahri_S.M., Chia W., Yang X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ephydroidea; Dro
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pterygota; Neoptera; Endopterygota; Diptera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zinc finger/leucine zipper protein DALF isoform C1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The Drosophila homolog of AF10 is expressed in a striped pattern throughout blastoderm.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALHAMBRA OR CG1070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9BMZ8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ocal Similarity
S 8; Conserv
                                                                                                                                                                     600 AAAAAALS 607
                                                                                                                                                                                                                8 AAAAAALS 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 601 AAAAAALS 608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 AAAAAALS 15
                                                       PRELIMINARY;
                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jackle H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel.
                                                                                                                                                                                                                                             100.0%; F1.
                                                                                                                                                                                                                                                                         4.7%; Score 8;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17,
17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                               PRT; 1015 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                   5BB70FB144935276 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          975 AA.
                                                                                                                                                                                                                                                                                     DB 5; Length 975;
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RX MEDIJUS-20196006, PubMed-10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Berson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferrae C., Ferriera S., Fleischmann W.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Wei M.-H., Ibegwam C.,
RA Harris N.L., Harvey D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levisky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 40
Q9VI61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-BERKELEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9VI61;
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SEQUENCE 1015 AA; 100464 MW; CB24616CF13D4CF3 CRC64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Nepptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=7227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Shue B.C., Siden-Klamos I., Simpson M., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Williams S.M., Woodage T., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Weinstock G.M., Venter E., Wang X.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhong G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Zhu S.,
RA Gibbs R.A., Wyers E.W., Rubin G.M., Venter J.C.;
RA Gibbs R.A., Wyers E.W., Rubin G.M., Venter J.C.;
RA Gibbs R.A., Wyers E.W., Rubin G.M., Venter J.C.;
RA EMBL, AE00372; AAF54065.1; -
DR EMBL, AE0037471; Alhambra:
QU SEQUENCE 1164 AA; 119469 MW; F49C6BC7394D8B6A CRC64;
SEQUENCE 1164 AA; 119469 MW; F49C6BC7394D8B6A CRC64;
SEQUENCE 1164 AA; 119469 MW; F49C6BC7394D8B6A CRC64;
Best Local Similarity 100.0%; Pred No. 45;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 17 Secs
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Perfect score:
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length: 2000000000
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Gapop 60.0 ,
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172
1 MMLHIQIAAAAAAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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                           US-08-159-339A-154
PCT-US95-04121-52
US-08-523-2268-42
US-08-721-458B-42
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          154, App
242, Appl
242, Appl
242, Appl
203, App
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204, Appli
205, Appli
206, Appli
207, Appli
208, Appli
209, Appli

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US-08-286-690-12
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US-08-118-32
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US-09-568-480-5
US-09-568-480-5
US-09-68-1395-1
US-08-159-339A-159
US-08-1
Sequence 9, Appli
Sequence 14, Appli
Sequence 15, Appli
Sequence 15, Appli
Sequence 160, Appli
Sequence 25, Appli
Sequence 25, Appli
Patent No. 5169933
Patent No. 5169933
Patent No. 5169933
Sequence 5, Appli
Sequence 6, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 11, Appli
Sequence 5, Appli
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32, Appli
33, Appli
37, Appli
17, Appli
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11, Appli
11, Appli
12, Appli
13, Appli
15, Appli
16, App
                                                                                                                                                                                                              12, Appl
14, Appl
15, Appl
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## ALIGNMENTS

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RESULT 1
US-08-159-339A-154
                                                                                                                                                    В
                                             PCT-US95-04121-52; Sequence 52, Application PC/TUS9504121; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                  US-08-159-339A-154
                                                                                                 RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 154, Application US/08159339A Patent No. 6037135
                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                      Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Weber, Ellen Lauver REGISTRATION NUMBER: 32,762 REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: HLA FITTLE OF INVENTION: Uses
APPLICANT:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/103,396
APPLICATION NUMBER: US 08/103,396
PITTING DATE: 06-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM CO
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Two Emwarca
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/159,339A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                     Local Similarity les 7; Conserv
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Celis, Esteban
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Grey, Howard M.
                                                                                                                                                                                                                                                                                                                                                                                                                                     (415) 576-0300
                                                                                                                                                                                                                4.1%; Score 7; lilarity 100.0%; Pred. No. Conservative 0; Mismatcl
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   Haptenated Peptides and Uses Thereof 62
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; MOLECULE TYPE: peptide; FRAGMENT TYPE: internal PCT-US95-04121-52
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US-08-503-226B-42
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Best Local
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APPLICANT: Locker
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TELEFAX: (617) 466-6010
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 079.2PCT TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 466-6000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/2:
FILING DATE: APPLICATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTER: IBM PC COMPOTER:
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Calcineurin Inhib
TITLE OF INVENTION: Anchoring Protein
NUMBER OF SEQUENCES: 42
                                                        FILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/344,227
FILING DATE: 23-NOV-1994
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/404,731
FILING DATE: 15-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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CITY: Chicago
STATE: Illinoi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US95/04121 FILING DATE:
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les 7; Conserv
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                                                                                                                                                                                                                     CLASSIFICATION: 436
                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                         FILING DATE:
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27
                    NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
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    Marshall, O'Toole, Gerstein, Murray & Borun
    South Wacker Drive, 6300 Sears Tower

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VENTION: Calcineurin Inhibitory Compounds and
                                                                                                                                                                                                                                                                                                                                                                                                                                   United States of America
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100.0%; Pred. No. 2.2;
tive 0; Mismatches
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         27866/32861
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US-08-721-458B-42
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                      Query Match
   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 42, Application US/08721458B
Patent No. 6107104
GENERAL INFORMATION:
APPLICANT: Lockerbie, Robert Owen
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 27.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                     FILLING LOCAL PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/503,226
TITTING DATE: 17-JUL-1995
                                                                   MOLECULE TYPE:
                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/344,227
FILING DATE: 23-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 15-MAR-1995
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ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
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LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                  STRANDEDNESS:
TOPOLOGY: lin
                                                                                                                LENGTH: 14 amino acids TYPE: amino acid
                                                                                                                                                                                                                                               NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/721,458B
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                                                                                                                                                                                     312-4740448
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                                                                                 linear
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 4.1%;
100.0%;
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100.0%; Pred. No. 2.3;
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                                                                                                                                                                                                                                              38,659
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Score 7;
Pred. No.
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 DB 3;
             Length 14;
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Sequence 103, Application US/09586472
PATCHI NO. 6323335
GENERAL INFORMATION:
APPLICANT: Huang, Shi
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                                                                                                                                                                                               RESULT 6
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US-08-516-859A-103
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                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UNMER: US 08/399,411
FILING DATE: 06-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/292,683
FILING DATE: 18-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Huang, Shi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Retinoblastoma Proteins TITLE OF INVENTION: Zinc Finger Proteins NUMBER OF SEQUENCES: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 18-AU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: San Diego
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                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                          NUMBER OF SEQUENCES:
                                                                                   TITLE OF INVENTION: Retinoblastoma Protein - Interacting
                                                                                                                                                                                                                                               6 AAAAAAL 12
                                                                                                                                                                                                                                                                             8 AAAAAAL 14
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                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                22 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Campbell & Flores LLP 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08516859A
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                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Retinoblastoma Protein - Interacting
                                                                                                                                                                                                                                                                                                                           4.1%; Score 7; DB 3; 100.0%; Pred. No. 3.6;
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                                                          106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103:
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                                                                      Finger Proteins
                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                           0; Indels
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FILING DATE: 18 AUG-1995
APPLICATION NUMBER: US 08/399,411
FILING DATE: 18 AUG-1995
APPLICATION NUMBER: US 08/399,411
FILING DATE: 18 AUG-1994
APPLICATION NUMBER: US 08/292,683
FILING DATE: 18 AUG-1994
ATTORNEY,AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE,DOCKET NUMBER: P-LJ 4130
TELECOMMUNICATION INFORMATION:
TELEPAX: (619) 535-9001
TELEPAX: (619) 535-9001
TELEPAX: (619) 535-8449
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 103, Application US/09528706 Patent No. 6468985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Prote:
TITLE OF INVENTION: Zinc Finger Proteins
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                 COMPUTER READABLE FORM:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 92122
                                        CLASSIFICATION:
                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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APPLICATION NUMBER: US/09/586,472
FILING DATE: 01-Jun-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/528,706
FILING DATE: 17-MAR-2000
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE DESCRIPTION: SEQ ID NO: 103:
                                                                                                                                                                                                                                                                                              SSEE: Campbell & Flores LLP
T: 4370 La Jolla Village Drive, Suite 700
San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 22 amino acids
                                                                                                                                                                                                                                                                                 California
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                                                                                      US/09/528,706
    US 08/516,859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 18-AUG-1994
ATTORNEY/AGENT INFORMATION:
ANAME. CARNEY I CATTORN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: P-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MSWORD Version 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                  APPLICATION NUMBER: US 07/486,333
FILING DATE: 28-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 07/409,217
FILING DATE: 19-SEP-1989
ATTORNBY/AGENT INFORMATION:
AND ATTORNBY/AGENT INFORMATION:
AND ATTORNBY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cronan, Charles L.
TITLE OF INVENTION: METHOD OF EXPRESING ANTIFREEZE PROTEINS
TITLE OF INVENTION: IN YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
NAME: Kryshak, Thad REGISTRATION NUMBER: 35,433 REGISTRATION NUMBER: 66-005-9234-1 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Thad Kryshak, Quarles & Brady
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815
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                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Milwaukee
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Barney, Michael C.
Bower, Patricia A.
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Huige, Nick
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                                                                                                                                                                                                                                                                                   US/08/180,524
                                                                                                                                                                                                            US/07/917,216
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o. 3.6;
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APPLICANT: Rhodes, Thomas
APPLICANT: Rotes, Nick
APPLICANT: Kot, Edward
APPLICANT: Kot, Edward
APPLICANT: Chicoye, Etzer
APPLICANT: Barney, Michael C.
APPLICANT: Bower, Patricia A.
APPLICANT: Cronan, Charles L.
TITLE OF INVENTION: METHOD OF EXPRESING ANTIFREEZE PROTEINS
TITLE OF INVENTION: IN YEAST
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Thad Kryshak, Quarles & Brady
'11 Fast Wisconsin Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-180-524-8
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                                                                            APPLICATION NUMBER: US 07/486,333
FILING DATE: 28-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/409,217
FILING DATE: 19-SEP-1989
ATTORNEY/AGENT INFORMATION:
NAME: Kryshak, Thad
RECISTRATION NUMBER: 35,433
RECISTRATION NUMBER: 35,433
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INFORMATION FOR SEO ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: single
TELEFAX: (414) 277-559 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
            REFERENCE/DOCKET NUMBER: 66-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5707
TELEFAX: (414) 277-5591
                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: MSWORD Version 5.0
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: 1
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                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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5849537
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linear
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114) 277-5591
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100.0%; Pro
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                                                                   66-005-9234-1
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; Pred. No.
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6;
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APPLICATION
FILING DATE:
FILING DATE:
APPLICATION NUMBER: US 07/486,333
FILING DATE: 28-FEB-1990
PROOR APPLICATION DATA:
APPLICATION NUMBER: US 07/409,217
FILING DATE: 19-SEP-1989
ATTORNEY/AGENT INFORMATION:
NAME: KIYSHAK, Thad
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 66-005-923
FELECOMMUNICATION INFORMATION:
TELEPAN: (414) 277-5591
INFORMATION FOR SEQ ID NO: 9:
TELEPAN: (414) 277-5591
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
US-08-180-524-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 4.1%; Score 7; Best Local Similarity 100.0%; Pred. No. Matches 7; Conservative 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Tripp,
                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MSWORD Version 5.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Cronan, Charles L.
TITLE OF INVENTION: METHOD OF EXPRESING ANTIFREEZE PROTEINS
TITLE OF INVENTION: IN YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein HYPOTHETICAL: NO
               LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 AAAAAAL 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Milwaukee
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Barney, Michael C.
Bower, Patricia A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhodes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Huige,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lusk, Lance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thad Kryshak, Quarles & Brady
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matthew
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                                                                                                                                                   66-005-9234-1
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; MOLECULE TYPE:
; HYPOTHETICAL: N
; ANTI-SENSE: NO
US-08-180-524-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 53202
ZIP: 53202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
COMPUTER: LIBM PC COMPATIBLE
COMPANIENTER: PC-DOS/MS-DOS
PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                          TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Cronan, Charles I.
TITLE OF INVENTION: METHOD OF EXPRESING ANTIFREEZE PROTEINS
TITLE OF INVENTION: IN YEAST
                                                                                                                                          REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 66-005-9234-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5707
                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-I
SOFTWARE: MSWORD Version 5.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Thad Kryshak, Quarles & Brady
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA: APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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MOLECULE TYPE: HYPOTHETICAL:
                                                                                                                                                                                                                APPLICATION NUMBER: US 0: FILING DATE: 19-SEP-1989 ATTORNEY/AGENT INFORMATION: NAME: Kryshak, Thad
                                                                                                                                                                                                                                                                              FILING DATE: 28-FEB-1990 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/07/917,216
FILING DATE:
APPLICATION NUMBER: US 07/486,333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Milwaukee
STATE: Wisconsi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                          TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                  TOPOLOGY:
                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity
7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       411 East Wisconsin Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.1%; Score 7; DB dilarity 100.0%; Pred. No. 6; Conservative 0; Mismatches
                                                                                37 amino acids
                           linear
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Barney, Michael C.
Bower, Patricia A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rhodes, Thomas
Huige, Nick
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lusk, Lance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tripp,
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                 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Edward
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US-08-975-166-8
US-08-975-166-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 4.1%; Score 7; DB 3
Best Local Similarity 100.0%; Pred. No. 6;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/486,333

FILING DATE: 28-FEB-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/409,217

APPLICATION NUMBER: US 07/409,217

FILING DATE: 19-SEP-1989

ATTORNEY/AGENT INFORMATION:
NAME: KLYSHAK, Thad
REGISTRATION NUMBER: 35,433
REGISTRATION NUMBER: 35,433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                       TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Chicoye, Etzer
APPLICANT: Barney, Michael C.
APPLICANT: Bower, Patricia A.
APPLICANT: Cronan, Charles L.
TITLE OF INVENTION: METHOD OF EXPRESING ANTIFREEZE PROTEINS
TITLE OF INVENTION: IN YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
                 ANTI-SENSE:
                              MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 66
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                                     SEQUENCE CHARACTERISTICS:
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OTTY: Milwaukee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                                                   TOPOLOGY:
                                                                                STRANDEDNESS:
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                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wisconsin
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                                                                                                                 37 amino acids
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                 NO
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                                                                   linear
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                                                                                                                                                                                        (414)
                                                                                 single
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                                                                                                                                                                                            277-5707
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[00.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10
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; ANTI-SENSE:
US-08-975-166-9
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US-08-975-166-9
 Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 53202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
                                                                                           TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 66
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5707
                                                                                 HYPOTHETICAL:
                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/409,217
FILING DATE: 19-SEP-1989
ATTORNEY/AGENT INFORMATION:
NAME: Kryshak, Thad
REGISTRATION NUMBER: 35,433
PREPERSON FORWER: 35,433
PREPERSON FORWER: 35,433
                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07
FILING DATE: 28-FEB-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-D SOTTWARE: MSWORD Version 5.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Thad Kryshak, Quarles & Brady
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Chicoye, Etzer
APPLICANT: Barney, Michael C.
APPLICANT: Bower, Patricia A.
APPLICANT: Cronan, Charles L.
TITLE OF INVENTION: METHOD OF EXPRESING ANTIFREEZE PROTEINS
TITLE OF INVENTION: IN YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                           TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                               TYPE:
                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/07/917,216 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Milwaukee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 AAAAAAL 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/08975166
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                                                                 NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rhodes, Tho
Huige, Nick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lusk, Lance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                             linear
                                                                                                                          single
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   100.0%;
                 4.18;
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Score 7; I
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Pred. No.
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DB 2;
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RESULT 15
US-09-117-121-42
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                                                                       ; Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
US-09-117-121-39
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                                                                          Sequence 42, Application US/09117121 Patent No. 6307020
                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                      Query Match
GENERAL INFORMATION:
APPLICANT: Hew, Choy
APPLICANT: Gong, Zhiyuan
TITLE OF INVENTION: Intracellular antifreeze Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 39:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Hew, Choy
APPLICANT: Gong, Zhiyuan
                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/CA97/00062
FILING DATE: 30-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANI.
TITLE OF INVENTION: Intraction:
TITLE OF INVENTION: and Nucleic Acids
TITLE OF STOMENCES: 46
                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Weber, Kenneth A. REGISTRATION NUMBER: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 20 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                        6 AAAAAAL 12
                                                                                                                                                                                                     8 AAAAAAL 14
                                                                                                                                                                                                                                      Similarity 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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                                                                                                                                                                                                                                                 4.1%; Score 7; DB 4; 100.0%; Pred. No. 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Intracellular Antifreeze Polypeptides
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CORRESPONDENCE ADDRESS:

ADDRESSEE:

Two Embarcadero Center, Eighth Floor

Townsend and Townsend and Crew LLP

NUMBER OF SEQUENCES:

TITLE OF INVENTION:

and Nucleic Acids

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                                                           US-09-344-529-4
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                                                                                                                                                                             SEQ ID NO 4
LENGTH: 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/09344529 Patent No. 6429293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                     APPLICANT: Hew, Choy L.
APPLICANT: HSC Research and Development Limited Partnership
APPLICANT: HSC Research and Development Limited Partnership
TITLE OF INVENTION: Sculpin-Type Antifreeze Polypeptides and Nucleic Acids
FILE REFERENCE: 016252-002620US
FILE REFERENCE: 016252-002620US
CURRENT APPLICATION NUMBER: US/09/344,529
CURRENT FILING DATE: 1999-06-24
EARLIER APPLICATION NUMBER: US 60/090,794
EARLIER FILING DATE: 1998-06-26
EARLIER FILING DATE: 1998-06-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 42:
                                                                                                                                                                                                                      EARLIER APPLICATION NUMBER: US 60/095,713
EARLIER FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.0
                                                                          OTHER INFORMATION: Winter flounder liver-type antifreeze polypeptide OTHER INFORMATION: (wflafP-6)
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                       FEATURE:
                                                                                                                                         ORGANISM: Pleuronectes americanus
                                                                                                                                                              TYPE: PRT
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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FILING DATE: 30-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
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CITY: San Francisco
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100.0%; Pred. No.
tive 0; Mismatc
  4.1%;
100.0%;
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  Score 7; DB 4; Pred. No. 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                     Length 37
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                                                                                                                                                             RESULT 18
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                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 7; Conserv
                                 GENERAL INFORMATION:
APPLICANT: Caceci,
APPLICANT: Toth, The APPLICANT: Szumans)
                                                                                                       Sequence 1, Application US/07812421 Patent No. 5932697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/588
APPLICATION NUMBER: US 07/588
FILING DATE: 25-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Whitham, Michael E.
REGISTRATION NUMBER: 32,635
REFERENCE/DOCKET NUMBER: CIT.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-191-2510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 703-391-9035
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Caceci, Thomas
APPLICANT: Toth, Thomas E.
APPLICANT: Szumanski, Maria B.W.
TITLE OF INVENTION: SYNTHETIC ANTIFREEZE PEPTIDE AND
TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS: LENGTH: 38 amino acids
                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: peptide
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: VA COUNTRY: US ZIP: 20191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Reston Intl. Center, 11800 Sunrise Valley Dr., STREET: Suite 900 CITY: Reston
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 AAAAAAL 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 AAAAAAL 14
                                                                                                                                                                                                                                                    8 AAAAAAL 14
                                                                                                                                                                                                                 6 AAAAAAL 12
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                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
   Szumanski, Maria B.W.
VENTION: SYNTHETIC ANTIFREEZE PEPTIDE AND
VENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
                                                     Toth, Thomas E.
                                                                    Caceci, Thomas
                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WHITHAM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                      4.1%; Score 7; DB 2; 100.0%; Pred. No. 6.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US 07/588,437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/07/814,220
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                                                                                                                                                                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                                          Length 38;
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NUMBER OF SEQUENCES:

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CURRENT APPLICATION NUMBER: US/09/325,932A
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 144
LENGTH: 109
TYPE: PAT
ORGANISM: Eucalyptus grandis
US-09-325-932A-144
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                                                                                                                                                                                                                                                                                                                                                                   US-09-325-932A-144; Application US/09325932A; Patent No. 6451604
                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-07-812-421-1
                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Flinn, Barry
APPLICANT: Lasham, Anne
                                                                   Matches
                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                              APPLICANT: Lasham, Annette
TITLE OF INVENITION: Compositions affecting programmed cell
TITLE OF INVENITION: death and their use in the modification of forestry plant develo
                                                                                                                                                                                                                                                                             FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/588,437
EILING DATE: 25-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Whitham, Michael E.
REGISTRATION NUMBER: 32,635
REFERENCE/DOCKET NUMBER: CIT.016
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-391-2510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 703-391-9035 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 703-391-9035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 23-DEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: WHITHAM, CURTIS & WHITHAM
STREET: Reston Intl. Center, 11800 Sunrise Valley Dr.,
STREET: Suite 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
18 AAAAAAL 24
                             8 AAAAAAL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 AAAAAAL 12
                                                              4.1%;
Similarity 100.0%;
7; Conservation
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23-DEC-1991
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100.0%; Pred. No.
7ative 0; Mismatcl
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                                                            0;
                                                                          Score 7; ; Pred. No.
                                                           Mismatches
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                                                                                        DB 4;
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                                                                                        Length 109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                         Indels
                                                     0;
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                                                     0;
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US-08-444-083-3
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 20
US-08-233-609-3
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

Best Local Similarity 100.0%; Pred. No.
Matches 7; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEPAX: 415/52-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Baker,
                                                                       APPLICANT: Chien, Kenneth
APPLICANT: King, Kathleen
APPLICANT: Pennica, Diane
APPLICANT: Wood, William
TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
NUMBER OF SEQUENCES: 8
                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech
                                                                                                                                                                                  APPLICANT: Baker, Joffre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: King, Kathleen APPLICANT: Pennica, Diane APPLICANT: Wood, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Chien, Kenneth
APPLICANT: King, Kathleen
CITY: South San Francisco
                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 25-APP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                       91 AAALSVL 97
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         E: Genentech, Inc.
460 Point San Bruno Blvd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              203 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-APR-1994
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lo. 31;
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COUNTRY:

USA

94080

STATE: California

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TOPOLOGY: US-08-444-083-3
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Best Local Similarity luv.
"---hes 7; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 203 amino acids
TYPE: amino acid
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,304
FILING DATE: 05-AUG-1994
CLASSIFICATION 25-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION UMBER: 08/233609
FILING DATE: 25-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Baker,
APPLICANT: Chien,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 894
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/233609
FILING DATE: 25-APR-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/2
FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Pennica, Diane
APPLICANT: Wood, William
TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/01 FILING DATE: 17-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415/952-9881
TELEX: 910/371-7168
                                                                                                                                                                                                                                                                                                     ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                      STATE:
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                                                                                                                                                                                                                                                                                    California
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King, Kathleen
                                                                                                                                                                                                                                                                    USA
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100.0%; Pred. No. 31;
ative 0; Mismatches
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US-08-442-745-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Baker, Joirre
APPLICANT: Chien, Kenneth
APPLICANT: King, Kathleen
APPLICANT: Pendica, Diane
APPLICANT: Wood, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 89-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEPHAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,745
FILING DATE: 17-may-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                        REFERENCE/DOCKET NUMBER: 89
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
                                                                                                                                                                                                                      APPLICATION NUMBER: 08/28
FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/233609
FILING DATE: 25-APR-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 203 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94080
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                                     TYPE:
                                                                                                           TELEFAX: 415/952-9881
TELEX: 910/371-7168
                                                                                                                                                                                                      REGISTRATION NUMBER:
                 TOPOLOGY: linear
                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91 AAALSVL 97
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                                   t: 203 amino acids amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                               IUMBER: 08/286304
05-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cardiac Hypertrophy Factor and Uses Therefor
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RESULT 25
US-08-443-952-3
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUIENCE CHARACTERISTICS:
FRIGTH: 203 amino acids
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Sequence 3, Application US/08443952
                                                                                                                                      Query Match 4.1%; Score 7; 1
Best Local Similarity 100.0%; Pred. No.
Matches 7; Conservative 0; Mismatc)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING LATE: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/233609
APPLICATION STAPE: 25-APR-1994
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Best Local Similarity
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APPLICANT: Baker,
APPLICANT: Chien,
                                                                                                                                                                                                                                                                                                                                                              FILING DATE: (null)
ATTORNEY/AGENT INFORMATION:
NAME: TOrchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 415/225-8674
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/2 FILING DATE: 05-AUG-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 460 Point San Bruno Blyd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Pennica, Diane APPLICANT: Wood, William TITLE OF INVENTION: Cardia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                    TELEPHONE: 415/252-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08 FILING DATE: 17-MAY-1995
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                                                                                                           11 AAALSVL 17
                                                                               91 AAALSVL 97
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Chien, Kenneth
King, Kathleen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.1%; Score 7; DB 1; 100.0%; Pred. No. 31;
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Wo. 31;
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; Patent No. 5723585
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Best Local S
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                                                                                                                                           APPLICANT: Baker, Joffre APPLICANT: Chien, Kenneth APPLICANT: King, Kathleen APPLICANT: Pennica, Diane APPLICANT: Wood, William
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APPLICATION NUMBER: 08/233
ETILING DATE: 25-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/286
ETILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
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                                                                        CORRESPONDENCE ADDRESS
                                                                                                       TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb f
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
**ADDITANTON NUMBER: NF //18 / 1443 .95
                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 415/225-8674
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STATE:
              STREET: 460 Point San Bruno Blvd CITY: South San Francisco
                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 203 amino acids TYPE: amino acid
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TELEX: 910/371-7168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 894P1D4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Torchia, Timothy E. REGISTRATION NUMBER: 36,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/0 FILING DATE: 17-MAY-1995 CLASSIFICATION: 435
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CITY: South San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                    91 AAALSVL 97
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California
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                                                      Genentech, Inc
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US-08-898-911-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 894P1D3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEPHONE: 415/225-8674
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APPLICATION NUMBER: 08/233609
FILING DATE: 25-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/286304
FILING DATE: 05-AUG-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: TOYCHIA, Timothy E.
REGISTRATION.NUMBER: 36,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/233609
FILING DATE: 25-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/286304
FILING DATE: 05-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                  FILING DATE: 05-AUG-
PRIOR APPLICATION DATA:
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                                                                                                                                                                  APPLICATION NUMBER: US/08/898,911 FILING DATE: 23-Jul-1997
                                                                                                                                                                                                                                                                                                                                                                    CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
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                                                                                                                                                      CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
APPLICATION NUMBER:
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08/452555
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To. 31;
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                            QY
Дb
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                Matches
                                                                                            Query Match
                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/233
APPLICATION NUMBER: 25-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 25-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Conley, Deirdre L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 650/225-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb :
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NUMBER OF SEQUENCES
                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 203 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 89
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: PO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 203 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Conley, Deirdre L. REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: Linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                   TELEPHONE: 415/225-18
TELEFAX: 415/952-9881
TELEX: 910/371-7168
                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE
                                                            Local Similarity
les 7; Conserv
                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91 AAALSVL 97
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91 AAALSVL 97
                                 11 AAALSVL 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                 Conservative
                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.1%; Score 7; DB 3;
100.0%; Pred. No. 31;
tive 0; Mismatches
                                                                 4.1%; Score 7; DB 5;
100.0%; Pred. No. 31;
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cardiotrophin and Uses Therefor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           360 Kb floppy disk
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                                                                                                     Length 203;
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US-08-508-761B-32
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Best Local Similarity
"atches 7; Conserve
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; ORGANISM: Fibrobacter succinogenes
US-09-286-690-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 55-96

CURRENT APPLICATION NUMBER: US/09/286,690

CURRENT FILING DATE: 1999-04-05

EARLIER APPLICATION NUMBER: US 60/027,882

EARLIER FILING DATE: 1999-10-04

EARLIER APPLICATION NUMBER: PCT/US97/17811

EARLIER FILING DATE: 1997-10-03

NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-286-690-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver.
SEQ ID NO 12
LENGTH: 228
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APPLICANT: Ljungdahl, Lars G.
APPLICANT: Chen, Huizhong
TITLE OF INVENTION: Lichenase and Coding Sequences
                  NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: P58525NA
TELECOMMUNICATION INFORMATION:
                                                                                         PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: F8 91/09870
FILING DATE: 02-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: System for Protein Expression and TITLE OF INVENTION: Secretion Especially in Corynebacteria NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Joliff, Gwennael APPLICANT: Guyonvarch, Arme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                 APPLICATION NUMBER: FR 91/09652 FILING DATE: 29-JUL-1991
                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/508,761B FILING DATE: 31-JUL-1995
                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Jacobson, Price, Holman & Stern, PLLC STREET: 400 Seventh St. N.W. CITY: Washington D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 AAAAAAL 21
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                                                                                                                                                                                                                                                                                                                                                                                                         U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Renaud, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Duchiron, Francis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Purification, Relano
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                                                                                                                                                                                                                                                                                                       IBM PC compatible SYSTEM: PC-DOS/MS-DOS
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(202) 638-6666
                                                                                                                                                                                                                                                                                                                                                  Floppy disk
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100.0%; Pred. No.
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RESULT 31
US-08-107-676-30
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                                                                                                                        INFORMATION FOR SEQ ID NO: 30: SEQUENCE CHARACTERISTICS: LENGTH: 325 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP92/00268
FILING DATE: 07-FEB-1992
                                IMMEDIATE SOURCE:
                                                                ORIGINAL SOURCE
                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: 612-332-5300
                                                                                                                                                                                                                                                                                               FILING DATE: 07-FEB-1992
PRIOR APPLICATION NUMBER: EP 91400388.4
                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                      FILING DATE: 14-FEB-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: DeWit, Lucas
APPLICANT: DeBruyn, Jacqueline
TITLE OF INVENTION: Mycobacterium Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding Them for Diagnosis and Control of
TITLE OF INVENTION: Tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                           TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
   CLONE:
                  CLONE:
                                          ORGANISM: Mycobacterium kansasii
                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 04-OC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity es 7; Conserv
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from M.kansasii
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      Partial protein sequence from antigen 85B
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DeWit, Lucas
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100.0%; Pred. No.
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RESULT 32
US-09-161-241-9
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US-07-792-885A-1
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CURRENT APPLICATION NUMBER: US/09/161,241
CURRENT FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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APPLICANT: Sullivan, John K
APPLICANT: Theill, Lars E
APPLICANT: Wang, Daguang
TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 350
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Goldring, Steven R.
APPLICANT: Gorn, Alan H.
APPLICANT: Lin, Herb Y.
TITLE OF INVENTION: MAMMALIAN CALCITONIN RECEPTOR
NUMBER OF SEQUENCES: 2
                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM ps/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WORDPERFECT (Version 5.1)
                                                                                   APPLICATION NUMBER: US FILING DATE: 19911115 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,1
                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.0%; Pred. No. hes 7; Conservative 0; Mismath
                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                CITY:
                                                                                                                                                                                                                                                                                                                                STREET:
                                                                   APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                Boston
                                                                                                                                                                                                                                                                                                 Massachusetts
                                                                                                                                                                                                                                                                                                                                  225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.18;
                                                                                                                                         US/07/792,885A
     30,162
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GENERAL INFORMATION:
APPLICANT. ...
US-08-142-439A-7
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Best Local :
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                      TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 482 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTER: IBM P
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APPLICATION NUMBER: PCT/1
FILING DATE: 23-MAR-93
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                             ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                      STRANDEDNESS: Si
TOPOLOGY: linear
MOLECULE TYPE: pro
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                                                                                                                                                   HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Harrington, James J
REGISTRATION NUMBER: 38,7
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/142,439A FILING DATE: 24-NOV-93
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                                              ORGANISM:
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                                          Sus scrofa
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US-08-869-477-7
   RESULT 36
US-09-172-952-26
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                                                                                                                                              Matches
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Best Local
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 212 867 0123
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APPLICATION NUMBER: PCT/I
FILING DATE: 23-MAR-93
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US,
FILING DATE: 24-NOV-93
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                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 3756.204-US
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                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: sir
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                                                                          431 AAAAAAL 437
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10174-6201
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7; Conservative
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100.0%; Pred. No. 72
tive 0; Mismatches
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100.0%; Pred. No. 72
Live 0; Mismatches
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US-09-382-256-10
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GENERAL INFORMATION:
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CURRENT FILING DATE: 1998-10-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Hoch, James
APPLICANT: Dartois, Veronique
TITLE OF INVENTION: METABOLIC SELECTION METHODS
FILE REFERENCE: 234/191
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TYPE: PRT
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MEDIUM TYPE: Diskette, 3

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect
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HELDIN, Carl-Henrik
TITLE OF INVENTION: ACTIVIN RECEPTOR LIKE KINASES, PROTEINS
HAVING SERINE THREONINE KINASE DOMAINS,
AND THEIR USE
                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 YNMSLGE 122
                                                                FILING DATE: May 28, 1993
APPLICATION NUMBER: 9313763.6
FILING DATE: July 2, 1993
                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/382,256A FILING DATE: 24-Aug-1999 CLASSIFICATION: 514
APPLICATION NUMBER: 9316099.2 FILING DATE: August 3, 193 APPLICATION NUMBER: 321344.5 FILING DATE: October 15, 1993
                                                                                                                                                                     APPLICATION NUMBER: GB 9224057.1 FILING DATE: No. 6207814ember 17, APPLICATION NUMBER: GB 9304677.9 FILING DATE: March 8, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: New York City
STATE: New York
                                                                                                                    APPLICATION NUMBER: GB 930468
FILING DATE: March 8, 1993
APPLICATION NUMBER: 9311047.6
                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/GB93/02367 FILING DATE: No. 6207814ember 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Fulbright & Jaworski L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/09382256A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               10103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRANZEN, Petra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TEN DIJKE, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     666 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
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Pred. No.
                                                                                                                                                        GB 9304680.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             3.25 inch, 1.44mb
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                                                                                                                                                                                                             1992
                                                                                                                                                                                                                                                 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 498;
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RESULT 38
US-09-395-115-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/436,265
FILING DATE: 30-October-1995
APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: 17-No. 6271365ember-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
APPLICANT: Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
TITLE OF INVENTION: Having Serine Threonine Kinase Domains and Their Use
                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9304677.9
FILING DATE: 8-March-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                    PRIOR APPLICATION DATA:
                                                                                                                                    FILING DATE: 8-March-1993 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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                                                                             PRIOR APPLICATION DATA:
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Local Similarity 100.0%;
nes 7; Conservativo
                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 9224057.1 FILING DATE: 17-No. 6271365ember-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: New York City
APPLICATION NUMBER:
                                          FILING DATE:
                                                           APPLICATION NUMBER:
                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
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REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5298.1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 503 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 AAAAAAL 14
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6271365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (212) 318-3000
TELEFAX: (212) 752-5958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                        2-July-1993
                                                                                                 28-May-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diskette, 3.5 inch, 360 kb storage
                                                             9313763.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29
                                                                                                                                                                               9304680.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/09/395,115
                                                                                                                  9311047.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (212) 838-3884 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Miyazono, HAPPLICANT: Franzen, RAPPLICANT: Franzen, RAPPLICANTION: AND TITLE OF INVENTION: HAPPLICANT OF SEQUENCES:
                                                                                                              FILING DATE: 8-March-1993
PRIOR APPLICATION DATA:
9311047.6
                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9304677.9
FILING DATE: 8-March-1993
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APPLICATION NUMBER:
                                 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                  PRIOR APPLICATION DATA:
                                                                                                  APPLICATION NUMBER: FILING DATE: 28-Ma;
                                                                                                                                                                                                                                                       APPLICATION NUMBER: 9224057.1 FILING DATE: 17-No. 6316217ember-1992
                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/43 FILING DATE: 30-October-1995 CLASSIFICATION: 435
                                                  FILING DATE:
                                                                                                                                               APPLICATION NUMBER: 9304680.3 FILING DATE: 8-March-1993
                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/GB93/02367 FILING DATE: 17-No. 6316217ember-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acids
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                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
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APPLICATION NUMBER: 913609 FILING DATE: 3-August-1993
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5. 6316217
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Similarity 100.0%;
7; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSEE: Felfe & Lynch I: 805 Third Avenue New York City
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                                                                                                                                                                                                                                                                                                                                                                                                                          Wordperfect
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diskette, 3.5 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-October-1993
                                                 2-July-1993
                                                                                                   28-May-1993
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Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
Activin Receptor-Like Kinase Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Having Serine Threonine Kinase Domains And Their Use
                                                                                                                                                                                                                                                                                                                                                                                        US/08/436,265
                                                                  9313763
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RESULT 40
US-09-679-187-10
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; MOLECULE TYPE: protein
US-08-436-265-10
                                                                                                                                         APPLICATION NUMBER: 9224057.1
FILING DATE: 17-No. 6331621ember-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9304677.9
FILING DATE: 8-March-1993
PRIOR APPLICATION NUMBER: 9304680.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                 FILING DATE: 28-May-1993
PRIOR APPLICATION DATA:
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SEQUENCE CHARACTERISTICS:
LENGTH: 503 amino acids
TYPE: amino acid
                                                                                                        APPLICATION NUMBER: 930460
FILING DATE: 8-March-1993
PRIOR APPLICATION DATA:
FILING DATE: 2-July-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/GB93/02367
FILLING DATE: 17-No. 6331621ember-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/430
FILING DATE: 30-October-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/679,187
FILING DATE: 03-OCT-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
APPLICANT: Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
TITLE OF INVENTION: Having Serine Threonine Kinase Domains And Their Use
NUMBER OF SEQUENCES: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cli.
STATE: No.
10022
                  APPLICATION NUMBER: FILING DATE: 2-July
                                                                                        APPLICATION NUMBER: 9311047.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
SOFTWARE: Wordper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Felfe & Lynch STREET: 805 Third Avenue CITY: New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Kohlei, Vineet
REGISTRATION NUMBER: 37,003
REFERENCE/DOCKET NUMBER: LUI
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FILING DATE: 15-October-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 AAAAAAL 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (212) 688-9200
(212) 838-3884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diskette, 3.5 inch, 360 kb storage
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                                                                                                                            ; MOLECULE TYPE: protein US-09-679-187-10
                                                                                Query Match
Best Local :
                                                                Matches
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TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                           TYPE: amino acids
TOPOLOGY: line
MOLECUTE TYPE: TYPE: AMINO ACID
                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: LUD 5298
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 9136099.2 FILING DATE: 3-AUGUST-1993 PRIOR APPLICATION DATA: 321344.5 FILING DATE: 15-October-1993
                                                                                                                                                                                                                                                                                                                          FILING DATE: 15-October-1
ATTORNEY/AGENT INFORMATION:
                                                              Local Similarity
les 7; Conserv
                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                         NAME:
21 AAAAAAL 27
                            8 AAAAAAL 14
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                                                        4.1%; Score 7; DB 4; ilarity 100.0%; Pred. No. 75; Conservative 0; Mismatches
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Search completed: July 6, 2003, 14:22:34 Job time: 21 secs

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Minimum DB :
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Perfect score:
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                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                           : /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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: /cgn2_6/ptodata/2/pubpaa/US00_PUBCOMB.pep:*
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                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6, 2003, 14:22:40; Search time 24 Seconds (without alignments) 824:116 Million cell updates/sec
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         Sequence 25, Appl Sequence 7, Appl Sequence 7, Appl Sequence 165, App Sequence 105, App Sequence 104, Appl Sequence 770, App Sequence 770, App Sequence 2737, App Sequence 2737, App Sequence 2737, App Sequence 444, Appl Sequence 42364, Appl Sequence 4364, Appl Sequence 3, Appli Sequence 3, Appli
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US-10-156-761-9085
US-10-156-761-9085
US-10-156-761-9085
US-10-063-547-8
US-09-907-824-236
US-09-906-746-236
US-09-907-942-236
US-09-907-955-236
US-09-907-955-236
US-09-907-957-236
Sequence 9684, Ap

Sequence 12779, A

Sequence 157, Appli

Sequence 316, Appli

Sequence 236, Appli
                 sequence
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ORGANISM: Drosophila melanogaster US-10-108-605-25
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US-09-864-761-42679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 25, Application US/10108605 Patent No. US20020160934A1
                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             Sequence 42679, Application US/09864761
Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 25
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Best Local
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APPLICANT: Kamdar, Kim
APPLICANT: Kamdar, Kim
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
FILE REFERENCE: 31133B
CURRENT APPLICATION NUMBER: US/10/108,605
CURRENT FILING DATE: 2002-03-27
CURRENT FILING DATE: 2002-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Broadus, Julie APPLICANT: Stam, Lynn
                                                                                                                                                                                   TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE REFERENCE: Acomica-x-1 CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/176,418 PRIOR FILING DATE: 2000-01-14 NUMBER OF SEQ ID NOS: 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 09/761,142 PRIOR FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                              APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R.
                                           PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
                                                                                                                                                                                                                                                                           APPLICANT: Hanzel, David K. APPLICANT: Chen, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.1
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94
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                                                                                                                                   PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
                                                                                                                                                PRIOR FILING DATE: 2000-02-04
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TYPE: PRT
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            APPLICATION NUMBER: US 60/236,359 FILING DATE: 2000-09-27
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8; Conserv
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Bachmann, Jane
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lve 0; Mismatches
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US-10-223-083-50

US-09-909-320-236

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Sequence 236, App
Sequence 8, Appli
Sequence 4875, Ap
Sequence 10782, A
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Sequence 50, Appl
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                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/10024450 Publication No. US20030032606A1
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Annomax Sequence Listing Engine vers. 1.1 SEQ ID NO 42679
                                                               SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR PRIOR
                                                                                                                                                                                                                               APPLICANT: Huang, Shi
APPLICANT: Chadwick, Robert B.
TITLE OF INVENTION: Methods of Detecting and Treating
TITLE OF INVENTION: Microsatellite-Instability Positive Tumors Using
FILE REFERENCE: P-LJ 5101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/608,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR PRIOR
                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/024,450 CURRENT FILING DATE: 2001-12-17 PRIOR APPLICATION NUMBER: US 60/256,582 PRIOR FILING DATE: 2000-12-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN BRAIM, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.7

OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.86

OTHER INFORMATION: EXPRESSED IN PLACEMTA, SIGNAL = 0.86

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN LIVER, SIGNAL = 1.4
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                   LENGTH: 22
TYPE: PRT
                                                                                                              NUMBER OF SEQ ID NOS: 15
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ORGANISM: Homo sapien
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OR APPLICATION NUMBER: PCT/USO1/00668
OR EILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/USO1/00663
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/USO1/00662
OR FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00667
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US-10-311-111-29
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 29
LENGTH: 23
Type: nom
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GENERAL INFORMATION:
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Publication No. US20030050455A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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TITLE OF INVENTION: 64 Human Secreted Proteins
EILE REFERENCE: PZ011
CURRENT APPLICATION NUMBER: US/09/776,724A
CURRENT FILING DATE: 2001-02-06
CURRENT FILING DATE: 2001-02-06
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Matches 7; Conserv
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PRIOR APPLICATION NUMBER: 09/669,688
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: 09/229,982
PRIOR FILING DATE: 1999-01-14
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CURRENT APPLICATION NUMBER: US/10/311,111
CURRENT FILING DATE: 2002-12-13
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TYPE: PRT
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                                                                  FILING DATE: 1997-07-16
APPLICATION NUMBER: 60/052,874
FILING DATE: 1997-07-16
                                                                                                                                                                               APPLICATION NUMBER: 60/052,661 FILING DATE: 1997-07-16
                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US98/14613 FILING DATE: 1998-07-15
                                  APPLICATION NUMBER: 60/052,873 FILING DATE: 1997-07-16
                                                                                                                        FILING DATE: 1997-07-16
APPLICATION NUMBER: 60/052,871
                                                                                                                                           APPLICATION NUMBER: 60/052,872 FILING DATE: 1997-07-16
APPLICATION NUMBER: 60/052,870 FILING DATE: 1997-07-16
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D. 17;
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; TYPE: PRT; ORGANISM: Hepatitis US-10-106-487-1
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US-10-106-487-1
                                                                                                                                                                      SOFTWARE: PatentIn Ver. SEQ ID NO 1 LENGTH: 41
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APPLICANT: FIRAT, H
APPLICANT: LEMONNI
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Matches 7; Conserv
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APPLICANT: LANGLADE-DEMOYEN, PIERRE
APPLICANT: MICHEL, MARIE-LOUISE
APPLICANT: MICHEL, MARIE-LOUISE
TITLE OF INVENTION: DESIGN OF A POLYEPITOPIC CONSTRUCT FOR THE INDUCTION
TITLE OF INVENTION: OF
TITLE OF INVENTION: HLA-A2.1 RESTRICTED HIV 1 SPECIFIC CTL RESPONSES USING
TITLE OF INVENTION: HHD MICE
FILE REFERENCE: 03495.0196 SEQUENCE LISTING
CURRENT APPLICATION NUMBER: US/10/106,487
CURRENT FILING DAIFE: 2002-03-27
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APPLICATION NUMBER: 60/053,440
FILING DATE: 1997-07-22
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   4.1%;
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                                                                                                                                                                                                                                                                 SOFTWARE: Annomax Sequence Listing Engine vers. 1.1 SEQ ID NO 40439
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NUMBER OF SEQ ID NOS: 49117
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/180,312 PRIOR FILING DATE: 2000-03-04 PRIOR APPLICATION NUMBER: US 60/207,456 PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 09/632,366 PRIOR FILING DATE: 2000-08-03
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
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N: EXPRESSED IN BONE MARROW, SIGNAL = 2

N: EXPRESSED IN FETAL LIVER, SIGNAL = 2

N: EXPRESSED IN LUNG, SIGNAL = 2

N: EXPRESSED IN PLACENTA, SIGNAL = 2.5

N: EXPRESSED IN BOULT LIVER, SIGNAL = 2.5

N: EXPRESSED IN HELA, SIGNAL = 3.6

EXPRESSED IN HEART, SIGNAL = 2.6
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; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1 ; OTHER INFORMATION: EST_HUMAN HIT: AU131227.1, EVALUE 3.00e-05 US-09-864-761-40439
Query Match
Best Local Similarity
7; Conserve
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                                                                                    US-10-092-154-770
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                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 2003

Prior Application removed -
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 770
SEQ ID NO 770
                                                                                                                                                                                                                                                                                                                                                                           Publication No. US20
GENERAL INFORMATION:
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LENGTH: 78
TYPE: PRT
ORGANISM: Artificial sequence
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Best Local
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CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 60/185,755
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Meyers, Rachel
TITLE OF INVENTION: 32253 TRANSPERASE FAMILY MEMBERS AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 38155-20004.00
                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/092,154
CURRENT FILING DATE: 2002-03-07
                                                                                                                                                                                                                                                                                                                           APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC009C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                      LENGTH: 79
                                                                                                    OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                    NAME/KEY: misc_feature
                                                                                                                                                    FEATURE:
                                                                                                                                                                    ORGANISM: Homo sapiens
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                                                                                                                    LOCATION: (73)
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100.0%; Pred. No.
                               4.1%;
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                                 Score 7; 1; Pred. No.
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lo. 35;
                                   DB 9;
o. 51;
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RESULT 12
US-09-764-891-2737
; Sequence 2737, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
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US-10-219-220-144
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Best Local
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TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of the set of the s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Flinn, Barry APPLICANT: Lasham, Anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Eucalyptus grandis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/764,847
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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llarity 100.0%; Pred. No.
Conservative 0; Mismatc)
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Pred. No.
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US-09-164-615-44
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APPLICANT: Hanley-Bowdoin, Linda
APPLICANT: Settlage, Sharon
TITLE OF INVENTION: Geminivirus Resistant Transgenic Plants
FILE REFERENCE: 5051-433
CURRENT APPLICATION NUMBER: US/09/164,615B
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 49
LENGTH: 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-764-891-2737
                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                Sequence 49, Application US/09164615B Patent No. US20020073442A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 44
LENGTH: 131
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Patent No. US20020073442A1
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APPLICANT: Settlage, Sharon
TITLE OF INVENTION: Geminivirus Resistant Transgenic Plants
FILE REFERENCE: 5051-433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/164,615B
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin Ver. 2.0
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TITLE OF INVENTION: Nucleic Acids, Proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: TYCLV mutant OTHER INFORMATION: C3 (mC3#67)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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NAME/KEY: SITE
LOCATION: (103)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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TYPE: PRT
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nes 7; Conserv
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100.0%; Pred. No.
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5. 73;
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; OTHER INFORMATION: Description of Artificial Sequence: TGMV AL3; OTHER INFORMATION: mutant (mAL3#67)
US-09-164-615-49
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US-09-864-761-42364
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PRIOR FILLING DATE: 2000-02-04
PRIOR PELLING DATE: 2000-05-26
PRIOR FILLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILLING DATE: 2000-08-03
PRIOR FILLING DATE: 2000-10-04
PRIOR FILLING DATE: 2000-10-04
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Patent No. US20020048763A1
GENERAL INFORMATION:
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                                                                SOFTWARE: Annomax Sequence Listing Engine vers. SEQ ID NO 42364
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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K
APPLICANT: Chen, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: PCT/US01/00666 PRIOR FILING DATE: 2001-01-30 PRIOR APPLICATION NUMBER: PCT/US01/00667 PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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                                                                                                                                                      PRIOR FILING DATE: 2000-06-30 PRIOR APPLICATION NUMBER: US 09/774,203
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                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/234,687 PRIOR FILING DATE: 2000-09-21
                                                                                                              NUMBER OF SEQ ID NOS: 49117
                                                                                                                                      PRIOR FILING DATE:
ORGANISM: Homo sapiens
                       TYPE: PRT
                                             LENGTH: 161
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nes 7; Conserv
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APPLICATION NUMBER: PCT/US01/00670
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                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US01/00661
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                                                                                                                                                                                                      APPLICATION NUMBER: US 09/608,408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US01/00665
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; 100.0%; Pr
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o. 80;
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US-10-107-931-3
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APPLICANT: Andrew D. MURDIN, Raymond P. OOMEN, Joe WANG, Pamela DUNN
APPLICANT: Andrew D. MURDIN, Raymond P. OOMEN, Joe WANG, Pamela DUNN
TITLE OF INVENTION: Chlamydia antigens and corresponding DNA fragments and uses th
FILE REFERENCE: 77813-37
CURRENT APPLICATION NUMBER: US/09/747,348
CURRENT FILING DATE: 2000-112-22
PRIOR APPLICATION NUMBER: US 60/171,525
PRIOR FILING DATE: 1999-12-22
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/10107931
Publication No. US20030054550A1
GENERAL INFORMATION:
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Best Local
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Best Local Similarity
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.6
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.8
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.6
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.9
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.9
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.8
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                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                   COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                              TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor NUMBER OF SEQUENCES: \boldsymbol{\theta}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 GHTDERG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 GHTDERG 112
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COMPUTER: IBM PC compatible
                                                                                        COUNTRY:
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                                                                      94080
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Wood, William
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King, Kathleen
                                                                                          USA
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100.0%; Pred. No.
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 Mismatches

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o. 96;
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US-09-896-856-3
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                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/896,856
FILING DATE: 29-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity nes 7; Conserv
                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wood, William
TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Baker, Joffre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: HASAK, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 894P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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FILING DATE: 30-Jul-1999
APPLICATION NUMBER: 08/286,304
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 203 amino acids
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APPLICATION NUMBER: US/10/107,931
FILING DATE: 26-Mar-2002
CLASSIFICATION: <Unknown>
                          APPLICATION NUMBER: US 08/733,850
FILLING DATE: 18-OCT-1996
APPLICATION NUMBER: US 08/471,112
FILLING DATE: 06-JUN-1995
APPLICATION NUMBER: 08/233,609
FILLING DATE: 25-APR-1994
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FILING DATE: 05-AUG-1994
                  APPLICATION NUMBER: 08/286304
                                                                                                                                                                   CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                    CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Genentech, Inc. STREET: 460 Point San Bruno Blvd
                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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King, Kathleen
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100.0%; Pr
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b; Pred. No. 1.2
0; Mismatches
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D. 1.2e+02;
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US-09-864-761-36691
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Patent No. US20020048763A1
                          PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: GB 24263,6 PRIOR FILING DATE: 2000-10-04
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TELEX: 910/371-7168
INFORMATION FOR SEG ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 203 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 2000-09-27
R APPLICATION NUMBER: PCT/US01/00666
FILING DATE: 2001-01-30
                                                                                                                                                        APPLICATION NUMBER: PCT/US01/00663 FILING DATE: 2001-01-30
                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US01/00665 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US01/00667 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/236,359 FILING DATE: 2000-09-27
             APPLICATION NUMBER: US 60/234,687
                                                                                                                    FILING DATE: 2001-01-30
                                                                                                                                    APPLICATION NUMBER: PCT/US01/00662
                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                          FILING DATE:
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FILING DATE: 17-MAY-1995
ATTORNEY/AGENT IMPORMATION:
NAME: Conley, Deirdre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: 90894PlD2C1
TELECOMMUNICATION INFORMATION:
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2000-09-21
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100.0%; Pred. No. 1.2e+02;
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OTHER INFORMATION: MAP TO AC006460.2

OTHER INFORMATION: EXPRESSED IN LING, SIGNAL = 4.5

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.1

OTHER INFORMATION: EXPRESSED IN HELLA, SIGNAL = 2.7

OTHER INFORMATION: EXPRESSED IN HELLA, SIGNAL = 3.7

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.4

OTHER INFORMATION: EXPRESSED IN BJ011T LIVER, SIGNAL = 2.3

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.8

OTHER INFORMATION: SWISSPROT HIT: Q62722, EVALUE 0.00e+00

OTHER INFORMATION: EST_HUMAN HIT: AU131373.1, EVALUE 1.00e-114
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RESULT 21
US-10-156-761-12279
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                                                                                                                                                                                                                                                                                  ; ORGANISM: Streptomyces avermitilis US-10-156-761-9684
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PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 36691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9684, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                Query Match 4.1%;
Best Local Similarity 100.0%;
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PRIOR FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL FOLYNUCLEOTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER: OF SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: OMURA, SATOSHI APPLICANT: IKEDA, HARUO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                             157 AAAAAAL 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IKEDA, HARUO
ISHIKAWA, JUN
HORIKAWA, HIROSHI
                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                             4.1%; Score 7; DB 9; Le
100.0%; Pred. No. 1.6e+02;
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o. 1.5e+02;
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Sequence 12279, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SAKAKI, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
APPLICANT: HATTORI, MASAHIRA
APPLICANT: HATTORI, NOVEL POLYNUCLEOTIDES
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
TILE REFERENCE: 249-262
CURRENT PILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9015
LENGTH: 319
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Streptomyces avermitilis US-10-156-761-9015
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PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 12279
LENGTH: 300
В
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APPLICANT:
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FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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                                                                                                                                                           / Match 4.1%; Score 7; DB (Local Similarity 100.0%; Pred. No. 1.8 es 7; Conservative 0; Mismatches
    301 AAAAALS 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43 AAAAAAL 49
                                                                                  · 9 AAAAALS 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 AAAAAAL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HATTORI, MASAHIRA
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SAKAKI, YOSHIYUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISHIKAWA, JUN
HORIKAWA, HIROSHI
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1.7e+02;
                                                                                                                                                                                                                        DB 9; Le
b. 1.8e+02;
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; Sequence 15, Application US/10281024

RESULT 23 US-10-281-024-15

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RESULT 25
US-09-905-291A-236
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US-10-156-761-9858
                                Sequence 236, Application US/09905291A Patent No. US20020160374A1 GENERAL INFORMATION:
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SEQ ID NO 9858
LENGTH: 340
TYPE: PRT
                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                             Query Match
 APPLICANT: Genentech, Inc
APPLICANT: Ashkenazi, Av:
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APPLICANT:
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SEQ ID NO 15
LENGTH: 324
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/156,761 CURRENT FILING DATE: 2002-05-29
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APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: OMURA, SATOSHI APPLICANT: IKEDA, HARUO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 249-262
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CURRENT FILING DATE: 2002-10-25
PRIOR APPLICATION NUMBER: US/09/674,337A
PRIOR FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: PCT/JP99/02305
PRIOR FILING DATE: 1999-04-30
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APPLICANT: Kyoko Higuc
                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                             122 ERRAVAV 128
                                                                                                                                               199 ERRAVAV 205
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Ashkenazi, Avi
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HORIKAWA, HIROSHI
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Pred. No. 1.8e+02;
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D. 1.9e+02;
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                                                                                                                                                                                                     0;
                                                                ; ORGANISM: Homo sapiens US-09-905-291A-236
   Matches
                                                                                                                            NUMBER OF SEQ ID NOS: 423
SEQ ID NO 236
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                                                                                                                                                                                                                            FILING DATE: 1999-12-20
                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT, FILING DATE: 1999-11-29
                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 1999-11-30
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                                                                                                                350
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Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
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Mather, Jennie P.
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Hillan, Kenneth, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Godowski, Paul J.
Grimaldi, Christopher J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pan, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Goddard, A.
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PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PCT/US00/00219
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PRIOR FILING DATE: 1999-12-20
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PRIOR EILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
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  y Match
Local Similarity 100.0%; Pred. No.
hes 7; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US99/28565
FILING DATE: 1999-12-02
APPLICATION NUMBER: PCT/US99/30095
FILING DATE: 1999-12-16
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     Mismatches
                               DB 9; L
o. 1.9e+02
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338 AAAAAAL 344

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RESULT 26
US-09-976-736-9
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                                                                                                                                     ORGANISM: Homo Sapien US-10-063-547-8
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CURRENT APPLICATION NUMBER: US/09/976,736
CURRENT FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: US/09/161,241
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Sullivan, John K
APPLICANT: Theill, Lars E
APPLICANT: Wang, Daguang
TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
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                                                                                                  Query Match
                                                                                                                                                                                                          SEQ ID NO 8
                                                                                                                                                                                                                                                          APPLICANT: WOOD, WILLIAM I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,547
CURRENT FILING DATE: 2002-05-02
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NUMBER OF SEQ ID NOS: 170
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ORGANISM: Human
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les 7; Conserv
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Local Similarity 100.0%; P
Concervative 0;
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338 AAAAAAL 344
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Conservative
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                                                                     Score 7; DB 9; Ler; pred. No. 1.9e+02; 0; Mismatches 0;
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US-09-902-853-236
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: 10466-14
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CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US/09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
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                 SEQ ID NO 236
                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: PCT.
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NEWSCORP.
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PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
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                                                   PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
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PRIOR APPLICATION NUMBER: PCT/US99/28214
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PRIOR FILING DATE: 1999-09-15
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PRIOR FILING DATE: 1999-09-13
                                    NUMBER OF SEQ ID NOS: 423
                                                                                                                                                                                 PRIOR APPLICATION NUMBER: PCT/US99/30095 PRIOR FILING DATE: 1999-12-16
                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: PCT/US99/28565
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PRIOR FILING DATE: 1999-11-30
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ENGTH:
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Filvaroff, Ellen
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Stewart, Timothy A.
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Mather, Jennie P.
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Hillan, Kenneth, J.
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Grimaldi, Christopher J.
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PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR PRIOR APPLICATION NUMBER: US 60/143,048
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PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/907,824
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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OR APPLICATION NUMBER: PCT/US99/21547
OR FILING DATE: 1999-09-15
OR APPLICATION NUMBER: PCT/US99/23089
OR FILING DATE: 1999-10-09
OR APPLICATION NUMBER: PCT/US99/28214
OR FILING DATE: 1999-11-29
OR APPLICATION NUMBER: PCT/US99/28313
OR FILING DATE: 1999-11-30
OR APPLICATION NUMBER: PCT/US99/28564
OR APPLICATION NUMBER: PCT/US99/28564
OR FILING DATE: 1999-12-02
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FILING DATE: 1999-09-13
APPLICATION NUMBER: PCT/US99/21090
FILING DATE: 1999-09-15
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FILING DATE: 1999-09-08
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Williams, P. Mickey
Wood, William, I.
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Stewart, Timothy A.
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Hillan, Kenneth, J.
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Mather, Jennie P.
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Grimaldi, Christopher J.
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Eaton, Dan L.
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D. US20020197671A1
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f, Ellen
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PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
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; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-824-236
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PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
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PRIOR APPLICATION NUMBER: PCT/US99/20944 PRIOR FILING DATE: 1999-09-13
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LENGTH: 350
                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/907,841
CURRENT ETLING DATE: 2001-11-20
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
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Best Local Similarity
                                 PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
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Hillan, Kenneth, J.
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Stewart, Timothy A.
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Mather, Jennie P.
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Grimaldi, Christopher
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Eaton, Dan L.
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                               1999-09-08
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-841-236
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LENGTH: 350
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PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-29
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Ashkenazi, Avi
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CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: 09/655,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 2000-02-22
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                                                                                     PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
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                                                  APPLICATION NUMBER: US 60/146,222 FILING DATE: 1999-07-28
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                 APPLICATION NUMBER: PCT/US99/20594 FILING DATE: 1999-09-08
APPLICATION NUMBER: PCT/US99/20944
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Eaton, Dan L.
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Botstein, David
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Gerritsen, Mary E.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
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Grimaldi, Christopher J.
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o. US20030003530A1
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Mather, Jennie P.
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US-09-904-011-236
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                                                                                                                                                                                                     SEQ ID NO 2
LENGTH: 350
TYPE: PRT
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Best Local S
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LENGTH: 350
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PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-11-09
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-29
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PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
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APPLICANT: Ruben, Steven M.
APPLICANT: Ruben, Steven M.
APPLICANT: Ruben, Steven M.
APPLICANT: Ruben, Steven M.
APPLICANT: PROVENT STEVEN CONTROL OF THE REPERBNCE: 1488.061002
CURRENT APPLICATION NUMBER: US/10/201,310
CURRENT FILING DATE: 2002-07-24
PRIOR APPLICATION NUMBER: US 60/033,870
PRIOR FILING DATE: 1996-12-20
PRIOR FILING DATE: 1996-12-20
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NUMBER OF SEQ ID NOS: 36
                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 08/993,198
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                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.1
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APPLICATION NUMBER: PCT/US99/30911
FILING DATE: 1999-12-20
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FILING DATE: 1999-12-02
APPLICATION NUMBER: PCT/US99/30095
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FILING DATE: 1999-11-30
APPLICATION NUMBER: PCT/US99/28564
FILING DATE: 1999-12-02
                                                                                                     Local
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FILING DATE: 1999-12-20
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  338 AAAAAAL 344
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                                       8 AAAAAAL 14
                                                                              Similarity 100.0%;
7; Conservative
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100.0%; Pred. No.
rative 0; Mismatch
                                                                                      4.1%; Score 7; DB 9; Len 100.0%; Pred. No. 1.9e+02;
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o. 1.9e+02;
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RESULT 33 US-10-063-616-8

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RESULT 34
US-09-906-742-236
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APPLICANT: Williams, F. Mickey
APPLICANT: Wood, William, T.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
CURRENT APPLICATION NUMBER: US/09/906,742
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION UNMBER: 09/665,350
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR APPLICATION NUMBER: PCT/US00/04414
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APPLICANT:
APPLICANT:
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APPLICANT: Filvaroff, El
APPLICANT: Gerritsen, Ma
APPLICANT: Goddwrd, Audr.
APPLICANT: Godowski, Pau
APPLICANT: Grimaldi, Chr.
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APPLICANT:
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Publication No. US20030013855A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 170
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CURRENT APPLICATION NUMBER: US/10/063,616
CURRENT FILING DATE: 2002-05-03
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Stewart, Timothy A.
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Hillan, Kenneth, J.
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Grimaldi, Christopher J.
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Gerritsen, Mary E.
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Eaton, Dan L.
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Filvaroff, Ellen
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Botstein, David
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                                                                                                                                                                                                                                               Nicholas F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sherman
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APPLICANT: Filvaroff, Ellen
APPLICANT: Filvaroff, Mary E.
APPLICANT: Goddard, Andrey
APPLICANT: Goddwski, Paul J.
                                                                  SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, application US/10063502 Publication No. US20030023042A1 GENERAL INFORMATION:
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APPLICANT:
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                                                                                                        CURRENT APPLICATION NUMBER: US/10/063,502
CURRENT FILING DATE: 2002-05-01
Prior Application removed - See File Wrap
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                                                                                                                                                                   TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3230R1C1
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                                                                                       NUMBER OF SEQ ID NOS: 170
                                                                                                                                                                                                                                                                                                                  APPLICANT:
ORGANISM: Homo Sapien
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PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
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PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
                                               LENGTH: 350
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PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
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PRIOR FILING DATE: 1999-10-05
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PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
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PRIOR FILING DATE: 1999-12-02
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PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
DELICA ETITUS CAMBER: US 60/146,222
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PRIOR APPLICATION NUMBER: PCT,
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Local Similarity 100.0%; Pred. No. 1:
Les 7; Conservative 0; Mismatches
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Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
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                                                                                                 See File Wrapper or Palm
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No. 1.9e+02;
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Matches 7; Conserv
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CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 2000-02-22
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PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
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PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
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                                                   PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-11-30
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PRIOR FILING DATE: 1999-09-15
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                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US99/21090
              APPLICATION NUMBER: PCT/US99/28564 FILING DATE: 1999-12-02
APPLICATION NUMBER: PCT/US99/28565
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Filvaroff, Ellen
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Botstein, David
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Wood, William,
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Hillan, Kenneth, J.
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Eaton, Dan L.
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Stewart, Timothy A.
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ms, P. Mickey
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100.0%; Pred. No.
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o. 1.9e+02;
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PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR APPLICATION E 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR HILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
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        CURRENT APPLICATION NUMBER: US/09/907.613
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/21090
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LENGTH: 350
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Best Local Similarity 100.0%; Pred. No. 1.5
Matches 7; Conservative 0; Mismatches
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Filvaroff, Ellen
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Wood, William, I.
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Hillan, Kenneth, J.
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Grimaldi, Christopher J.
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Eaton, Dan L.
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Stewart, Timothy A.
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Mather, Jennie P.
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PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILLING DATE: 1999-11-30
PRIOR FILLING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILLING DATE: 1999-12-16
PRIOR FILLING DATE: 1999-12-16
PRIOR PRIOR APPLICATION NUMBER: PCT/US99/30991
PRIOR PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILLING DATE: 1999-12-20
PRIOR FILLING DATE: 1990-12-20
PRIOR FILLING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14 CURRENT APPLICATION NUMBER: US/09/907,942 CURRENT FILING DATE: 2002-01-22 PRIOR APPLICATION NUMBER: PCT/US00/04414
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Publication No. US20030027146A1
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PRIOR FILING DATE: 1999-11-29
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Local Similarity 100.0%; P
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                                                                                                                              Williams, P. Mickey Wood, William, I.
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Stewart, Timothy A.
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Hillan, Kenneth, J.
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Grimaldi, Christopher J.
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Botstein, David
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Eaton, Dan L.
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SEQ ID NO 236
LENGTH: 350
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, Davi
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PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
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PRIOR FILING DATE: 1999-12-20
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PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
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PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
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PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
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             Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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                                                                                Godowski, Paul J.
Grimaldi, Christopher J.
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Gerritsen, Mary E.
Pan, James
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; ORGANISM: Homo Sapien US-09-904-820-236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 236
LENGTH: 350
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CURRENT FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
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PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
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PRIOR FILING DATE: 2000-02-22
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                                                                                                                          Sequence 236, A Publication No.
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PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
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PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
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PRIOR FILING DATE: 1999-09-13
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APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: PCT/US00/00219 PRIOR FILING DATE: 2000-01-05
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PRIOR FILING DATE: 1999-11-29
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PRIOR FILING DATE: 1999-10-05
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PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
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Local Similarity 100.0%; Pred. No. 1.9e+02;
nes 7; Conservative 0. No. 1.9e+02;
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Stewart, Timothy A.
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                                                                                                                                 Application US/09904859 o. US20030036060A1
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LENGTH: 350
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CURRENT FILING DATE: 2001-07-12
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PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
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    Query Match 4.1%; Score 7; DB Best Local Similarity 100.0%; Pred. No. 1. Matches 7; Conservative 0; Mismatches
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Matches
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PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
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PRIOR APPLICATION NUMBER: PCT/US99/28313
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NUMBER OF SEQ ID NOS: 423
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                                                                                               ORGANISM: Homo Sapien
                                                                                                              TYPE: PRT
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FILING DATE: 1999-12-20
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Mather, Jennie P.
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Hillan, Kenneth, J.
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Stewart, Timothy A.
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Conservative
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o. 1.9e+02;
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Search completed: July 6, 2003, 14:26:44 Job time : 24 secs

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Database :
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          122
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                                                                                         OMPA_ESCBL
OMPA_KLEPN
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TP50_TREPA
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MOTY_VIBAN
MOTY_VIBPA
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OMPA_SALTY
OMPA_ESCHE
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OMP4_NEIMA
Y899_MYCTU
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OMPA_ESCFE
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P24016 citrobacter
P02936 salmonella
P24754 escherichia
P24754 escherichia
O99124 escherichia
O99124 escherichia
P09146 enterobacte
P24017 klebsiella
P57414 buchnera ap
O9s399 vibrio angu
P46233 vibrio para
P04845 serratia ma
P38369 treponema p
P28612 bacillus su
P24755 serratia od
P46827 bacillus me
                                                                                                                                                    P38368
P45996
P45996
P22263
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P37726
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5 shigella dy
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7 mycobacteri
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bescherichia
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USG_PSEAE  DACD_SALTY YNS7_CORGL YC39_CYAPA H181_PSEAE DP3B_MYCTU SYEB_MYCTU ITH1_MESAU UCR1_RHOCA NIFS_ENTAG	YTXE_BACEV YTXE_BACEV YTXE_BACEV G6P2_STRCO MOTB_HELPV COOS_RHORU PMPE_CHLTR DTD_DEIRA TRMU_CHLPW DP3B_BACSU SAHTHEMA G6P1_STRCO HE_PARLI ITH1_HOUSE VTL2_RAT ITH1_MOUSE VTL2_RAT ITH1_MOUSE VTL2_RAT ITH1_NOUSE ACVS_NOCLA TCR1_BCOLI PSA1_DROWE PMP9_CHLPN Y421_BTJA Y105_SULSO ITH3_RAT ITH1_FOOM PMP9_CHLPN Y421_BAD TCR1_ECOLI PSA1_DROWE PMP9_CHLPN Y421_BAD TCR1_COCI PSA1_DROWE PMP9_CHCPN Y421_BAD PMP9_CHCPN Y421_BAD PMPYCLE COST_MYCHE PROB_XYLFA VANTB_METBA DPO1_ECOLI 194K_TRVSY VATB_METBA DPO1_ECOLI PSA1_WYCPN Y054_MYCPN PYRC_ECOST PILS_MYCH POIN_SETV WOTB_SALTY Y054_MYCH POIN_SETV WOTB_SALTY Y054_MYCHU POIN_SETV MOTB_SALTY Y054_MYCHU POIN_SETV MOTB_SALTY YN96_YEAST LPRE_MYCTU PYRC_ECOLI PHEA_NEIGO CYSN_BUCAI CALX_HELTU PYRC_DEIRA P15_CAEEL HMEN_DROME DCPY_ZYMMO	IB_ECOL

7 methanosarc 2 saccharomyc 3 mycobacteri 4 xylella fas

Q9ji51 rattus norv
Q61702 mus musculu
P27743 nocardia la
P02982 escherichia
P12881 drosophila
Q9z398 chlamydia p
Q57864 methanococc
P95879 sulfolobus
Q63416 rattus norv
Q03478 vibrio para
P00582 escherichia
P05080 tobacco rat

Q29052 sus scrofa Q48295 halobacteri

paracentrot streptomyce

5 drosophila 3 homo sapien 0 mesocricetu

mus musculu

P05649 bacillus su O51933 thermotoga

084877

6 rhodospiril
7 chlamydia t
1 deinococcus
5 chlamydia p

streptomyce helicobacte bacill

escherichia treponema

ALIGNMENTS

P02836 P06672 P53959 Q22918 Q9rvc3 P11031

mus musculu deinococcus caenorhabdi drosophila

zymomonas m saccharomyc mycobacteri

pseudomonas

pseudomonas mycobacteri mycoplasma mesocricetu

corynebacte salmonella

rhodobacter

Q9zhy3 P05020

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myxococcus

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2 salmonella 9 mycoplasma 8 escherichia

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01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Peptidoglycan-associated lipoprotein precursor
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-i- FUNCTION: VERY STRONGLY ASSOCIATED WITH THE PEPTIDOGLYCAN (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96198174; PubMed=8626299;
Rodriguez-Herva J.J., Ramos-Gonzalez M.I., Ramos J.L.;
"The Pseudomonas putida peptidoglycan-associated outer membrane lipoprotein is involved in maintenance of the integrity of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P43036
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P07176;
01-APR-1988
01-APR-1988
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PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
PROSITE; PS01068; OMPA; 1.
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PF00691; OmpA; 1.
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Pred. No. 9.8e-22;
4; Mismatches 46
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PEPTIDOGLYCAN-ASSOCIATED LIPOPROTEIN
N-ACYL DIGLYCERIDE (BY SIMILARITY).
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Peptidoglycan-associated lipoprotein precursor.
PAL OR EXCC OR B0741 OR Z0909 OR ECS0776.
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OShima T., Aiba H., Baba T., Fujita K., Hayashi K., Kashimoto K., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Kimura S., Kitagawa M., Makino K., Masauda S., Miki T., Mizobuchi K., Kimura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N., Sanpei G., Seki Y., Tagami H., Takemoto K., Wada C., Yanamoto Y., Yano M., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F. Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
MBU B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lazzaroni J.-C., Portalier R.;
"The excC gene of Escherichia coli K-12 required for cell envelope integrity encodes the peptidoglycan-associated lipoprotein (PAL)."; Mol. Microbiol. 6:735-742(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Nucleotide sequence of the gene for the peptidoglycan-associated lipoprotein of Escherichia coli K12.";
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                                                                                Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyi Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe i lida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunak Kuhara S., Shiba T., Hattori M., Shinagawa H.; "Complete genome sequence of enterohemorrhagic Escherichia coli "Complete genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                      Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kikkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potemousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 277:1453-1474(1997).
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"A 718-kb DAR sequence of the Escherichia
corresponding to the 12.7-28.0 min region
DNA Res. 3:137-155(1996).
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STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
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MEDLINE=21074935; PubMed=11206551;
MEDLINE=90078104; PubMed=2687247;
                   STRAIN-JM105
                                  SEQUENCE OF 1-30 FROM N.A.
                                                                                                                                                                                                                                                                         Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                       "genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
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                                                                       8:11-22(2001).
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on the linkage map.";
                                                                                                                                                      Yasunaga T.,
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RESULT 3
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Best Local :
P10324;
01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
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peptidoglycan-associated lipoprotein from Escherichia coll.";
Acta Crystallogr. D 57:317-319(2001).
-1- FUNCTION: Thought to play a role in bacterial envelope integrity.
--- Very strongly associated with the peptidoglycan.
--- currelinnar LOCATION: Attached to the outer membrane by a lipid
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                                                                                                                              PAL_HAEIN
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PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
PROSITE; PS01068; OMPA; 1.
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ECOGENE, EG10684; pal.
InterPro, IPR001145; Bac_OmpA.
Pfam; PF00691; OmpA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; S20547; S20547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Abergel C., Walburger A., Chenivesse S., Lazdunski C.; "Crystallization and preliminary crystallographic study of the peptidoglycan-associated lipoprotein from Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: TO OTHER PAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           their products, components of a multistep translocation system Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21111468; PubMed=11173492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Levengood S.K., Webster R.E.;
"Nucleotide sequences of the tolA and tolB genes and localization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteriol. 171:6600-6609(1989).
                                                                                                                                                                                                                                                                                                                                                                                                 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M28232; -; NOT_ANNOTATED_CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AE000177; AAC73835.1; -. D90713; BAA35407.1; -. AE005252; AAG55077.1; -. AP002553; BAB34199.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X05123; CAA28771.1; -. X65796; CAA46673.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MMLHIQIAAAAAALSVLTFMTGCANKSTSQVMVAPNAPTGY----TGVIYTGVAPLVDND 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity
67; Conser
                                                                                                                                                                                                                                                            EYNISLGERRANAVKMYLQGKGVSADQISIVSYGKEKPAVLGHDEAAYSKNRRAVLVY
                                                                                                                                                                                                                                                                                                    EYNMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELSY
                                                                                                                                                                                                                                                                                                                                                                                 EQARLQMQQLQQNNIVYFDLDKYDIRSDFAQMLDAHANFLRSNPSYKVTVEGHADERGTP 115
                                                                                                                                                                                                                                                                                                                                                                                                                                            ETVKALASKLP--SLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSR 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MQLNKVLKGLMIALPVMAIAACSSNKNASN-----DGSEGMLGAGTGMDANGGNGNMSSE 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105
173 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal; Lipoprotein; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                149
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37.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18824 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 285.5;
Pred. No. 5.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OMPA-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEPTIDOGLYCAN-ASSOCIATED LIPOPROTEIN
                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           449F9959C0274430 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DIGLYCERIDE.
                                                                                                                           153
   update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .9e-19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 173;
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Best Local
                    Query Match
                                                                                          CHAIN
LIPID
                                                                                                                                      PRINTS; PR01021; OMPADOMAIN.

Prodom; PD000930; Bac_OmpA; 1.

PROSTIE; PS00013; PROKAR_LIPOPROTEIN; 1.

PROSITE; PS01068; OMPA; 1.

Outer membrane; Signal; Lipoprotein; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;
                                                                                                                                                                                                                               Pfam; PF00691; OmpA;
                                                                                                                                                                                                                                                                                                                      EMBL; M19391; AAA24994.1; -. EMBL; M18878; AAA24940.1; -. EMBL; U32722; AAC22039.1; -.
                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Deich R.A., Metcalf B.J., Finn C.W., Farley J.E., Green B.A.;
"Cloning of genes encoding a 15,000-dalton peptidoglycan-associated outer membrane lipoprotein and an antigenically related 15,000-dalton protein from Haemophilus influenzae.";
J. Bacteriol. 170.480.400.7007
                                                         SEQUENCE
                                                                           DOMAIN
                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                      TIGR; HI0381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Outer membrane protein P6 precursor (OMP P6) (15 kDa peptidoglycan-associated lipoprotein) (PC protein).
PAL OR OMPP6 OR HI0381.
                                                                                                                                                                                                                                                                                         PIR; A28543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: TO OTHER PAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein P6.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=88085463; PubMed=3257200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND PARTIAL SEQUENCE MEDLINE=88115138; PubMed=2828309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95350630; PubMed=7542800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Rd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nelson M.B., Apicella M.A., Murphy T.F., Vankeulen H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning and sequencing of Haemophilus influenzae outer membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rekosh D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Infect. Immun. 56:128-134(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteriol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                                                                                                                                                         A27558;
     Similarity
                                                                                                                                                                                                                                                  IPR001145; Bac_OmpA
                                                       153 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KW20
                                                                                                                                                                                                                                                                                       A28543
                                                                                                                                                                                                                                                                                                         A27558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     170:489-498(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / ATCC 51907;
                                                       16108 MW;
30.7%;
   Pred.
 Score 264; DB 1; Pred. No. 4.4e-17;
                                                                        OMPA-LIKE
                                                                                      OUTER MEMBRANE PROTEIN P6
N-ACYL DIGLYCERIDE.
                                                       3DF358122EF17A11 CRC64;
                Length 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spotila L.D.,
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Matches

Conservative

20;

Mismatches

Indels

0;

Gaps

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RESULT 4
PAL_PASMU
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                                                          Query Match
Best Local
                                            Matches
                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                      EMBL; U16849; AAA79373.1; --
EMBL; AE006136; AAK03050.1; --
InterPro; IPR001145; Bac_OmpA.
                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Pasteurella multocida produces a protein with homology to the outer membrane protein of Haemophilus influenzae."; Infect. Immun. 63:989-993(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Outer membrane protein P6 precursor (OMP P6) (P6-like) (Peptidoglycan-associated lipoprotein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q51886;
                                                                                                                                                                  Outer membrane; Signal; Lipoprotein; Complete proteome SIGNAL 1 19 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pasteurella multocida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                              PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.; "Complete genomic sequence of pasteurella multocida Pm70."; "Complete genomic Sci. U.S.A. 98:3460-3465(2001).

Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).

-1- SUBCELLULAR LOCATION: ATTACHED TO THE OUTER MEMBRANE BY A LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-Pm7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hirsh D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-95172751; PubMed-7868272;
Kasten R.W., Hansen L.M., Hinojoza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pasteurella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAL OR PM0966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAL_PASMU
                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                           Pfam; PF00691; OmpA; 1
                                                                                                                                       LIPID
                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21145866; PubMed=11248100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANCHOR (By similarity).
SIMILARITY: TO OTHER PAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 NYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELSY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111 GYLAGKGVDAGKLGTVSYGEEKPAVLGHDEAAYSKNRRAVLAY 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70
              70
                                            50;
                                                            Similarity
                                                                                                                                                                                                                                PD000930;
                                                                                                                                                                                                                                              PR01021; OMPADOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VYFGFDKYDITGEYVQILDAHAAYLNATPAAKVLVEGNTDERGTPEYNIALGQRRADAVK 110
VYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVR
                                                                                                                                                                                                PS01068; OMPA;
                                                                                                  20
20
82
150
                                            Conservative
                                                                                                         ĀΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                              Bac_OmpA; 1.
PROKAR_LIPOPROTEIN; 1
                                                                                                     20 1
126 (
16213 MW;
                                                          30.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gamma subdivision; Pasteurellaceae;
                                            19;
                                                          Score 258; DB 1;
Pred. No. 1.5e-16;
                                                                                                                                                     OUTER MEMBRANE PROTEIN
                                                                                                                        OMPA-LIKE
                                                                                                                                    N-ACYL DIGLYCERIDE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                         170E7B13D2E9ED6C CRC64;
                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      150 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bieber D., Ruehl W.W.,
                                              34;
                                                                          Length 150
                                            Indels
                                            0
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                                            Gaps
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RESULT 5
PAL_LEGPN
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Qy
                                              Query Match
Best Local
                                 Matches
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                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaborate between the Swiss Institute of Bioinformatics and the EMBL outstatise the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1992 (Rel.
01-AUG-1992 (Rel.
01-OCT-1994 (Rel.
                                                                                                                                                        Lipoprotein; Outer membrane; SIGNAL 1 21
                                                                                                                                                                                     proDom; PD000930; Bac_OmpA; 1.
proSITE; pS00013; pROKAR_LIPOPROTEIN; 1.
proSITE; pS01068; OMPA; 1.
                                                                                                                                                                                                                                              InterPro; IPR001145; Bac_OmpA. Pfam; PF00691; OmpA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ludwig B., Schmid A., Marre R., Hacker J.;
"Cloning, genetic analysis, and nucleotide sequence of a determinant coding for a 19 kiloaliton peptidoglycan-associated protein (Ppl) of reciprolis and processing ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=91310296; PubMed=1855972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=AA100 / Serogroup 1;

MEDLINE=92114778; PubMed=1766377;

Englaberg N.C., Howe D.C., Rogers J.E., Arroyo J., Eisenste:

"Characterization of a Legionella pneumophila gene encoding"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAL OR PPLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antigen)
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                                                                                             SEQUENCE
                                                                                                          DOMAIN
                                                                                                                                          CHAIN
                                                                                                                                                                                                                                  PRINTS; PR01021; OMPADOMAIN
                                                                                                                                                                                                                                                                                PIR;
                                                                                                                                                                                                                                                                                                             EMBL; X60543; CAA43033.1;
                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: TO OTHER PAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Attached
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Legionella pneumophila.";
Infect. Immun. 59:2515-2521(1991).
-i- FUNCTION: VERY STRONGLY ASSOCIATED WITH THE PEPTIDOGLYCAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Legionellaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Legionella pneumophila
                                                                                                                          LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Legionellaceae; Legionella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lipoprotein antigen.";
dol. Microbiol. 5:2021-2029(1991).
                                                                                                                                                                                                                                                                              A60337; A60337
S16631; S16631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48
 29 SQVMVAPNAPTGYTGVIYTGVAPLVDNDETVKAL-----ASKLP----
                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYLSAKGVQAGQVSTVSYGEEKPAVLGHDEAAYSKNRRAVLAY 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELSY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VYFGFDKYNIEGEYVQILDAHAAFLNATPATKVVVEGNTDERGTPEYNIALGQRRADAVK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PPL).
                                                                                             176
                               Conservative
                                                                                             ĀΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . 23, Created)
. 23, Last sequence. 30, Last annotation.
                                                                                             18911 MW;
                                                                                                                                                                                                                                                                                                                                                        license agreement (See http://www.isb-sib.ch/announce/
                                               28.5%;
36.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                 30;
                                               Score 245;
Pred. No. 2
                                                                                                                                                          Antigen; Signal. POTENTIAL.
                                                                                                             OMPA-LIKE
                                                                                                                          N-ACYL DIGLYCERIDE (PROBABLE)
                                                                                                                                          PEPTIDOGLYCAN-ASSOCIATED LIPOPROTEIN.
                                   Mismatches
                                                                                             7D9C3EBECBE621DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to the outer membrane by a lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176
                                                 DB 1;
.7e-15
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15 SAVLVAACSKTPGSA---DGGAAVGDGDATAQGLGQMTHFAGQEPGESYTTQAPHNQLYL 71

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Q05146;
Q1-OCT-1994 (Rel.
01-OCT-1994 (Rel.
01-FEB-1995 (Rel.
                                                                                                                                                                                                                                                  PROSITE; PS01068; OMPA; 1.

Outer membrane; Transmembrane; Porin; Antigen; Signal.

POTENTIAL.

POTENTIAL.

POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salmonella typhimurium.";
J. Bacteriol. 174:7729-7742(1992).
-!- FUNCTION: STRUCTURAL PROTEIN THAT MAY PROTECT THE INTEGRITY OF
                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                        Pfam; PF00691; OmpA;
                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                              ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           membrane protein from Bordetella avium and expression of the gene in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=93077456; PubMed=1447140;
Gentry-Weeks C.R., Hultsch A.-L., Kelly S.M., Keith J.M.,
                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M96550; AAA22979.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane -!- SIMILARITY: BELONGS TO THE OMPA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Curtiss R. III;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BORAV
                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001145; Bac_OmpA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning and sequencing of a gene encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bordetella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bordetella avium
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138 NQASVEIISFGEERPIAFGTNEEAWSQNRRAEL 170
                                                                                        56
                                                                                                          18 TFMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVKALASKLPSLVYFDFDSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     132 LRMAGVSRQQIRVVSYGKERPANYGHDEASHAQNRRVEFIY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 LLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELSY 172
                                                                                                                                                 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72 FAYDDSTLASKYLPSVNAQAEYLKTHPGARVMIAGHTDERGSREYNVALGERRADTVAEI 131
                                                                                                                                                                                                                                                                                                      PD000930; Bac_OmpA; 1.
                                                                                                                                                              Similarity
                        TLKPEGRQLLDQVAQQARAIDLETIIAVGNTDSIGTEAYNMKLSERRAASVKAYLVSKGI 154
                                                     EIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGKGI
                                                                                TGIPGCDGVPVAQQPKEKPAPM------AAKVVFNADT------FFDFDKS
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                                                                                                                                                                                                         194 AA;
                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                        OMPADOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30, Created)
30, Last sequence update)
31, Last annotation update)
                                                                                                                                                                                                      165 (
21115 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           beta subdivision; Alcaligenaceae;
                                                                                                                                               22;
                                                                                                                                                          Score 185.5; DB 1
Pred. No. 7.3e-10;
                                                                                                                                                                                                                     OMPA-LIKE
                                                                                                                                                                                                                                   PRO-RICH.
                                                                                                                                                                                                                                                 OUTER MEMBRANE PROTEIN
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                                                                                                                                             Mismatches
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OM51_HAEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO1021; OMPADOMAIN.
PRODOM; PD000930; Bac_OmpA; 1.
PROSITE; PS01068; OMPA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 269:496-512(1995).
-!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
-!- SIMILARITY: BELONGS TO THE OMPA FAMILY.
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01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Outer membrane protein P5 precursor (OMP P5
OMPA OR OMPP5 OR HII164
Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Outer membrane; Transmembrane; Porin; Signal; Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities
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MEDLINE=95350630; PubMed=7542800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001145; Bac_OmpA.
InterPro; IPR000498; OmpA_tmen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=727;
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252 QATLDSIYGEMSQVKSAKVAVAGYTDRIGSDAFNVKLSQERADSVANYFVAKGVAADAIS 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF01389; OmpA_membrane; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF00691; OmpA;
                                               84 AAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGKGINQASVE 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P02934; 1QJP.
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                                                                                                                                                                                                                                   48;
                                                                                                                                                                                                                                                           Similarity
                                                                                                        PNTALNYNPWIGSINAGISYRFGQGAAPVVAAPEVVSKTFS-LNSDVTFAFGKANLKPQA
                                                                                                                                                                 PNAPTGY----TGVIY---TGVAPLVDNDETVKALASKLPSLVYFDFDSDEIKPQA 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 requires a license agreement
                                                                                                                                                                                                                                                                                                                                                 353 AA;
                                                                                                                                                                                                                                                                                                                                                                            326
272
                                                                                                                                                                                                                                Conservative
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BY SIMILARITY.
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                                                                                                                                                                                                                          61;
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144 IISFGEERPIAFGTNEE-----AWSQNRRAELS 171

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01-OCT-1994 (Rel. 3
01-OCT-1994 (Rel. 3
16-OCT-2001 (Rel. 4
                                                                                                                                                                                                                                                                                                                                DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of BioInformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   de Mot R., Proost P., van Damme J., Vanderleyden J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO THE OMPA FAMILY. STRONG, PSEUDOMONAS SPECIES OPRF.
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279 QVLVKDGVAPSRITAVGYGESRPVADNATEAGRAVNRRVEAS 320
                                                                                                        219 VKFDFDKSVVKPNSYGDVKNLADFMAQYPATNVEVAGHTDSIGPDAYNQKLSQRRADRVK 278
                                              130 NYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELS 171
                                                                                                                                                                70 VYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVR 129
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                                                                                                                                                                                                                       14;
                                                                                                                                                                                                                                                 Score 174; DB 1; Length 326, Pred. No. 1.5e-08;
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PORF\_PSEAE STANDARD; PRT; 350 AA. p13794; 01-JAN-1990 (Rel. 13, Created) 01-JAN-1990 (Rel. 13, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update)

Outer membrane porin F precursor.

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RESULT 9
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01-OCT-1994 (Rel. 30, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation updat
01-NOV-1995 (Rel. 32, Dast annotation updat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L20309; AAA03346.1; -. HSSP; P02934; 1QJP.
InterPro; IPR001145; Bac_OmpA.
InterPro; IPR000498; OmpA_tmen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Munson R.S. Jr., Grass S., West R.;
"Molecular cloning and sequence of the gene for outer membrane
protein P5 of Haemophilus influenzae.";
Infect. Immun. 61:4017-4020(1993).
-i- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
-i- SIMILARITY: BELONGS TO THE OMPA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND STRAIN=1613 / Serotype
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P38368;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00691; OmpA; 1. Pfam; PF01389; OmpA_membrane; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=93366472; PubMed=8359929
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                                                                                                                                          144 IISFGEERPIAFGTNEE------AWSQNRRAELS 171
                                                                                                                                                                                                                                                                                                                      193 PNTAINYNPWIGSINAGISYRFGQGAAPVVAAPEVVSKTFS-LNSDVTFAFGKANLKPQA
                                                                                  312 ATGYGKANPVTGATCDQVKGRKALIACLAPDRRVEIA 348
                                                                                                                                                                                                    252 QATLDSIYGEMSQVKSAKVAVAGYTDRIGSDAFNVKLSQERADSVANYFVAKGVAADAIS
                                                                                                                                                                                                                                                            84 AAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGKGINQASVE 143
                                                                                                                                                                                                                                                                                                                                                                             35 PNAPTGY-----TGVIY---TGVAPLVDNDETVKALASKLPSLVYFDFDSDEIKPQA 83
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316 O)
37594 MW;
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30.6%; Pred. No. 1.8e-08;
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RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Garber R.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
opportunistic pathogen.";
RI "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
opportunistic pathogen.";
RI Nature 406:959-964(2000).
C. -!- FUNCTION: HAS PORIN ACTIVITY, FORMING SMALL WATER-FILLED CHANNELS.
C. -!- FUNCTION: HAS PORIN ROLE IN DETERMINING CELL SHAPE AND ABILITY
C. -I SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
C. -!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
C. -!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
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C. -!- SUBCELLULAR LOCATION: OF THE ONDER PRESENT.
C. -!- SUBCELLULAR LOCATION: OF THE ONDER PRESENT.
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Duchene M., Schweizer A., Lottspeich F., Krauss G., Marget J
Vogel K., von Specht B.-U., Domdey H.;
"Sequence and transcriptional start site of the Pseudomonas aeruginosa outer membrane porin protein F gene.";
                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR01021; OMPADOMAIN.
ProDom; PD000930; Bac_Ompa; 1.
PROSITE; PS01068; OMPa; 1.
                                                                                                                                                                                                                    SEQUENCE
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MEDLINE=20437337; PubMed=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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130 NYLLGK-GINQASVEIISFGEERPIAFGTNEEAWSQNRRAE 169 : |: |: |: |: || | | : || | |
                                                        242 VKFDFDKSKVKENSYADIKNLADFMKQYPSTSTTVEGHTDSVGTDAYNQKLSERRANAVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AE004603; AAG05166.1; -.
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                                                                                                                                                         Similarity
                                                                                               VYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVR 129
                                                                                                                                                                                                                                                                                                                                                                          proteome.
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350
195
191
193
193
                                                                                                                                                                                                                321 (
37639 MW;
                                                                                                                                                       19.9%;
                                                                                                                                                   Score 171.5; DB 1
Pred. No. 2.7e-08;
                                                                                                                                                                                                                                                                                                           OUTER MEMBRANE PORIN F.

3 X 2 AA TANDEM REPEATS OF
                                                                                                                                                                                                                                    OMPA-LIKE
                                                                                                                                                                                                                D1F758F076874383 CRC64;
                                                                                                                                       Mismatches
                                                                                                                                                                        DB 1; Length
                                                                                                                                     Indels
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RESULT 11

OND53_HAEIN
ID ONA53_H
AC P4595
DT 01-NOV
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RESULT 12
PORF_PSESY
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Best Local
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DOMAIN
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-i- FUNCTION: ACTS AS A FIMBRIAE SUBUNIT.

-i- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00691; OmpA; 1. Pfam; PF01389; OmpA_membrane; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-NTHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OMPA OR OMPP5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (Rel. 01-NOV-1995 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Outer membrane; Transmembrane; Porin; Signal; Fimbria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD000930; Bac_OmpA; 1. PROSITE; PS01068; OMPA; FALSE_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L08448; AAA24959.1; -. HSSP; P02934; 1BXW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sirakova T., Kolattukudy P.E., Murwin D., Billy J., Leake E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Outer membrane protein P5 precursor (OMP P5) (Fimbrin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P45996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR01021; OMPADOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000498,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO THE OMPA FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lim D., Demaria T., Bakaletz L.;
"Role of fimbriae expressed by nontypeable Haemophilus influenzae in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=94222575; PubMed=7909539;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001145; Bac_OmpA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HAEIN
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                                                                                                                                                                                                                                                                                    84 AAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGKGINQASVE 143
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                                                                                                                                                                           IISFGEERPIAFGTNEE---
                                                                                                                                                                                                                                 QATILDSVYGEISQVKSRKVAVAGYTNRIGSDAFNVKLSQERADSVANYFVAKGVAADAIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pean Bioinformatics Institute. The
non-profit institutions as long
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                                                                                                                                                                                                                                                                                                                                                                                                PNAPTGY-----TGVIY---TGVAPLVDNDETVKALASKLPSLVYFDFDSDEIKPQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              359 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38340 MW;
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29.9%;
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 165.5; DB Pred. No. 9.9e-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OUTER MEMBRANE PROTEIN P5
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OMPA-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              576B1C59B4818C37 CRC64;
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                                                                                                                                                                        -AWSQNRRAELS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         There are no restrictions on ng as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 359;
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                                                                                                                                                                   RESULT 13
YIAD_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical lipoprotein yiaD precursor.
YIAD OR B3552.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Outer membrane; Transmembrane; Porin; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Bacteriol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ullstrom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=91100367; PubMed=1898935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-ATCC 19310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas syringae (pv. syringae)
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01-AUG-1991 (Rel.
15-JUL-1999 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00691; OmpA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              family Pseudomonadaceae: sequence of the Pseudomonas syringae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *Conservation of the gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hancock R.E.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PORF_PSESY
                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Integral membrane protein. PTM: TWO DISULFIDE BONDS ARE PRESENT. SIMILARITY: BELONGS TO THE OMPA FAMILY. STRONG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: HAS PORIN ACTIVITY, FOR ALSO HAS A STRUCTURAL ROLE IN DET TO GROW IN LOW-OSMOLARITY MEDIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A39139; A39139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PSEUDOMONAS SPECIES OPRF.
                                                                                                                                                                                                                                            296 QVLVNQYGVGASRVNSVGYGESKPVADNATEAGRAVNRRVE
                                                                                                                                                                                                                                                                                130 NYLLGK-GINQASVEIISFGEERPIAFGTNEEAWSQNRRAE 169
                                                                                                                                                                                                                                                                                                                         236
                                                                                                                                                                                                                                                                                                                                                             70
                                                                                                                                                                                                                                                                                                                                                                                                  36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PD000930; Bac_OmpA; 1. : PS01068; OMPA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PR01021; OMPADOMAIN.
                                                                                                                                                                                                                                                                                                                                                         VYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVR
                                                                                                                                                                                                                                                                                                                     VKFDFDKSVVKPNSYGDIKNLADFMQQYPQTTTTVEGHTDSVGPDAYNQKLSERRANAVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR001145; Bac_OmpA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .A., Siehnel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           344 AA;
                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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19,
38,
                                                                                                                                                                                                                                                                                                                                                                                                              19.0%;
35.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36567 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for outer membrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Woodruff W., Steinbach
                                                                                                                                                                                                                                                                                                                                                                                                14;
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 163.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OMPA-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OUTER MEMBRANE PORIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5B463D9AD973D755 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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         RESULT 14
OMP3_NEIGO
ID OMP3_NI
AC P07050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restricted the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO THE OMPA FAMILY. STRONG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning and nucleotide sequence of bisC, the structural gene for biotin sulfoxide reductase in Escherichia coli.";
J. Bacteriol. 172:2194-2198(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner i "Analysis of the Escherichia coli genome. V. DNA sequence of the region from 76.0 to 81.5 minutes."; Nucleic Acids Res. 22:2576-2586(1994).
                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR01021; OMPADOMAIN. ProDom; PD000930; Bac_OmpA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EcoGene; EG12271; yiaD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M34827; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE000432; AAC76576.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U00039; AAB18529.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- CAUTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=K12 / MG1655;
MEDLINE=94316500; PubMed=8041620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein; Membrane; Lipoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS01068; OMPA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90202748; PubMed=2180922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-104 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFT IN POSITION 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Attached to the membrane
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  211
                                      167
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                                                                                                                        107
                                                                                                                                                                 95
                                                                                                                                                                                                     47 TGVAPLVDNDETVKALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAG 106
                                                                                                                                                                                                                                                                    Similarity
                                                                                                                        HTDERGSREYNMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNR
                                        RAELS
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RVEIT
                                                                                YTDSTGGHDLNMRLSQQRADSVASALITQGVDASRIRTQGLGPANPIASNSTAEGKAQNR
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                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                     148.
                                                                                                                                                                                                                                                                                                                             AA;
  215
                                        171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bac_OmpA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROKAR_LIPOPROTEIN; 1.
                                                                                                                                                                                                                                                                                                                                                                      20
219
21
                                                                                                                                                                                                                                                                                                                             22169 MW;
                                                                                                                                                                                                                                                                  17.9%;
31.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bac_OmpA.
                                                                                                                                                                                                                                           21;
                                                                                                                                                                                                                                                          Score 154; Db 1
                                                                                                                                                                                                                                                                                                                                                     OMPA-LIKE
                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL LIPOPROTEIN YIAD.
N-ACYL DIGLYCERIDE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                             8EDED55A0A66E368 CRC64;
                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plunkett G. III, Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             as its content
                                                                                                                                                                                                                                                                                     ۳.
                                                                                                                                                                                                                                               61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Usage
                                                                                                                                                                                                                                                                                     Length 219;
                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
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OMP3\_NEIGO STANDARD; P07050; 01-APR-1988 (Rel. 07, Created)

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Best Local
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DISULFID
            P24747;
01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Outer membrane protein A (Outer membrane protein)
                                                                                             ESCFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The DNA sequence of the structural gene of gonococcal protein III and the flanking region containing a repetitive sequence. Homology protein III with enterobacterial OmpA proteins.";
J. Exp. Med. 165:471-482(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neisseria gonorrhoeae.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1988 (Rel. 07, Last sequence update) 01-FEB-1994 (Rel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=87139801; PubMe Gotschlich E.C., Seiff
                                                                               OMPA_ESCFE
                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X05105; CAA28752.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                         REPEAT
                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Outer membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom; PD000930; Bac_Ompa; 1. PROSITE; PS01068; OMPA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR01021; OMPADOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=485
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                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane. MISCELLANEOUS: PIII IS CLOSELY ASSOCIATED MITH PART, BUT NOT ALL OF THE PI MOLECULES IN THE GONCOCCAL OUTER MEMBRANE.
MISCELLANEOUS: A PORTION OF THE PIII IS EXPOSED TO THE SURFACE I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTACT GONOCOCCI; THE PROTEIN CAN BE LABELED WITH IODINE AND REACTS WITH MABS.
SIMILARITY: BELONGS TO THE OMPA FAMILY. STRONG, TO N.MENINGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A27894; A27894.
rPro; IPR001145; Bac_OmpA.
                                                                                                                                                143 YNQALSERRAYVVANNLVSNGVPASRISAVGLGESQ 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF00691; OmpA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             membrane
                                                                                                                                                                                                                               56
                                                                                                                                                                                                                                                           35
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                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                         YNMSLGERRAVAVRNYLLGKGINQASVEIISFGEER 151
                                                                                                                                                                                                    DETISLSAKTL-----FGFDKDSLRAEAQDNLKVLAQRLSRTNVQSVRVEGHTDFMGSEK
                                                                                                                                                                                                                               DETVKALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSRE
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                                                                                                                                                                                                                                                          Conservative
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                                                                               STANDARD;
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76
70
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175
                                                                                                                                                                                                                                                                                                              25540 MW;
                                                                                                                                                                                                                                                                       17.6%;
36.5%;
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                                                                                                                                                                                                                                                          13;
                                                                                                                                                                                                                                                                       Score 151.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                            BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                          OUTER MEMBRANE PROTEIN P.II
4 X 2 AA TANDEM REPEATS OF
                                                                                                                                                                                                                                                                                                                                         OMPA-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                DAE9AAECA66FB199
            membrane protein II) (Fragment).
                                                                                                                                                                                                                                                         Mismatches
                                                                               243
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                                                                               A
                                                                                                                                                                                                                                                                                   DB 1;
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                                                                                                                                                                                                                                                          43;
                                                                                                                                                                                                                                                                                                                CRC64;
                                                                                                                                                                                                                                                                                  Length 236;
                                                                                                                                                                                                                                                          Indels
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Matches 42
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J. Gen. Microbiol. 137:1911-1921(1991).
-!- FUNCTION: REQUIRED FOR THE ACTION OF COLICINS K AND L AND FOR T
                                                                                                                                                                                                                                                                                                                                                                           VARIANT
NON_TER
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=ATCC 35471, ATCC 35469, a MEDLINE=92065252; PubMed=1955870
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                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lawrence J.G., Ochman H., Hartl D.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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SUBUNIT: MONOMER (PROBABLE).
SUBURITAR LOCATION: Integral membrane protein. Oute
SUBCELLULAR LOCATION: TOTOGYRAIN THAT OF STRAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE OMPA FAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STABILIZATION OF MATING AGGREGATES IN CONJUGATION. SERVES AN RECEPTOR FOR A NUMBER OF T-EVEN LIKE PHAGES. ALSO ACTS AS A WITH LOW PERMEABILITY THAT ALLOWS SLOW PENETRATION OF SMALL
                                                                                      166
                                         160
                                                                                                                                  107
                                                                                                                                                                              106
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PF01389; OmpA_membrane;
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                                                                                                                                                                                                                                                                                         Similarity
LIDCLAPDRRVEI 238
                                                                                                                                                                         VAPAPAPAPEVQTKHFTLKSDVLFNFNKATLKPEGQAALDQLYSQLSNLDPKDGSVVVLG
                                                                                      YTDRIGSDAYNQGLSERRAQSVVDYLISKGIPADKISARGMGESNPVTGNTCDNVKQRAA
                                       --EAWSQNRRAEL 170
                                                                                                                                HTDERGSREYNMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNE------
                                                                                                                                                                                                                      VAPLVDNDETVKALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTT--NQTARVLVAG
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31.6%;
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E -> D (IN STRAIN ATCC 35469).
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STRAIN-0157:H7 / RIMD 0509952;
MEDLINE-21156231; PubMed-11258796;
Hayashi T., Makino K., Ohnishi M.,
Han C.-G., Ohtsubo E., Nakayama K.,
                                                                                                                                                                                                                                 Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K. Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7\text{-}28.0 min region on the linkage manna Res. 3:137\text{-}155(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N. Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Blattner F.R., Piunkett G. III, Bloch C.A., Perna N.T., Burland Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F. Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Movva N.R., Nakamura K., Inouye M.;
"Gene structure of the OmpA protein, a major surface protein
"Secherichia coli required for cell-cell interaction.";
                                                                                                                                                                                 Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=0157:H7 / EDL933 / ATCC 700
MEDLINE=21074935; PubMed=11206551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=K12 / MG1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli, and Escherichia coli 0157:H7.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                     SEQUENCE FROM
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21-JUL-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=81170587; PubMed=6260961;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Nucleotide sequence of the gene cmpA coding the outer membrane protein II of Escherichia coli K-12."; Nucleic Acids Res. 8:3011-3024(1980).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complete genome sequence of Escherichia coli K-12."; nce 277:1453-1474(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83334;
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                                 Kurokawa
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      Tanaka
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   Yokoyama
Tobe T.,
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"Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";

DNA Res. 8:11-22(2001).
                           beta-barrel membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98291876; PubMed=9629924;
Molloy M.P., Herbert B.R., Walsh B.J., Tyler M.I., Traini M.,
Sanchez J.-C., Hochstrasser D.F., Williams K.L., Gooley A.A.;
"Extraction of membrane proteins by differential solubilization
separation using two-dimensional gel electrophoresis.";
Electrophoresis 19:837-844(1998).
                        "Structural and functional roles of the surface-exposed loops of the beta-barrel membrane protein OmpA from Escherichia coli.";
                                                                               Koebnik R.;
                                                                                                        MEDLINE=99296577;
                                                                                                                                       TOPOLOGY
                                                                                                                                                                                                                                                                                           MEDLINE=94148615;
                                                                                                                                                                                                                                                                                                                                                                                                                          Sugawara E., Nikaido H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-K12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Bacteriophage receptor area of outer membrane protein OmpA of Escherichia coli K-12.";
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STRAIN=K12 / W3110;
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Link A.J., Robison K., Church G.M.;
"Comparing the predicted and observed properties
in the genome of Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=K12 / W3110;
Pasquali C., Sanchez J.-C., Ravier F., Golaz O., Hughes G.J
Frutiger S., Paquet N., Wilkins M., Appel R.D., Bairoch A.,
Hochstrasser D.F.;
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Chen R., Schmidmayr W., Kramer C., Chen-Schmeisser
"Primary structure of major outer membrane protein
of Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                          TOPOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                    "Pore-forming activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=92129334;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Electrophoresis 18:1259-1313(1997).
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embrane protein OmpA from 181:3688-3694(1999).
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                                                                                                        PubMed=10368142;
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II (ompA protein)
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SWISS-2DPAGE; P02934; COLI.

SWISS-2DPAGE; P02934; COLI.

ECOZDBASE; F024.5; GTH EDITION.

ECOZDBASE; F028.0; GTH EDITION.

ECOZDBASE; F033.0; GTH EDITION.

ECOZDBASE; F033.1; GTH EDITION.

ECOZDBASE; F033.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- FUNCTION: REQUIRED FOR THE ACTION OF COLICINS K AND L AND FOR THE ACTION OF COLUMN RECEPTOR FOR A NUMBER OF T-EVEN LIKE PHAGES. ALSO ACTS AS A WITH LOW PERMEABILITY THAT ALLOWS SLOW PENETRATION OF SMALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE005286; AAG55443.1; -. EMBL; AP002554; BAB34464.1; -.
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PDB; 18XW; 30-DEC-98.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; V00307; CAA23588.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       spectrometry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Proteomics on full-length membrane proteins using mass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20222957; PubMed=10757971;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pautsch A., Schulz G.E.; "High-resolution structure of the OmpA membrane domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kaback H.R., Faull K.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20229895; PubMed=10764596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Structure of the outer membrane protein A transmembrane domain.";
"at. Struct. Biol. 5:1013-1017(1998).
[17]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               le Coutre J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [16]
X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 22-192.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              {-RAY CRYSTALLOGRAPHY (1.65 ANGSTROMS)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: MONOMER (PROBABLE).
SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
MASS SPECTROMETRY: MM-35177; METHOD-ELectrospray; RANGE-22-346.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE OMPA FAMILY.
                                         160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AE000198; AAC74043.1; -. D90733; BAA35715.1; -. D90734; BAA35722.1; -.
                                                                                                                                                                                                       200
                                                                                                                                                                                                                                                        49
                                                                                                                                                                                                                                                                                                          42;
                                                                                                                                                                                                                                                                                                                                   Similarity
                                      --EAWSQNRRAEL 170
                                                                                                                                       HTDERGSREYNMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGINE-----
                                                                                                                                                                                            VAPAPAPAPEVQTKHETLKSDVLENFNKATLKPEGQAALDQLYSQLSNLDPKDGSVVVLG
                                                                                     YTDRIGSDAYNQGLSERRAQSVVDYLISKGIPADKISARGMGESNPVTGNTCDNVKQRAA
                                                                                                                                                                                                                                             VAPLVDNDETVKALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTT--NQTARVLVAG
                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           298:273-282(2000).
                                                                                                                                                                                                                                                                                                                                17.2%;
31.6%;
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                                                                                                                                                                                                                                                                                                  Score 148.5; DB 1;
Pred. No. 3.2e-06;
0; Mismatches 60;
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                                                                                                                                                                                                                                                                                                                                                    Length 346;
                                                                                                                                                                                                                                                                                                     Indels
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  Best Local Similarity
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P02935;
21-JUL-1986
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Nucleic Acids Res. 10:2367-2378(1982).

"I FUNCTION: REQUIRED FOR THE ACTION OF COLICINS K AND L AND FOR THE STABILIZATION OF MATING AGGREGATES IN CONJUGATION. SERVES AS A RECEPTOR FOR A NUMBER OF T-EVEN LIKE PHAGES. ALSO ACTS AS A PORIN WITH LOW PERMEABILITY THAT ALLOWS SLOW PENETRATION OF SMALL
                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR01021; OMPADOMAIN. ProDom; PD000930; Bac_Ompa; 1. PROSITE; PS01068; OMPA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001145; Bac_OmpA.
InterPro; IPR000498; OmpA_tmem.
Pfam; PF00691; OmpA; 1.
Pfam; PF01389; OmpA_membrane; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=82221414; PubMed=6283478; Braun G., Cole S.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SHIDY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; V01344; CAA24638.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shigella
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                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The nucleotide sequence coding for major outer membrane protein OmpA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=622;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOLUTES (BY SIMILARITY).
SUBUNIT: MONOMER (PROBABLE).
SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
SIMILARITY: BELONGS TO THE OMPA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            320 LIDCLAPDRRVEI 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane; Phage recognition; Signal; Repeat;
                                                                                                                                    351
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126
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207
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306
                                                                                  37741
17.2%;
31.6%;
                                                                                MW;
Score 148.5; DB 1 Pred. No. 3.3e-06;
                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                         BY SIMILARITY
                                                                                                                                    OMPA-LIKE
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4 X 2 AA TANDEM REPEATS OF A-P
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                                                                                1499AA5F5395B35B CRC64;
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                                                                                                                                                                                                                                                                                                            Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Melson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Cotton M.D., Scarlato V., Massignan V., Pizza M., Grandi G., Sun L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *Sequence of the structural gene (rmpM) for the class 4 outer membrane protein of Neisseria meningitidis, homology of the protein to gonococcal protein III and Escherichia coli OmpA, and construction of meningococcal strains that lack class 4 protein. *; Infect. Immun. 57:2066-2071(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C., Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd Jagels K., Leather S., Moule S., Mungall K., Quail M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G., "Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OMP4_NEIMA
P38367;
                                                                                                                                                       MC58.";
Science 287:1809-1815(2000).
Science 287:11AR LOCATION: Integral membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CCUG 18241 / M986 / Serogroup B / SMEDLINE=89277523; PubMed=2499543; Klugman K.P., Gotschlich E.C., Blake M.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neisseria meningitidis (serogroup A), Neisseria meningitidis (serogroup B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Outer membrane protein class 4 precursor. RMPM OR NMA2105 OR NMB0382.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1994 (Rel. 30, Created)
16-OCT-2001 (Rel. 40, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                   Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=MC58 / Serogroup B;
MEDLINE=20175755; PubMed=10710307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature
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MEDLINE=20222556; PubMed=10761919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                    "Complete genome sequence of Neisseria meningitidis serogroup B
European
                                                                                                                                                 SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160
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      Bioinformatics Institute.
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   restrictions
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tions on its
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Q10557;
01-OCT-1996;
01-OCT-1996;
15-JUN-2002;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein Rv0899.
RV0899 OR MT0922 OR MTCY31.27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PROSITE; PS01068; OMPA; 1.
                                                                                                                                                                                                                  MEDLINE-98295987; PubMed-9634230;
                                                                                                                                                                                                                                          STRAIN-H37Rv;
                                                                                                                                                                                                                                                                                                                          Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis.
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                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1773;
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Pfam; PF00691; OmpA; 1.
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242 AA;
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BY SIMILARITY.
MISSING (IN ST
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I -> V (IN STRAIN MC58).
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OMPA_CITER
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                 01-MAR-1992 (Rel. 21, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Outer membrane protein A (Outer membrane protein
                                                                                                                                 01-MAR-1992 (Rel.
01-MAR-1992 (Rel.
01-NOV-1995 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom; PD000930; Bac_OmpA; 1.
PROSITE; PS01068; OMPA; FALSE_NEG.
Hypothetical protein; Transmembrane; Complete proteome.
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                                                                                                                                                                              OMPA_CITER P24016;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 393:537-544(1998).
SEQUENCE FROM N.A STRAIN=OS60;
                                                            Citrobacter
                                                                        Bacteria; Proteobacteria;
                                                                                        Citrobacter freundii
                                                                                                      OMPA
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                                          NCBI_TaxID=546;
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                                                                                                                                                                                                                                                                      281 VADYLVARGVAGDHIATVGLGSVNPIASNATPEGRAKNRRVEI 323
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                                                                                                                                                                                                                                                                                                    VRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAEL 170
                                                                                                                                                                                                                                                                                                                                                               --VYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVA 127
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33574 MW;
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23.3%;
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                                                                                                                                                               Created)
                                                                       gamma subdivision; Enterobacteriaceae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 143; DB 1; Pred. No. 9.5e-06;
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"Molecular and evolutionary relationships among enteric bacteria.";
J. Gen. Microbiol. 137:1911-1921(1991).
-i- FUNCTION: REQUIRED FOR THE ACTION OF COLICINS K AND L AND FOR TH
                                                                                                                                                                                 OMPA_SALTY P02936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                               21-JUL-1986 (Rel. 01, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Outer membrane protein A precursor (Outer membrane protein A precursor (Outer membrane major heat-modifiable protein).
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REPEAT
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                                                                                                                                                                                                                                           SALTY
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Pfam; PF01389; OmpA_membrane; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M63354; AAA23095.1; -. HSSP; P02934; 1QJP.
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SUBUNIT: MONOMER (PROBABLE).
SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane
SIMILARITY: BELONGS TO THE OMPA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STABILIZATION OF MATING AGGREGATES IN CONJUGATION. SERVES AS RECEPTOR FOR A NUMBER OF T-EVEN LIKE PHAGES. ALSO ACTS AS A 1 WITH LOW PERMEABILITY THAT ALLOWS SLOW PENETRATION OF SMALL
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                                                                                                                                                                                                                                                                                                                                                                                                    148 GEERPIAFGINE-----EAWSQNRRAEL 170
                                                                                                                                                                                                                                                                                                                                                  202 GESNPVTGNTCDNVKARAALIDCLAPDRRVEI 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                     142 MYSQLSNLDPKDGSVVVLGFTDRIGSDAYNQGLSEKRAQSVVDYLISKGIPSDKISARGM 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90 QAQFLTT--NQTARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGKGINQASVEIISF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82 GLLSVGVSYRFGQQEEAAPVVVAPAPAPEVQTKHFTLKSDVLFNFNKATLKPEGQQALDQ 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43 GVIYTGV-----APLVDNDETVKALASK---LPSLVYFDFDSDEIKPQAAAILDE 89
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28.3%;
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Pred. No. 9.9e-06;
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Salmonella OMPA OR STM1070

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     SEQUENCE
                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                           ProDom; PD000930; Bac_OmpA; 1. PROSITE; PS01068; OMPA; 1.
                                                                                                                                                                                                                                                                                                                                           StyGene; SG10263; ompA.
InterPro; IPR001145; Bac_OmpA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBUNIT: MONOMER (PROBABLE).
-!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
-!- SIMILARITY: BELONGS TO THE OMPA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
McClelland M., Sanderson K.E., Spiet
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MEDLINE=83287368; PubMed=6349993;
                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A03436; MMEBAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Freudl R., Cole S.T., {}^{\prime} "Cloning and molecular characterization of the ompA gene from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 413:852-856(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Waterston R., Wilson R.K.;
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SUBUNIT: MONOMER (PROBA
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                                                                                                                                                                                                                                                                                                                                                                                         P02934;
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BY SIMILARITY.
V -> F (IN REF. 1).
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Pfam; PF01389; OmpA_membrane;
ProDom; PD000930; Bac_OmpA; 1.
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EMBL; M63347; AAA24238.1;
HSSP; P02934; 1BXW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lawrence J.G., Ochman H., Hartl D.L.; "Molecular and evolutionary relationships among enteric bacteria."; J. Gen. Microbiol. 137:1911-1921(1991).
                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                          Outer membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content
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01-NOV-1995 (Rel.
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SUBUNIT: MONOMER (PROBABLE).
SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 324 LIDCLAPDRRVEI 336
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4 X 2 AA TANDEM REPEATS OF A-P.
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bred. No. 1.7e-05;
                                                                                                                                                                      POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lawrence J.G., Ochman H., Hartl D.L.;
"Molecular and evolutionary relationships among enteric bacteria.";
J. Gen. Microbiol. 137:1911-1921(1991).
-!- FUNCTION: REQUIRED FOR THE ACTION OF COLICINS K AND I. AND FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
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                                            InterPro; IPRO01145; Bac_OmpA.
InterPro; IPRO00498; OmpA_tmem.
Pfam; PF006591; OmpA; 1.
Pfam; PF01389; OmpA_membrane; 1.
ProDom; PD00930; Bac_OmpA; 1.
                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-ATCC 33429; ATCC 29907, and ATCC 33430;
MEDLINE-92065252; PubMed-1955870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia
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                                                                                                                                                                                                     EMBL; M63344; AAA24239.1; -. EMBL; M63345; AAA24242.1; -. HSSP; P02934; 10JP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
Outer membrane; Transmembrane; Phage recognition; Repeat; Porin
                                                                                                                                                                                                                                                                        EMBL; M63344; AAA24235.1; -. EMBL; M63344; AAA24239.1; -.
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                               PROSITE; PS01068; OMPA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: MONOMER (PROBABLE).
SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF STRAIN ATCC 33429.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STABILIZATION OF MATING AGGREGATES IN CONJUGATION. SERVES AS A RECEPTOR FOR A NUMBER OF T-EVEN LIKE PHAGES. ALSO ACTS AS A PORIN WITH LOW PERMEABILITY THAT ALLOWS SLOW PENETRATION OF SMALL
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OMPA-LIKE.
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01-MAR-1989 (Rel. 10, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
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                                                                                                             "Molecular characterization of the gene coding for major outer membrane protein OmpA from Enterobacter aerogenes.";

Eur. J. Biochem. 137:495-500(1983).

-i- FUNCTION: REQUIRED FOR THE ACTION OF COLICINS K AND L AND FOR THE STABILIZATION. SERVES AS A RECEPTOR FOR A NUMBER OF T-EVEN LIKE PHACES. ALSO ACTS AS A PORIN WITH LOW PERMEABILITY THAT ALLOWS SLOW PENETRATION OF SMALL
                                                                                                                                                                                                                                                                                                                 Outer membrane protein A precursor
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           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                       OMPA.
                                                                                                                                                                                                                                                                                                                                                                   P09146;
                                                                                                                                                                                                                                                                                                                                                                               OMPA_ENTAE
                                                                                                                                                                                                      Braun G., Cole S.T.;
                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE-84108348; Pubmed-6363059;
                                                                                                                                                                                                                                                   NCBI_TaxID=548;
                                                                                                                                                                                                                                                                  Enterobacter
                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                          Enterobacter aerogenes (Aerobacter aerogenes).
                                                              SOLUTES (BY SIMILARITY).
SUBBURIT: MONOMER (PROBABLE).
SUBCELLULAR LOCAFION: Integral membrane protein. Outer membrane.
SIMILARITY: BELONGS TO THE OMPA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148 GEERPIAFGINE-----EAWSONRRAEL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145 LYTQLSNLDPKDGAVVVLGYTDRIGSDAYNQRLSQQRAQSVVDYLVSKGIPAGKITAQGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85 GMLSVGVSYRFGQDEAAPVVAPAPAPAPQVQTKHFTLKSDVLFNFNKSTLKPEGQQALDQ 144
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27.0%; Pred. No. 1
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V -> G (IN STRAIN ATCC 29907).

W -> M (IN STRAIN ATCC 33430).

MISSING (IN STRAIN ATCC 33430).

N -> S (IN STRAIN ATCC 29907 AND STRAIN ATCC 33430).

K -> Q (IN STRAIN ATCC 29907 AND
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Nguyen T.N., Samuelson P., Sterky F., Merle-Poitte C., Robert A., Baussant T., Haeuw J.F., Uhlen M., Binz H., Stahl S.; "Chromosomal sequencing using a PCR-based biotin-capture method allowed isolation of the complete gene for the outer membrane pro
                                                                                                                                                                                                                                                                                            P24017; 069435;
01-MAR-1992 (Rel. 21, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                         MEDLINE=98192544; PubMed=9524233;
                                                                                                               STRAIN=RV 308;
                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                          Klebsiella pneumoniae
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Pfam; PF01389; OmpA_membrane; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 AFGT 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96 T--NQTARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 NAPTGYTGVIYTGVAPLVDNDETVKALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 137.5; DB 1
Pred. No. 3.2e-05;
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the outer membrane protein
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                                                                                                                                                                                                                                                                                                                            DISULFID CONFLICT
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Molecular and evolutionary relationships among enteric bacteria.",
J. Gen. Microbiol. 137:1911-1921(1991).

-i- FUNCTION: REQUIRED FOR THE ACTION OF COLICINS K AND L AND FOR THE
STRAILIZATION OF MATING AGGREGATES IN CONJUGATION. SERVES AS A
RECEPTOR FOR A NUMBER OF T-EVEN LIKE PHAGES. ALSO ACTS AS A PORI
WITH LOW PERMEABILITY THAT ALLOWS SLOW PENETRATION OF SMALL
                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00691; OmpA, 1.
Pfam; PF01389; OmpA_membrane; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Outer membrane; Transmembrane; Phage recognition; Signal; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M63355; AAA25119.1; -. HSSP; P02934; 1QJP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOLUTES (BY SIMILARITY).
-1- SUBUNIT: MONOMER (PROBABLE).
-1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
-1- SIMILARITY: BELONGS TO THE OMPA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A of Klebsiella pneumoniae.";
Gene 210:93-101(1998).
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS01068; OMPA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProDom; PD000930; Bac_OmpA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR01021; OMPADOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001145; Bac_OmpA
InterPro; IPR000498; OmpA_tmer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AJ000998; CAA04450.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=92065252; PubMed=1955870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=LD119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lawrence J.G.,
                                                                                                                                                                                                                               Local
                                                         124
                                                                                                                                                                                                                            Similarity
RAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEI 330
                                                  RAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNE----
                                                                                                                                               LPSLVYFDFDSDEIKPQAAAILDEQAQFLTT--NQTARVLVAGHTDERGSREYNMSLGER
                                                                                                 LKSDVLFNFNKATLKPEGQQALDQLYTQLSNMDPKDGSAVVLGYTDRIGSEAYNQQLSEK
                                                                                                                                                                                                                                                                                                   344 AA;
                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93-335 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ochman H., Hartl D.L.;
                                                                                                                                                                                                                                                                                                                         344
28
60
760
7100
1119
151
173
190
206
200
200
200
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335
                                                                                                                                                                                                                                                                                                   37061 MW;
                                                                                                                                                                                                                            15.9%;
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                                                                                                                                                                                                   20;
                                                                                                                                                                                                                            Pred.
                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
Y -> I (IN REF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                Score 136.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                      OMPA-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
4 X 2 AA TANDEM REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OUTER MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                              AC88AAE3B7871B16 CRC64;
                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                            No.
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                                                                                                                                                                                                                          3.9e-05
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                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                 50;
                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                 Indels
                                                  ----EAWSQNRRAEL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q.
                                                                                                                                                                                                 11;
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OMPA\_BUCAI

RESULT 26

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RESULT 27
MOTY_VIBAN
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                                                 밁
                                                                                                                                                   Matches
                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of the endocellular bacterial symbiont Buchnera sp. APS.";
Nature 407:81-86(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001145; Bac_OmpA.
InterPro; IPR000498; OmpA_tmem.
Pfam; PF00691; OmpA; 1.
Pfam; PF01389; OmpA_membrane; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-Tokyo 1998;
MEDLINE-20445173; PubMed-10993077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       symbiotic bacterium).
Bacteria; Proteobacteria; gamma subdivision; Buchnera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OmpA-like protein precursor. OMPA OR BU332.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P57414;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR01021; OMPADOMAIN. ProDom; PD000930; Bac_Ompa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                               Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=118099;
                                                                                                                                                                                                                                       NIAMOC
                                                                                                                                                                                                                                                      TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO THE OMPA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: MONOMER (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: ACTS AS A PORIN WITH LOW PERMEABILITY THAT ALLOWS SLOW PENDERATION OF SMALL SOLUTES (BY SIMILARITY).
                                                                                                                          54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P02934; 1QJP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AP001119; BAB13037.1; -.
                                                                                                                                                   34;
                                                                                                                                                                Similarity
                                                                       RGSREYNMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNE 159
                                                                                                                      DNDETVKALASKLPSLVYFDFDSDEIKPQA---AAILDEQAQFLTTNQTARVLVAGHTDE 110
                                                                                                DDSEPLNEQYSVLNENINFPFNSTELKPSSYDKLNKLDDDIKDMQLKNVSIVLL-GHADK
                                                IGSDEYNQKLSEDRAYSIKNYLASRGFSRDKITVKGMGKLYPL---TNQ 319
                                                                                                                                                                                                   349
                                                                                                                                                                                                             1
23
27
63
78
106
120
154
171
193
207
267
                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                               Porin;
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                                                                                                                                                                                                                                                                                                                                                                                        OMPA;
                                                                                                                                                                                                                                                                                                                                                                                                     Bac_OmpA; 1.
                                                                                                                                                                                                               349
40
75
75
116
135
1165
1204
2187
3311
                                                                                                                                                                                                   39303 MW;
                                                                                                                                                             15.7%;
31.2%;
                                                                                                                                                                                                                                                                                                                                                                           Signal;
                                                                                                                                                                                                                                                                                                                                                                                        FALSE_NEG
                                                                                                                                                 23;
                                                                                                                                                             Score 135.5; DB 1;
Pred. No. 4.9e-05;
                                                                                                                                                                                                             OMPA-LIKE.
BY SIMILARITY
                                                                                                                                                                                                                                                                                                   POTENTIAL.
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                                                                                                                                                                                                                                                                POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                          Complete proteome.
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                                                                                                                                                                                                  CC14AB1BD590CF58 CRC64;
                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            349 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sakaki Y., Ishikawa H.;
                                                                                                                                                 45;
                                                                                                                                                 Indels
                                                                                                                                                                       Length 349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of aphids
                                                                                                                                                7;
                                                                                                                                               Gaps
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PN OCC
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                                                                                                                                                                                                                                                                                 MOTY_VIBPA
                                                                                                                                                                                                                                                                                                           RESULT 28
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
[SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Wilton D.L.;
in ac
                                                                                                                                                01-NOV-1995
01-NOV-1995
01-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOTY_VIBAN
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16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                              MOTY_VIBPA
P46233;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The role of motility in adherence and invasion of a fish cell line by Vibrio anguillarum.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PLAYS THE ROLE OF A STATOR IN THE SODIUM FLAGELLAR MOTOR, STABILIZING THE FORCE-GENERATING UNIT THROUGH DIRECT INTERACTION WITH THE CELL WALL. INVOLVED IN ADHERENCE AND INVASION OF FISH CELL LINE.
                                             Vibrio parahaemolyticus.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Flagella; Signal.
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vibrio anguillarum (Listonella anguillarum).
Bacteria; Proteobacteria; gamma subdivision;
                                                                                                                           Sodium-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS01068; OMPA; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001145; Bac_OmpA.
InterPro; IPR001035; MotY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein).
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                        NCBI_TaxID=670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProDom; PD000930;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00691; OmpA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF176946; AAD51752.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: Membrane-associated (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183
                                                                                                                                                                                                                                                                                                                                                                                    243 VLRDYFKSLGLPEDRIQVQGYGKRRPIADNASPIGKDKNRRVVIS
                                                                                                                                                                                                                                                                                                                                                                                                                                         127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l Similarity
30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PR01023; NAFLGMOTY. PR01021; OMPADOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                 AVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELS 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TILHYDRDNVQLNKASQKRLAQIADYIRYNQDIDLVLVSTYTDSVDSRGVSQDLSERRAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTA-RVLVAGHTDERGSREYNMSLGERRAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the Swiss Institute of Bioinformatics and the EMBL
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293 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
flagellar protein motY precursor (Polar flagellum motor
                                                                                                                     (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 33, Last annotation update)
flagellar protein MOTY precurso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                         STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bac_OmpA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21
293
264
33725
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                                                gamma subdivision; Vibrionaceae; Vibrio.
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Pred. No. 0.00021;
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; 5618435B49F40D3B CRC64;
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13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                          "DNA sequence analysis of the Serratia marcescens ompA gene: implications for the organisation of an enterobacterial outer membrane protein.";
Mol. Gen. Genet. 195:321-328(1984).
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=85035845; PubMed=6092858;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Outer membrane protein A precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Bacteriol. 176:4219-4225(1994).
-!- FUNCTION: PLAYS THE ROLE OF A STATOR IN MOTOR, STABILIZING THE FORCE-GENERATING
                                                                                                                                                                                                                                                                           Braun G., Cole S.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Serratia marcescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OMPA_SERMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00691; OmpA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001035; MotY.
                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=615;
                                                                                                                                                                                                                                                                                                                                                                                                            Serratia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001145; Bac_OmpA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "MotY, a component of the sodium-type flagellar motor.";
WITH LOW SOLUTES (SUBUNIT:
                                                  FUNCTION: REQUIRED FOR THE ACTION OF COLICINS K AND L AND FOR THE STABILIZATION OF MATING AGGREGATES IN CONJUGATION. SERVES AS A RECEPTOR FOR A NUMBER OF T-EVEN LIKE PHAGES. ALSO ACTS AS A PORIN WITH LOW PERMEABILITY THAT ALLOWS SLOW PENETRATION OF SMALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERACTION WITH THE CELL WALL.
SUBCELLULAR LOCATION: Membrane-associated (Potential).
SIMILARITY: BELONGS TO THE OMPA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 AVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELS 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 TILHYERQGDQLTKASKKRLAQIADYVRHNQDIDLVLVATYTDSTDGKSESQSLSERRAE 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243 SLRTYFESLGLPEDRIQVQGYGKRRPIADNGTPIGKDKNRRVVIS 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83
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293 AA;
                            (BY SIMILARITY)
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     MONOMER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 E
293 S
264 C
  (PROBABLE).
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SODIUM-TYPE FLAGELLAR PROTEIN MOTY.
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Best Local S
Matches 34
                                                                                                                                                                                                               TP50_TREPA STANDARD;
p38369; Q56358;
O1-OCT-1994 (Rel. 30, Created)
O1-OCT-1994 (Rel. 30, Last seq
16-OCT-2001 (Rel. 40, Last anno
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                                                                                                                            Treponema pallidum.
Bacteria; Spirochaetales;
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                    MEDLINE=94156449;
                                             STRAIN=Nichols;
                                                               SEQUENCE FROM N.A.
                                                                                                       NCBI_TaxID=160;
                                                                                                                                                                         TPN50 OR TP0292
                                                                                                                                                                                             Outer membrane protein TPN50 precursor (Antigen TPP57).
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                                                                                                                                                                                                                                                                                                                                                                                                                 272 TDAVGSDQYNQKLSEQRAQSVVDYLVSKGIPSDKISARGMGEADAVTGNT
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J.M., Stamm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TDERGSREYNMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGT
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118
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PubMed=8112835;
nm L.V.;
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                                                                                                                              Spirochaetaceae; Treponema
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Pred. No. 0.00084;
9; Mismatches 49
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                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD000930; Bac_OmpA; 1. PROSITE; PS01068; OMPA; 1.
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                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane; Porin; Signal; Outer membrane; Antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00691; OmpA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cox D.L., Akins D.R., Porcella S.F., Norgard M.V., Radolf J.D.; "Treponema pallidum in gel microdroplets: a novel strategy for investigation of treponemal molecular architecture.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Nichols;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Identification and characterization of the Treponema pallidum tpn50 gene, an ompA homolog.";
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                                371 RYLQELGVVDAAHVYTRGCGAQQSIAPNDSEDGRRKNRRVEIT 413
                                                              130 NYLLGKG-INQASVEIISFGEERPIAFGTNEEAWSQNRRAELS 171
                                                                                          311 VQFDADSASLAPSEYEKLRKTAELLRAFPDRELLVSGHAARRGSVQDQQRISEERADVVA
                                                                                                                                                     253 SGGTVLRYQGTATAKNFAPERFDPARTVVELQETLKDL--HMPDAKVRETEEGVTISIEN 310
                                                                                                                       70 VYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVR 129
                                                                                                                                                                                    39 TGYTGVIYTGVA-------PLYDNDETVKALASKLPSL-------
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417 AA;
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27.0%;
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A -> E (IN REF. 2).
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RA Chois.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Entian K.D., Elmerson P.T.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Medina N., Mellado R., Liu H., Masuda S., Mauel C., Medigue C.,
RA Konone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parco V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Parco V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sato T., Tamakoshi A., Tanaka T., Tarahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
RA Winters P., Wipat A., Yamanoto H., Yasamoto K., Yata K.,
RA Koshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT Tengothiete genome sequence of the Gram-positive bacterium Bacillus
          PIR; B42882; B42882.
SubtiList; BG10689; motB.
                                                    PIR;
                                                                        EMBL; M77238; AAA22603.1; -.
                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                  the European Bioinformatics Institute.
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-!- FUNCTION: REQUIRED FOR THE ROTATION OF THE FLAGELLAR MOTOR. MIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mirel D.B., Lustre V.M., Chamberlin M.J.;
"An operon of Bacillus subtilis motility genes transcribed by the sigma D form of RNA polymerase.";
J. Bacteriol. 174:4197-4204(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98044033; PubMed=9384377;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Type II membrane protein. SIMILARITY: BELONGS TO THE MOTH FAMILY.
                                                                                                                                                                                                                                                                                                                                                   CELL WALL
                                                                                                                                                                                                                                                                                                                                                        BE A LINKER THAT FASTENS THE TORQUE-GENERATING MACHINERY
                                                      ; Z99111; CAB13241.1;
S27516; S27516.
                                                                                                                                                       STANDARD;
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InterPro;

IPR001145; Bac\_OmpA

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Best Local Similarity
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15-DEC-1998 (Rel. 37, Last annotation update)
Outer membrane protein A (Outer membrane protein II) (Fragment).
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P24755;
01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequ
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                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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HSSP; P02934; 1QJP.
InterPro; IPRO00145; Bac_OmpA.
InterPro; IPRO00498; OmpA_tmem.
Pfam; PF00691; OmpA; 1.
Pfam; PF01389; OmpA_membrane; 1.
                                                                                                                                                                                                                                                                                                                                       LAWRENCE J.G., Ochman H., Hartl D.L.;

"Molecular and evolutionary relationships among enteric bacteria.";

"Molecular and evolutionary relationships among enteric bacteria.";

J. Gen. Microbiol. 137:1911-1921(1991)

J. Gen. Microbiol. 137:1911-1921(1991)

J. Gen. Microbiol. 137:1911-1921(1991)

STABILIZATION OF MATING AGGREGATES IN CONJUGATION. SERVES AS A RECEPTOR FOR A NUMBER OF T-EVEN LIKE PHAGES. ALSO ACTS AS A PORIN WITH LOW PERMEABILITY THAT ALLOWS SLOW PENETRATION OF SMALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=92065252; PubMed=1955870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-ATCC 3307;
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                                                                                      EMBL; M63357; AAA26561.1; -.
                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE OMPA FAMILY.
                                                                                                                                                                                                                                                                                                       SOLUTES (BY SIMILARITY).
SUBUNIT: MONOMER (PROBABLE).
                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 RAVAVRNYLLGKGINQASV-EIISFGEERPIAFGTNEEAWSQNRRAEL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 DSIFFDSGKATIRKEDVPLAKEISNLLVINPPRNIIISGHTDNMPIKNSEFQSNWHLSVM 200
                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 SLYYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTD----ERGSREYNMSLGER 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81 DEVKKEKEEKEKNKKEKEKAADQEELENVKSQVEKFIKDKKLEHQLETKMTSEGLLITIK 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MMLHIQIAAAAAALSVLTFMTGCANKSTSQVMVAPNAPTGYTGVI-YTGVAP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.4%; 20.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 0.014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 106.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BED623BE2A84C6D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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YTXE_BACME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                    P46827;
01-NOV-1995
01-NOV-1995
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prodom; PD000930; Bac_OmpA; 1
prosite; PS01068; OMPA; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Outer membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                        This SWISS-PROT entry is copyright..It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                     Hueck C., Kraus A., Hillen W.;
"Sequences of copA and two downstream Bacillus megaterium genes with homology to the motAB operon from Bacillus subtilis.";
Gene 143:147-148(1994).
Gene 143:147-148 (1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON_TER
                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                Bacillus megaterium
                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical
                                                                                                                                                                                                                                                                                                                   MEDLINE=94259294; PubMed=8200532;
                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=1404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YTXE_BACME
            DOMAIN
                                              ProDom; PD000930; Bac_OmpA; 1.
Hypothetical protein; Transport; Transmembrane.
                                                                Pfam; PF00691; OmpA; 1. ProDom; PD000930; Bac_O
                                                                                                  EMBL; L26052; AAA22297.1; -
                                                                                                                                                                                                                            -i- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
                            TRANSMEM
                                                                                         InterPro;
                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 LKSDVLFNSAKSSLKPEGQQALDQLYTQLSSMDPKDGSVVYLGYTDPVGKDAANQKLSEA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 RARSVVDYLVSKGIPADKISARGMGEADQVTDSCGYKNGRATKAQIECLAPNRRVEI 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 RAVAVRNYLLGKGINQASVEIISFGEERPI-----AFGTNEEAWSONRRAEL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 LPSLVYFDFDSDEIKPQAAAILDEQAQFLTT--NQTARVLVAGHTDERGSREYNMSLGER 123
                                                                                        IPR001145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 AA;
                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 32, Last sequence update)
(Rel. 40, Last annotation update)
1 24.6 kDa protein in CCPA 3'region (ORF2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                 36
                            15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane; Phage recognition; Repeat; Porin
                                                                                                                                                                                                                                                                                                                                                                                                                                             32, Created)
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27
59
81
98
113
105
107
109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.1%; 29.1%;
                            14
35
                                                                                         Bac_OmpA.
                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 104; DB 1
Pred. No. 0.022;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 X 2 AA TANDEM REPEATS OF A-P
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                 EXTRACELLULAR (POTENTIAL)
                            POTENTIAL.
                                        CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        687CC9C10DDEC64C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         218 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
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SEQUENCE

218 AA;

24642 MW;

63622D730A4AE247 CRC64;

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RESULT 34
YFIB_ECOLI
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no will modified and this statement is not removed. Usage by and for commercia
                                                                                                                    MEDLINE=83141045; PubMed=6298574;
Bystroem A.S., Bjoerk G.R.;
"The structural gene (trmD) for the tRNA(mlG)methyltransferase is part of a four polypeptide operon in Escherichia coli K-12.";
MOL. Gen. Genet. 188:447-454(1982).
-I- SUBCELLUAR LOCATION: Attached to the membrane by a lipid anchor
                                                                                                                                                                                                                                                                                                                                      Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K., Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N., Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H., Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasundaram S. Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C. Yamagata S., Horiuchi T.;
                                                                                                                                                                                                                                  SHOWS THAT THE PROTEIN IS EXPRESSED
                                                                                                                                                                                                                                                                                     analysis of its sequence features.";
                                                                                                                                                                                                                                                                                              "Construction of a contiguous 874-kb sequence of the Escherichia coli-
K12 genome corresponding to 50.0-68.8 min on the linkage map and
                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97349980; PubMed=9205837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mau B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bystroem A.S., Hjalmarsson K.J., Wikstroem P.M., Bjoerk G.R.;
"The nucleotide sequence of an Escherichia coli operon containing genes for the tRNA(mlo)methyltransferase, the ribosomal proteins and L19 and a 21-K polypeptide.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97426617; PubMed=9278503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=84057772; PubMed=6357787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Putative lipoprotein yfiB precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1988 (Rel.
01-AUG-1992 (Rel.
16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBO J. 2:899-905(1983)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YFIB OR B2605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=562;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                      Res. 4:91-113(1997).
                                                                                                                  (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complete genome sequence of Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161 AARASGVIRYLTNHFSLSANRFEALGYGDTKPLVPNTSNDNLQKNRRVEI 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 LQEQVLFETGQADILKKGTPFLDELGRLFSTIPN-DIKVEGHTDNRPIHTYAYPSNWELS 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 LPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREY----NMSLG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ERRAVAVRNYLLGK-GINQASVEIISFGEERPIAFGTNEEAWSQNRRAEL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / MG1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07,
23,
40,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 100; DB 1
Pred. No. 0.045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB_1; Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
       and for commercial
                                                                      a collaboration
                                                                                                                                                                                                                                                                                                                                                 daram S.,
Wada C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOTB_TREPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
   Science 281:375-388(1998).

-:- FUNCTION: REQUIRED FOR THE ROTATION OF THE FLAGELLAR MOTOR.

BE A LINKER THAT FASTENS THE TORQUE-GENERATING MACHINERY TO CELL WALL (BY SIMILARITY).

-:- SUBCELLULAR LOCATION: Type II membrane protein. Inner membra.
                                                                                                                          Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S., Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOTB_TREPA
007887;
                                                                                           "Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

MEDLINE=96345631; PubMed=8755894;
                                                                                      spirochete."
                                                                                                                     Venter J.C.;
                                                                                                                                                                                                                                   MEDLINE=98332770; PubMed=9665876;
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                             Limberger R.J., Slivienski L.L., El-Afandi M.C.T., Dantuono L.A., "Organization, transcription, and expression of the 5' region of the fla operon of Treponema phagedenis and Treponema pallidum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOTE OR TP0724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Chemotaxis motB protein (Motility protein B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Preponema pallidum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prodom; PD000930; Bac_OmpA; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001145; Pfam; PF00691; OmpA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; S07952; S07952.
EcoGene; EG11152; yfiB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR01021; OMPADOMAIN.
                                                                                                                                                                                                                                                                                                a operon of Treponema phagedenis and Treponema pallidum, Bacteriol. 178:4628-4634(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 IPRSNLTTQGLGKKYPIASNKTAQGRAENRR 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 KLLPESQQQIQTMAAKLASTGLTHARMDGHTDNYGEDSYNEGLSLKRANVVADAWAMGGQ 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X01818; CAA25961.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78 EIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVRN-YLLGKG 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37 APTGYTGVIYTG-----VAPLVDNDETVKALAS-----KLPSLVYFDFDSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AE000346; AAC75654.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 APLVFTSLILTGCQSPQGKFTP-----EQVAAMQSYGFTESAGDWSLGLSDAILFAKNDY
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                                                                                                                                                                                                                                                                                                                                                                                                                            Spirochaetales; Spirochaetaceae; Treponema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lipoprotein; Signal; Complete proteome 1 18 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160 AA; 17244 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19
LOCATION: Type II membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.4%; Score 98.5; 23.8%; Pred. No. 0
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RESULT 36
MOTB_HELPY
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                                                                                                                                  SEQUENCE FROM N.A.

STRAIN-26695 / ATCC 700392;

MEDIJIE-97394467; PubMed=9252185;

MEDIJIE-97394467; PubMed=9252185;

Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,

Tomb J.-F., White O., Kerlavage A.R., Glayton G.J., Dougherty B.A.,

Relson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,

Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,

McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,

Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,

Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.

Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOTB_HELPY
P56427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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Chemotaxis; Flagella; Transmembrane; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U28219; AAB61254.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
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CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                    Chemotaxis motB protein (Motility protein B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=210;
                                                                                                                                                                                                                                                                                                                                                                                                      Helicobacter pylori (Campylobacter pylori)
                                                                                                                                                                                                                                                                                                                                                                                                                       MOTB OR HP0816.
                                                                                                                                                                                                                                                                                                                                                                       Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                Nature 388:539-547(1997)
                                                                                                   "The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE MOTB FAMILY.
                                 BE A LINKER THAT FASTENS THE TORQUE-GENERATING
                                                 FUNCTION: REQUIRED FOR THE ROTATION OF THE FLAGELLAR MOTOR
 SUBCELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TP0724;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53 VDNDETVKALASKLPSLVYFDFDSDEIK-PQAAAILDEQAQFLTTNQTA--RVLVAGHTD 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NRRVDI 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NRRAEL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVEVPEDGSTD-NWELSTRRAVRVLHYLTDFGAQENRFSLAGYADTRAKFSNESPEGRAY 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VTSDE--RGLVISLTSDSFFYPGSSDLNVEESREALLRVAQFLSDHALAGRRFRIEGHTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----ERGSREYNMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQ 164
                  WALL (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR001145; Bac_OmpA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26050 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.1%; 29.4%;
Type II membrane protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              257 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 238;
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                                    MACHINERY
     Inner membrane
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  REPORT OF THE PROPERTY OF THE 
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1995
01-FEB-1995
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Flagellar rotation; Complete proteome.

DOMAIN 1 16 CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00691; OmpA; 1.
ProDom; PD000930; Bac_OmpA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chemotaxis; Flagella; Transmembrane; Inner membrane;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BACSU
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                                                                                                                                                                                                                                                            "Identification of genes involved in utilization of acetoin in Bacillus subtilis."; mol. Microbiol. 10:259-271(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P39064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001145;
                                                                                                                                                                                                                                                                                                                                             Grundy F.J., Waters D.A., Takova T.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YTXE_BACSU
SEQUENCE FROM N.A
                                            Microbiology 143:3431-3441(1997).
                                                                        Lapidus A., Galleron N., Sorokin A., I sequencing and functional annotation in the 200 kb rrnB-dnaB region.";
                                                                                                                                                                                    STRAIN=168
                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95020526; PubMed=7934817;
                                                                                                                                                           MEDLINE=98048467; PubMed=9387221;
                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALSVLTFMTGCANKSTSQ----------VMVAPNAPTGYTGVIYTGVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YGSTNPIAPNDSLENRMKNNRVEIFF 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IQKLPKRVHINVRGFTDDTPLVKTRFKSHY--ELAANRAYRVMKVLIQYGVNPNQLSFSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PASQNTETKATIARKGEGSVLEQIDQGSILKLPSNLLFENATSDAINQDMMLYIERIAKI 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        \verb|ALFIALYAISAVNKSKVEALKTEFIKIFNYAPKPEAMQPVVVIPPDSGKEEEQMASESSK|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FGEERPIAFGTNEEAWSQNRRAELSY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   257 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel.
(Rel.
(Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein ytxE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      257
28849 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bac_OmpA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillales; Bacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 87;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
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                                                                                                            Ehrlich
n of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -KLPS-LVYFDFDSDEIKPQAAAILDEQAQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.82;
                                                                                                                                                                                                                                                                                                                                                        Henkin T.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88;
                                                                                                            S.D.;
Bacillus subtilis genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus.
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RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Bourschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Gulseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Honaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Liardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moseli D., Nakai S., Noback M.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Parro V., Pohl T.M., Portetelle B., Rapport G., Rey M., Reynolds S.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Sekiguchi A., Tanakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Viaria A., Wanden S., Vandenbol M., Vannier F., Vasarotti A.,
RA Winters P., Witz A., Yananoto H., Yanane K., Yasamoto K., Yata K.,
Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT The complete genome sequence of the Gram-positive bacterium Baciilus
                                                                                                                                                                                             Query Match
Best Local S
Matches 29
                                                                                                                                                                                                                                                                                                                                         SubtiList; BGI0366; ytxE.
InterPro; IPR001145; Bac_OmpA.
InterPro; IPR001145; Bac_OmpA.
Pfam; PF00691; OmpA; 1.
ProDom; PD00930; Bac_OmpA; 1.
Hypothetical protein; Transport; Transmembrane; Complete proteome.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z99119; CAB14950.1; PIR; S39642; S39642.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L17309; AAA68283.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98044033; PubMed=9384377;
183 AARASGVIQYFTSKEKLPSKRFIAVGYADTKPVKDNKTNEHMKENRRVEI
                                            122 ERRAVAVRNYLLGK-GINQASVEIISFGEERPIAFGTNEEAWSQNRRAEL 170
                                                                                                   124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF008220; AAC00301:1; -.
                                                                                                                                                                                                                   Similarity
                                                                                         LQEAVLFDTGEAKVLKNAETLLHQIAVLLQTIPN-DIQVEGHTDSRNISTYRYPSNWELS 182
                                                                                                                                         LPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREY----NMSLG 121
                                                                                                                                                                                                                                                                                         242 AA;
                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                       242
27595 MW;
                                                                                                                                                                                                                 10.0%;
                                                                                                                                                                                          13;
                                                                                                                                                                                                                 Score 86;
Pred. No.
                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL).
; 8BA7DDC103C1DFF5 CRC64;
                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                     DB 1; Length 242;
                                                                                                                                                                                                                   . 94;
                                                                                                                                                                                          62;
                                                                                                                                                                                          Indels
                                                                                                                                                                                        6;
                                                                                                                                                                                        Gaps
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RESULT 38

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MOTB_HELPJ
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                                                                                                                                                                                               Вb
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                                                                         RESULT 39
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                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                  Query Match
Best Local
MOTB_HELPJ STANDARD;
Q9ZL29;
16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                 ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quall M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Cronin A., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Glucose-6-phosphate isomerase 2 (EC 5.3.1.9) (GPI 2) (Phosphoglucose isomerase 2) (PGI 2) (Phosphohexose isomerase 2) (PHI 2).
PGI2 OR SC01942 OR SCC54.02C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AL035591; CAB38132.1; -.
HSSP; Q9N1E2; 1HOX.
HSSP; Q9N1E2; 1G6P_Isomerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coelicolor A3(2).";
Nature 417:141-147(2002).
                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00765; P_GLUCOSE_ISOMERASE_1; 1.
PROSITE; PS00174; P_GLUCOSE_ISOMERASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00662; G6PISOMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=A3(2) / M145;
MEDLINE=21996410; PubMed=12000953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Actinobacteria; Actinobacteria (class);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9Z523;
                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                               Isomerase; Gluconeogenesis; Glycolysis; Complete proteome ACT_SITE 390 390 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00342; PGI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- CATALYTIC ACTIVITY: D-glucose 6-phosphate = D-fructose 6-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hopwood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G6P2_STRCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PATHWAY: Involved in glycolysis and in gluconeogen-
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: BELONGS TO THE GPI FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phosphate.
                                                                                                                                                         90 QAQFLTTNQTARVLVAGHTDERGSREYNMSLG 121
                                                                                                                                                                                                                             30
                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D.A.;
                                                                                                                        MAGFADRVRTGE--WTGHTGRRIRNVVNIGIG 158
                                                                                                                                                                                                                             QVMVAPNAPTGYTGVIYTGVAPLVDNDETVKALASKLPSLVYFDFDSDEIKPQAAAILDE
                                                                                                                                                                                           QELAAATGVSGLRDAMFRGERINITEDRAVLHTALRAPRDAVIEVDGENVVPQVHAVLDK 128
                                                                                                                                                                                                                                                                                                                                 390
514
551 AA;
                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptomycineae; Streptomycetaceae; Streptomyces
                                                                                                                                                                                                                                                                                                                               514 E
                                                                                                                                                                                                                                                                            9.6%;
25.0%;
                                                                                                                                                                                                                                                                14;
                                                                                                                                                                                                                                                                            Score 83; I
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                 631BD4A76EB34643 CRC64;
                                                                                                                                                                                                                                                                Mismatches
                                     257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          551
                                                                                                                                                                                                                                                                              DB 1;
4.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gluconeogenesis
                                                                                                                                                                                                                                                                53;
                                                                                                                                                                                                                                                                                              Length 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Actinobacteridae
                                                                                                                                                                                                                                                                Indels
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                                                                                             COOS_RHORU
                                                                                                             RESULT 40
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 42
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Carbon monoxide dehydrogenase (EC 1.2.99.2) (
                                                               P31896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plagellar rotation; Complete proteome.
Plagellar rotation; Complete proteome.
CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G. Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Iv Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E.,
                                                                               COOS_RHORU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProDom; PD000930; Bac_OmpA; 1.
Chemotaxis; Flagella; Transmembrane; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00691; OmpA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID~85963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chemotaxis motB protein MOTB OR JHP0752.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE001506; AAD06331.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99120557; PubMed=9923682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helicobacter pylori J99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001145; Bac_OmpA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genomic sequence comparison of two unrelated isolates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics. Institute of Broinformatics and the EMBL outstation - European Bioinformatics. Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane SIMILARITY: BELONGS TO THE MOTE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BE A LINKER THAT FASTENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: REQUIRED FOR THE ROTATION OF THE FLAGELLAR MOTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CELL WALL (BY SIMILARITY)
                                                                                                                                                                                                                    149
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                                                                                                                                                          YGSTNPIAPNDSLENRMKNNRVEIFF
                                                                                                                                                                                      FGEERPIAFGTNEEAWSQNRRAELSY 172
                                                                                                                                                                                                                    IQKLPKRVHINVRGFTDNTPLNKTRFKSHY--ELAANRAYRVMKVLIQYGVDPNQLSFSS
                                                                                                                                                                                                                                                                               PASQNTETKATIARKGEGSVLEQIDQGSVLKLPSSLLFENATSDAINQDMMLYIERIAKI
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                                                                                                                                                                                                                                                                                                                                            ALFIALYAISAVNKSKVEALKTEFIKIFNYAPKPEAMQPVVVIPPDSGKEEEQMASESSK
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28838 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                     9.5%;
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a; epsilon subdivision; Helicobacter group;
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                                                                                                                                                                                                                                                                                                                                                                                                        25;
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 82;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
PERIPLASMIC (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04F8E7BF7833A9FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                             639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                             A
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    (CODH)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Doig P.C.
                                                                                                                                                                                                                                                                                                                                                                                                        48;
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Best Local
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Bacteriol. - i - FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Bacteriol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Rhodospirillum.
                                                                                                                                                                                                                                                                                                                               Oxidoreductase; Nickel; Iron; Zinc; Iron-sulfur.

METAL 50 50 IRON-SULFUR (BY SIM
METAL 53 53 IRON-SULFUR (BY SIM
METAL 72 72 IRON-SULFUR (BY SIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- INDUCTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fox J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genetic and physiological characterization rubrum carbon monoxide dehydrogenase system.
J. Bacteriol. 174:5284-5294(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=92355502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rhodospirillum rubrum.
                                                                                                                                                                                                                                                                                                                                                                                               Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U65510; AAC45123.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fox J.D., Kerby R.L., Roberts G.P., Ludden P.W.; ^{"}Characterization of the CO-induced, CO-tolerant hydrogenase from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-96198151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kerby R.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INDUCTION: By carbon monoxide; under anaerobic conditions. MISCELLANEOUS: METHYL VIOLOGEN CAN ACT AS ACCEPTOR. SIMILARITY: STRONG, TO C. THERMIACETICUM CARBON MONOXIDE DEHYDROGENASE BETA SUBUNIT AND SOME, TO M.SOEHNGENII CARBON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REDUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MONOXIDE DEHYDROGENASE ALPHA SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                              C42957; C42957
                             132
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                                                                                                                                                                                                                                                     42;
                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                         YVDLAKSLAKRNYLVLATGCAAGAFAKAGLMTSEATTQYAGEGLKGVLSAIGTAAGLGGP 521
RAGLGL 639
                             LLGKGI 137
                                                              LPTHVGSVPPVIGSQIVTKLVTETAKDLVGGYFIVDTDPK-----SAGDKLYAAIQER
                                                                                                                         LPLYMHMGSCVDNSRAV-ALATALANKLGVDLSDLPLVASAPECMSEKALAIGSWAVTIG
                                                                                                                                                                                                                    HIQIAAAAAALSVLTEMTGCANKSTSQV-MVAPNAPTGYTGVIYTGV--
                                                                                                                                                                                                                                                                                                                   639
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                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CODH MAY OXYDATE CARBON MONOXIDE COUPLED, VIA COOF, TO OF HYDROGEN CATION BY AN HYDROGENASE (POSSIBLY COOH).

ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IRON, NICKEL AND ZINC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178:1515-1524(1996).
                                                                                                                                                                                                                                                                                                                  AA;
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                                                                                                                                                                                                                                                                                                                  72
66854 MW;
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                                                                                           -QFLT--TNQTARVLVAGH----TDERGSREYNMSLGERRAVAVRNY 131
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Pred. No.
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IRON-SULFUR (BY SIMILARITY).
IRON-SULFUR (BY SIMILARITY).
DCADD7C13D8D85B8 CRC64;
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Search completed: July 6, 2003, 14:05:18 Job time : 39 secs

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Q47958 haemophilus Q92gc3 rickettsia Q45017 bartonella

Q45017 bartonella 025750 helicobacte Q9zk87 helicobacte

Q9zaw7 helicobacte Q8xwu0 ralstonia s Q9rnf4 helicobacte

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Result
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                  protein - protein search, using sw model
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   O93495 erwinia chr
O89496 erwinia chr
O89164 ralstonia s
O9a3h5 caulobacter
O8zgz0 yersinia pe
O98685 rhizobium I
O9pc85 xylella fas
O926c3 rhizobium m
O8u915 agrobacteri
O9kr12 vibrio choi
O9kr12 vibrio choi
O9l3q8 pasteurella
O92662 rickettsia
O44662 brucella ab
O44662 brucella ab
                                                                                                                                                                      Q51489 pseudomonas
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Q9X4R6
Q9XCZ4
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Q9S5J9
Q9SSJ9
Q9SOKG
G9CMNI
086254
Q9CMNI
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Q9X4R9
Q51778
Q52465
Q9X4S0
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5 08WS
6 08WS
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6 08WYHI1
7 09X4RS
7 09X4RS
7 09Y4RS
7 09Y4RS
7 09Y691
7 09X691
7 09X7
7 09WF
                                            Q9S3M1
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09PJE0
09XCZ6
09XCZ3
09XCZ3
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Q8VR19
Q46099
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Q9Z7C5
Q92ST9
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Q52465 pseudomonas
Q9x4s0 pseudomonas
Q9x4s0 pseudomonas
Q9pm14 campylobact
Q9x558 rhodospiril
Q9x4r6 pseudomonas
Q9xcz4 pseudomonas
      OBrmmO haemophilus OBrmmO haemophilus OBrm19 haemophilus O9s3m1 bordetella O9zid6 methylococc O8vpl3 pasteurella P96773 haemophilus
                                                                                                                                                                                       Q9wwt9 pseudomonas
Q9abm6 caulobacter
Q9abm6 caulobacter
Q9a56b8 pseudomonas
Q8reh8 fusobacteri
Q9a2r2 caulobacter
O51841 actinobacil
Q9x4s3 pseudomonas
Q9s5j9 actinobacil
Q8x93 fusobacteri
Q9s0k6 shewanella
Q9cmn1 pasteurella
Q9cmn1 pasteurella
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08rgn8 fusobacteri
031154 vibrio chol
051777 pseudomonas
048265 haemophilus
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Q9pgd9 xylella fas
Q51781 pseudomonas
Q51780 pseudomonas
Q51780 pseudomonas
Q51721 pseudomonas
Q5415 pseudomonas
Q9pgf9 xylella fas
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Q9x4r7 pseudomonas
Q9wwi5 pseudomonas
Q8r6jl fusobacteri
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Q51778
Q52465
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Q92705 chlamydia p
Q92st9 rhizobium m
Q98na9 rhizobium n
Q8vr19 myxococcus
Q46099 campylobact
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Q9aa59 caulobacter Q9hzu7 pseudomonas

Q8re60 fusobacter:

pasteurella haemophilus

4 pseudomonas
2 haemophilus
1 haemophilus
0 haemophilus
haemophilus

pseudomonas

Q9hxu8 pseudomonas Q8ubx6 agrobacteri Q8xrs0 ralstonia s Q8yhl1 brucella me

09xcz5 pseudomonas Q9xcz6 pseudomonas Q9xcz3 pseudomonas

084605 chlamydia t 09pje0 chlamydia m

Q9xCz7 pseudomonas Q9x4r8 pseudomonas Q9x4s1 pseudomonas

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RESULT 1

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ID Q5149
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Q51489;
Q1-NOV-1996 (TIEMBLTel. 01,
Q1-JAN-1998 (TIEMBLTel. 05,
Q1-JUN-2001 (TIEMBLTel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO1021; OMPADOMAIN. ProDom; PD000930; Bac_OmpA; 1. PROSITE; PS01068; OMPA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         outer-membrane peptidogiycan-associated lipoprotein (PAL) of Pseudomonas aeruginosa.";
Microbiology 143:1709-1716(1997).
EMBL; Z50191; CAA90573.1; -..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lim A., De Vos D., Brauns M., Mossialos D., Gaballa A., Hamers R.,
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pfam; PF00691; OmpA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Molecular and immunological characterization of OprL, the 18 kDa
                         Outer membrane protein OprL OPRL OR PA0973.
                                                                       01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last seq
01-MAR-2002 (TrEMBLrel. 20, Last ann
                                                                                                                                                                      Q914Z4
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                                                                                                                                                                                                                                                                                                                                                                                          62 RAITT----FYFEYDSSDLKPEAMRALDVHAKDL-KGSGQRVVLEGHTDERGTREYNMA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                      60 KALASKLPSLYYFDFDSDEIKPQAAAILDEQAQFLTINQTARVLVAGHTDERGSREYNMS 119
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                                                                                                                                                                           PRELIMINARY;
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40.9%; Pred. No. 7
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Q9KLT2
Q9I4T3
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006895
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Q52584
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Q9X4L6
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                                                        precursor.
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006895 campylobact
Q9x4s2 pseudomonas
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Q52584 pseudomonas
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haemophilus
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GRXFH6
ID CRXFH6
AC QRXFH
AC ACRA
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RA RA Watu
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pfam; pF00691; OmpA; 1.
pRINTS; PR01021; OMPADOMAIN.
proDom; pD000930; Bac_OmpA; 1.
pROSITE; PS01068; OMPA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Salmonella
                       SPECIES=S.typhi; STRAIN=CT18;
                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                            Nature 413:852-856(2001).
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

RETAINATEC 15692 / PAO1;

RETA
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Q1-MAR-2002 (TrEMBLrel. 20, Created)
Q1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Tol protein required for outer membrane integrity, uptake colicins, and translocation of phage DNA to cytoplasm
                                           McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Peptidoglycan-associated lipoprotein). PAL OR STM0749 OR STM0795.
                                                                                                                                                                                                                                                                                                                                             SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720; MEDLINE=21534948; PubMed=11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 RAITT-----FYFEYDSSDLKPEAMRALDVHAKDL-KGSGQRVVLEGHTDERGTREYNMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 QIAAAAAALSVLTFMTGCANK-----STSQVMVAPNAPTGYTGVIYTGVAPLVDNDETV
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Pfam; PF00691; OmpA; 1.
PRINTS; PR01021; OMPADOMAIN.
ProDom; PD000930; Bac_OmpA; 1.
PROSITE; PS01068; OMPA; 1.
Lipoprotein; Complete protecome.
                                                                                                                                                                                                                                                                                 Ray M.C., Vianney A., Cotte-pattat N., Lazzaroni J.; "Characterization of the Erwinia chrysanthemi tol-pal ge Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AJ297885; CAC82710.1; -
                                                                              SEQUENCE
                                                                                                                                                                         ProDom; PD000930; Bac_Ompa; 1.
PROSITE; PS01068; OMPA; UNKNOWN_1.
                                                                                                                                                                                                                                              InterPro; IPR001145; Bac_OmpA. Pfam; PF00691; OmpA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                      Lipoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=3937
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pectobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Erwinia chrysanthemi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptidoglycan-associated lipoprotein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=556;
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EMBL; AL627268; CAD05211.1; -.
This contains the con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Whitehead
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 33.6%;
Local Similarity 36.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 VY 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 RGTPEYNISLGERRANAVKMYLQGKGVSADQISIVSYGKEKPAVLGHDEAAYAKNRRAVL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 RGSREYNMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAEL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         171 SY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53 MSSEEQARLQMQQLQQNNIVYFDLDKYDIRSDFAAMLDAHANFLRSNPSYKVTVEGHADE 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MMLHIQIAAAAAALSVLTFWTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --NDETVKALASKLP--SLYYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDE 110
                                                                        168 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         174 AA; 18865 MW; A515624F96EBB5A5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.6%; Score 289; DB 16; illarity 36.8%; Pred. No. 3.7e-19; Conservative 33; Mismatches 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                 18433 MW;
                                                                                                                                21
   33.4%; Score 287.5;
                                                                                 PEPTIDOGLYCAN-ASSOCIATED LIPOPROTEIN
                                                                                                                          POTENTIAL.
                                                           1E315BCF52852DD5 CRC64;
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   DB 2;
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Length 168
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                                                                                       RESULT 6
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Q9A3H5;
                             Q9A3H5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00308; ANTIFREEZEI.
PRINTS; PR01021; OMPADOMAIN.
ProDom; PD000930; Bac_OmpA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS01068; OMPA; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandlar M., Choisne N., Claudel-Renard C., Cunnac S., Demange N Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of the plant pathogen Ralstonia solanacearum."; Nature 415:497-502(2002).
EMBL; AL646060; CAD14266.1; -.
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8Y1F4
Q8Y1F4;
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InterPro; IPR001145; Bac_Ompa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probable peptidoglycan-associated lipoprotein precursor. PAL OR RSC0736 OR RS05117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21681879; PubMed=11823852;
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                                                                                                                                                                                  123
                                                                                                                                                                                                                      123 RRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELSY 172
                                                                                                                                                                                                                                                                                                       63
                                                                                                                                                                                                                                                                                                                                        63 ASKLPSLYYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 SLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELSY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65;
                                                                                                                                                                                                                                                                                                                                                                                                         8 IKLAAIAALLALGACSSGVKLDDTSK-----NATGGAAAGADTRNVTPVDVSRDELTDPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 IQIAAAAAALSVLTFMTGCANKSTSQVMVAPNAPTG-YTGVIYTGVAPL-VDNDETVKAL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 LOMOELORNNIVYFDLDKYDIRPDFAOMLDAHAAFLRSNPSYKVTVEGHADERGTPEYNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ALASKLP--SLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREVNM 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 LMLALPVLAVAACSS-----NKHANNDQSSLNGGAGMEN-----GGNMSSAEQAR 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                           KRAEAVRRALSSLGVPDSQMESVSLGKEKPQASGHDEESWAQNRRSDIVY 172
                                                                                                                                                                                                                                                                                    SPLAKRSVYFDFDSYTVKPEYQGLLTQHARYLQSHNQRKVLIQGNTDERGTSEYNLALGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALGERRANAVQMYLQGKGVSADQISVVSYGKEKPAVLGHDEAAWSKNRRAVLVY 168
                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.3%; Score 286.5;
38.2%; Pred. No. 6.3e
htive 36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 4.9e-19;
                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5CFF28E6AE7702D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                   188 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.3e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 16; Length 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Demange N.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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RESULT 7

RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001
01-JUN-2001
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B., DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Kolonay J.F., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O., Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.; Complete genome sequence of Caulobacter crescentus."; Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caulobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR01021; OMPADOMAIN. ProDom; PD000930; Bac_OmpA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=ATCC 19089 / CB15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=155892;
STRAIN-CO-92 / BIOVAR ORIENTALIS:

MEDLINB=21470413: PUBMed=11586360;

Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,

Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,

Basker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,

Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

Chillingworth T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,

Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,

Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,

Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;

"Genome sequence of Yersinia pestis, the causative agent of plague."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE005987; AAK25191.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2002 (TIEMBLIEL 20, Created)
01-MAR-2002 (TIEMBLIEL 20, Last sequence update)
01-JUN-2002 (TIEMBLIEL 21, Last annotation update)
peptidoglycan_associated lipoprotein Pal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8ZGZ0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21173698;
                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAL OR YPO1125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8ZGZ0
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=632;
                                                                                                                                                                                                                                                                                                                                                                                                       Yersinia
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yersinia pestis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  family protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 NMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNR 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC3229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 GSVQDFVVNIGDRVYFDTDEYVIRADAQPVLAGQAQWLNRYSSVRIRIEGNADERGTREY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 IAAAAAALSVLTEMTGCANKSTSQVMVAPNA-----PTGYT----GVIYTGVAPLVDND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ETVKALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREY 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VGLAAASLA----ACASRPKPQPVTPPPAQPQPTQPTPYTPPAPPPVTSGILP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NLALGARRANAVRDFLIAQGVSSARIETISFGKERPIDPGSSEEAWAKNR 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR001145; Bac_OmpA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (TrEMBLrel.
1 (TrEMBLrel.
2 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       188 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OmpA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=11259647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20425 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33.3%; Score 286.5; 38.2%; Pred. No. 7.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17,
17,
20,
                                                                                                                                                                                                                                                                                                                                                                                                                                   gamma
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DF5703C15AEFB3EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                      subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.1e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 188;
            agent of plague.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21;
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                                                                                                                                                                                                               Qy
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                           Дb
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                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS01068; OMPA; 1.
Lipoprotein; Complete proteome.
SEQUENCE 168 AA; 18084 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 413:523-527(2001).
EMBL; AJ414146; CAC89968.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2001 (TrEMBLrel. 18, C
01-OCT-2001 (TrEMBLrel. 18, L
01-MAR-2002 (TrEMBLrel. 20, L
Hypothetical protein ml13887.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR01021; OMPADOMAIN. ProDom; PD000930; Bac_OmpA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001145; Bac_OmpA. pfam; PF00691; OmpA; 1.
                                                                                                                                                                                                                                                                                                                                                                           Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasa
Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno
Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q98F85
                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=MAFF303099;
MEDLINE=21082930; PubMed=11214968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q98F85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phyllobacteriaceae; Mesorhizobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rhizobium loti (Mesorhizobium loti)
                                                                                                                                                                                                                 PRINTS; PRO1021; OMPADOMAIN.

Probom; PD000930; Bac_OmpA; 1.

Hypothetical protein; Complete proteome.

SEQUENCE 168 AA; 17765 MW; 03E260D3BALECBB3 CRC64;
                                                                                                                                                                                                                                                                                                                      DNA Res.
                                                                                                                                                                                                                                                                                                                                      Mesorhizobium loti.
                                                                                                                                                                                                                                                                                                                                                   "Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                              Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Takeuchi C., Yamada M., Tabata S.;
                                                                                                                                                                                                                                                                            Pfam; PF00691; OmpA;
                                                                                                                                                                                                                                                                                           [nterPro; IPR001145; Bac_OmpA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 ALASKLP--SLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNM
130 NYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRA 168
                                                                                                                                                                                                                                                                                                         AP003003; BAB50682.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MMLHIQIAAAAALSVLTFMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MQLNKVLKGIMLALPVLAVAACSSNKSANNDQSGMGAGTG-----TENGSNLSSEEQAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66;
                           61 IFFDTDSSSIRADAQTTLARQAQWLNQYKQYAIVVEGHADERGTREYNLALGARRAAAAR 120
                                                        70 VYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVR 129
                                                                                        15 ALVAMLATAGCASKKT-----PNNAADLGLNG---AGAATPGSAQDFTV-----NIGDR 60
                                                                                                                     13 ALSVLTFMTGCANKSTSQVMVAPN--APTGYTGVIYTGVA-PLVDNDETVKALASKLPSL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALGERRASAVKMYLQGKGVSADQISIVSYGKEKPAVLGHDEAAFAKNRRAVLVY 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELSY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LQMQELQKNNIVYFGFDKYDIGSDFAQMLDAHAAFLRSNPSDKVVVEGHADERGTPEYNI
                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32.9%;
                                                                                                                                                                     31.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32; Mismatches
                                                                                                                                                        25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
                                                                                                                                                                     Score 269.5; DB 1
Pred. No. 2.3e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3AAA851E765F1994 CRC64;
                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            283; LL
NO. 1.3e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B
                                                                                                                                                                                         DB 16;
                                                                                                                                                          53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 168;
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                                                                                                                                                          Indels
                                                                                                                                                                                       Length 168;
                                                                                                                                                                                                                                                                                                                                                                                      Sugimoto M.,
                                                                                                                                                                                                                                                                                                                                                                                                                       Kimura T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sasamoto
                                                                                                                                                                                                                                                                                                                                                                                                          P.
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                                                                                                                                                             Gaps
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QΥ
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RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Barros M.H., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Guntinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Matsukuma A.Y.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Manni A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Menck C.F.M., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
Peixoto B.R., Roberto P.G., Santelli R.V., Sawasaki H.E.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA Genome Sequence of the Ninhola J.C.;
RT "The denome sequence of the Ninhola J.C.;
RT "The genome sequence of the Ninhola J.C.;
RT "The genome sequence of the Ninhola J.C.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The genome sequence of the plant Nature 406:151-159(2000).
EMBL; AE004009; AAF84702.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001145; Bac_Ompa. Pfam; PF00691; Ompa; 1. PRINTS; PR01021; OMPADOMAIN.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20365717; PubMed=10910347;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xylella fastidiosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Outer membrane protein P6 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9PC85
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137 NSVLYSLQANGASSGQLNVVSYGEERPVCTESTESCWSRNRRVEIVY 183
                                                                                                                        126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                   VAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELSY 172
                                                                                                                                                                                                                                                                                     LPSIVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MTGCANKSTSQVMV------AP--NAPTGYTGVIYTGVAPLVDNDETVKALASK 65
                                                                                                                                                                                                                                                                                                                                                                                                    LVACSKKVKEOPHVPVKTMAPTVSTPAPTTTAPTDSSG-LYT--AADLDTDACLR----
                                                                                                                                                                                            -QRVVYFDFDKDDVKKEFQTVLGCHAKYLRNRPSAHITLQGNTDERGSREYNIALGERRG 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATEMENT OF THE STATE OF THE S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20431 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.8%; Score 265.5; 35.9%; Pred. No. 6.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C8DD2F6233DB0C92 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pathogen Xylella fastidiosa."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54;
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RESULT 10
Q926C3
ID Q926C3
AC Q926C
DT Q1-DED

                       RAA RAA RAA
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Best Local :
SEQUENCE FROM N.A.

MEDILINE=21608550; PubMed=11743193;

WOOD D.W., SetubBal J.C., Kaul R., Monks D.E., Kitajima J.P.,

Wood D.W., SetubBal J.C., Kaul R., Monks D.E., Almeida N.F. Jr., Woo L.

Chen Y., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.

Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,

Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,

Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,

Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,

Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordo

Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry
                                                                                                                                                                                                                                                                                                                                                                                          Agrobacterium tumefaciens (strain C58 / ATCC Bacteria; Proteobacteria; alpha subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Omp16 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2002 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J., Botstard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S., Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F., "Analysis of the chromosome sequence of the legume symbiont Sinchizoblum meliloti strain 1021.", Sinchizoblum meliloti strain 1021.", Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
                                                                                                                                                                                                                                                                                                                              Rhizobiaceae; Rhizobium.
NCBI_TaxID-176299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PALA OR ATU3713 OR AGR_L_2246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8U9L5
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhizobiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133 LGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72 DTDSTSIRADAQATLDRQAQWLAKYPNYGITIEGHADERGTREYNLALGARRAAATRDYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 ALVMTLALAGCASKKN-----LPNDAAG-LGLGAGAATPGSQQDFTV-----NVGDRIFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73 DFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVRNYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 ALSVLTEMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVKALASKLPSLVYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 21, (TrEMBLrel. 21, (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18735 MW; A6F162CB35042268 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30.5%;
      Biddle P., Jung M., Krespan W., Perry M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 262.5; DB 1
Pred. No. 1.1e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  177 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bothe G., Ampe F., Batut J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 16; Length 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61;
                                                                                                                                                                                                                                                                                                                                                                                   33970).
Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                  Jr., Woo L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
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Q9KR12
Q9KR12
ID 09KR1
AC 09KR1
DT 01-OC
DT 01-OC
DT 01-DE
Pepti
GN VC1B3
OC Bacte
OC NCBI
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RN [1]
RN [1]
RR SEQUE
RA Heide
RA Heide
RA Heide
RA G111
RA MCDDN
RA SALEN
RA G111
RA MCDN
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Best Local
                                                                                                                                                                                                                                                                                                                       Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Houmiel K., Gordon J., Vaudin M., Tartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V., Nester E.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cielo C., Slater s.; the plant pathogen and biotechnology agent "Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58."; Science 294:2323-2328(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TremBLrel.
01-OCT-2000 (TremBLrel.
01-DEC-2001 (TremBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21608551; PubMed=11743194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9KR12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 294:2317-2323(2001).
PRINTS; PRO1021; OMPADOMAIN.
PRODOM; PD000930; Bac_OmpA; 1.
PROSITE; PS01068; OMPA; 1.
                                                                                                                                                                                                                                                                               Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptidoglycan-associated lipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9KR12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                 InterPro; IPR001145;
Pfam; PF00691; OmpA;
                                                                                                                                                                                                                             cholerae
                                                                                                                                                                                                                                      "DNA sequence of both chromosomes cholerae.":
                                                                                                                                                                                                   Nature 406:477-483(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AE009302; AAL44523.1; -. AE008312; AAK89692.1; -.
                                                                                                                                           VC1835;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 RIFFDTDSTSIRADAQQTLQRQAQWLSRYPNYAITVEGHADERGTREYNLALGARRAAAT 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20
                                                                                                                                                                      AE004259; AAF94983.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 AAAALSVLTFMTGCANKSTSQVMVAPNAPTGYTGVIYTGVA-PLVDNDETVKALASKLPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAV 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AVIAMTLALAGCANKKN-----MPNS-AGELGLGGAGSATPGSQQDFTV----NVGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RDFLASQGVPASRMKTISYGKEKPVAVCDDISCWSQNRRA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30.4%; Score 262; DB 16; 38.1%; Pred. No. 1.3e-16;
                                                                                                           Bac_OmpA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15, Created)15, Last sequence update)19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gamma subdivision; Vibrionaceae; Vibrio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                          of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 177;
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RESULT 13
Q9L3Q8
                                                                                                                         RESULT 14
Q9ZCH2
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Best Local
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                                                Q9ZCH2;
01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goswami P.P., Chaudhuri P., Grish K.S.; "cloning and sequencing of the gene encoding a 16 kDa outermembrane protein of Pasteruella maltocida p52.", Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AJ271673; CAB75338.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00691; OmpA; 1.
PRINTS; PR01021; OMPADOMAIN.
ProDom; PD000930; Bac_OmpA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9L3Q8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pasteurella multocida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9L3Q8
                                                                                                             Q9ZCH2
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                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS01068; OMPA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001145; Bac_OmpA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-P52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pasteurella
                                      Peptidoglycan-associated lipoprotein precursor (PAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64;
                                                                                                                                                                                 88 HYLSAKGVQAGQVSTVSYGEEKPAVLGHDEAAYSKNRRAVLAY 130
                                                                                                                                                                                                                                          28
                                                                                                                                                                                                                                                                   70 VYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVR 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YNIALGERRAQAVAKYLEALGVQAGQLSIVSYGEEKPLVLGQSEEAYAKNRRAVLVY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YNMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELSY
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                                                                                                                                                                                                                                       VYFGFDKYNIEGEYVQILDAHAAFLNATPATKVVVEGNTDERGTPEYNIALGQRRADAVK
                                                                                                                                                                                                            NYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELSY 172
                                                                                                                                                                                                                                                                                                                                                      130 AA;
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                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                               Bac_OmpA; 1.
                                                                                                                                                                                                                                                                                                                                                      14216 MW; 91E7D2C2A9A87F44 CRC64;
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48.5%;
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                                                                                                                                                                                                                                                                                                  19;
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                                                        Last annotation
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Pred. No. 2.3e-16;
                                                                                    Created)
                                                                    Last sequence update)
                                                                                                                                                                                                                                                                                                              Score 258; DB 2;
Pred. No. 1.9e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            803EFE81D17CDC69 CRC64;
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                                                                                                                155 AA
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                                                      update)
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                                                                                                                                                                                                                                              87
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Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;

Rickettsia prowazekii.

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AC CONTRACTOR REPORTED TO THE CONTRACTOR OF THE 
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Q44662
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Best Local Similarity
SPECIES-B.melitensis; STRAIN-16M / ATCC 23456 / BIOTYPE 1; MEDLINE-20020109; PubMed-11756688;
                                                                                                                                                               Tibor A., Aidant N., Letesson J.;
"The tol-pal region in Brucella e
of E. coli.";
                                                                                                                                                                                                                                                                                                                                                       Tibor A., Weynants V., Denoel P., Lichtfouse B., De Bolle X., Saman E., Limet J.N., Letesson J.J.; "Molecular cloning, nucleotide sequence, and occurrence of a 16.5-kilodalton outer membrane protein of Brucella abortus with similarity to pal lipoproteins.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                               Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                           SPECIES=B.melitensis; STRAIN=16M / ATCC 23456 / BIOTYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES-B.abortus 1, and B.melitensis; STRAIN-544, AND 16M; MEDLINE-94341863; PubMed-8063379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OMP16 precursor (PAL protein) (Peptidoglycan-associated
                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brucella melitensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brucella abortus 1, and
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                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                      Infect. Immun. 62:3633-3639(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=35802,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lipoprotein)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q44662;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome. SEQUENCE 155 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 396:133-140(1998).
EMBL; AJ235273; CAA15198.1; .
Interpro; IPR001145; Bac_OmpA.
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PRINTS; PR01021; OMPADOMAIN.
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"The genome sequence of Rickettsia prowazekii and the origin of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Andersson S.G.E., Zomorodipour A., Andersson J.O.,
Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99039499; PubMed=9823893;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 LANKGIAHNRLNTISYGKDKPAMIGNTEEAFSYNRRA 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 LLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53 FAFDSSSLSPKAKEELERQACWLSKHPEVKVTVEGHCDERGTREYNLALGERRAAAAKQF 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 FDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVRNY 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 ALSVLTFMTGC-ANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVKALASKLPSLVY 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56;
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                                                                                                                                                               region in Brucella encodes homologs of the Tol-Pal system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brucella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29459;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29.7%;
35.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 256; DB 16;
Pred. No. 3.8e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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RESULT 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                  outer membrane protein belonging to the family of PAL Res. Microbiol. 147:351-361(1996). EMBL; X89009; CAA61413.1; -. InterPro; IPR001145; Bac_OmpA.
                                                                                                                                                                                                                                                      ProDom; PD000930; Bac_OmpA; 1.

CHAIN 20 152 PALA OUTER MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00691; OmpA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINE-96298014; PubMed-8763621;

Frey J., Kuhnert P., Villiger L., Nicolet J.;

"Cloning and characterization of an Actinobac
"Cloning and characterization of the famil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOY-1996 (TrEMBLrel. 01, Created)
01-NOY-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                   PRINTS; PR01021; OMPADOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PALA outer membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q44157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=715;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Actinobacillus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal; Complete proteome. SIGNAL 1 24
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Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
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                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 MSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 LALGORRAAATRDELASRGVPTNRMRTISYGNERPVAVCDADTCWSQNRRA 159
8 LMIAAPA-----FVLAACSSSSDNANANANAGQFGGM-----TAEDLQT 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 TV-----NVGDRIFFDLDSSLIRADAQQTLSKQAQWLQRYPQYSITIEGHADERGTREYN 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF358662; AAK48919.1; -. AE009476; AAL51521.1; -.
                                                       5 IQIAAAAAALSVLTEMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVKALAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 TVKALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYN 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L27996; AAA59360.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MRRIQ-SIARSPIAIALEMSLAVAGCASKKN----LPN-NAGDLGLGAGAATPGSSQDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 MLHIQIAAAAAALSVLTFMT----GCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDE 57
                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                152 AA;
                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168 AA;
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                                                                                                                                                                                                                                             16235 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29.5%;
36.3%;
                                                                                                                                                    29.4%; Score 253.5; DB 2 37.5%; Pred. No. 6.3e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18232 MW;
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                                                                                                                              27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 254; DB 16;
Pred. No. 6.5e-16;
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                                                                                                                                                                                                                                       892C1E23E80406A7 CRC64;
                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                152 AA
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                                                                                                                                                                               DB 2;
                                                                                                                           55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65;
                                                                                                                                                                            Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 168;
                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lipoproteins.";
                                                                                                                        23;
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                                                                                                                     Gaps
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RESULT 17
1047958
AC 047959
AC 047959
DOI-NK
DT 01-NK
DT 01-NK
DT 01-NK
DT 01-NK
DT 01-NK
DT 01-NK
DT 01-DI
Bact
OC Haem
OC Haem
OC Haem
OC NCB:
RN (1]
RN [1]
RN [1]
RN [1]
RN [1]
RN MED
RA Spi
RT Hak
RX MED
RX M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δÃ
        RESULT 18
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Best Local
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haemophilus ducreyi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q47958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR01021; OMPADOMAIN. ProDom; PD000930; Bac_OmpA; 1. SEQUENCE 157 AA; 17051 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Infect. Immun. 64:1950-1955(1996).
EMBL; U42466; AAC44382.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spinola S.M., Hiltke T.J., Fortney K., Shanks K.;
"The conserved 18,000 molecular weight outer membrane protein
Haemophilus ducreyi has homology to PAL.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=85-023233;
MEDLINE=96239002; PubMed=8675292;
                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=730;
                                                                                                                                                                                                                                                                                                             Peptidoglycan-associated lipoprotein PAL OR RC1200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q92GC3
Ogata H., Audic S., Renesto-Audiffren P., Fourni
Samson D., Roux V., Cossart P., Welssenbach J.,
Raoult D.;
                                                                                                                 SEQUENCE FROM N.A. STRAIN-MALISH 7;
                                                                                                                                                                                                                            Bacteria; Proteobacteria; alpha subdivision; Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                   Rickettsia conorii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                         MEDLINE=21442074; PubMed=11557893;
                                                                                                                                                                                               NCBI_TaxID=781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             kDa outer membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 RRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELSY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pro; IPR001145; Bac_OmpA. PF00691; OmpA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 ASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KLPSLYYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERR 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADAVKNYLATKGANQVST--VSYGEEKPAVLGHTEADYAKNRRAVLEY 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RY-NTVYFGFDSYAVEGEYQQLLDAHAAYL-TSANGKVTVAGHADERGTPEYNIALGQRR 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QTRY-NTVYFNFDSYAVEGEYRQLLDAHAAYLTSS-NSKVTVTGHADERGTPEYNIALGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LMIAAPAFVLTACSSSSGKTDANANMNGDAMAVNQFGGM---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IQIAAAAAALSVLTFMTG--CANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVKAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RRADAVKNYLATKGVSQVST--VSYGEEKPSVLGHTEADYAKNRRAVLEY 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 246; up _.
No. 3.3e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D3CB01A763002654 CRC64; .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         155 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                           Fournier P.-E., Barbe
ch J., Claverie J.-M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52;
                                                                                                                                                                                                                                                                  Rickettsiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                        Barbe V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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RESULT 19
Q45017
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DE DE DE LE
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                                                                                          RESULT 20
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Best Local
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ProDom; PD000930; Bac_OmpA; 1.
Lipoprotein; Complete proteome.
SEQUENCE 155 AA; 17340 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Mechanisms of evolution in Rickettsia conorii and R. prowazekii."; Science 293:2093-2098(2001).
EMBL; AE008667; AAL03738.1; -.
InterPro; IPR001145; Bac_OmpA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q45017;
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                                                   025750
025750;
                                                                                                                                                                                                                                                                                            PRINTS; PRO1021; ÔMPADOMAIN.
PRODOM; PD000930; Bac_ompA; 1.
PROSITE; PS01068; OMPA; UNKNOWN 1
SEQUENCE 171 AA; 19354 MW; 3A
                                                                                                                                                                                                                                                                                                                                             InterPro; IPR0011145; Bac_OmpA.
Pfam; PF00691; OmpA; 1.
                                                                                                                                                                                                                                                                                                                                                                                   Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bartonellaceae; Bartonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bartonella bacilliformis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.5 kDa protein
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Arevalo J.I., Williams M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=774;
                                                                                                                                                                                                                                                                                                                                                                        EMBL; L47642; AAA78948.1;
                                                                                                                                                                                                                                                                                                                                                                                                               "Anonymous DNA sequence with ORF from
                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 GLGERRAAAAKKFLAHKGIDHNRLNTISYGKDRPAMMGNTEEAFAYNRRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 SLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSONRRA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40
                                                                                                                                                           130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 VKALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61;
                                                                                                                                  93 DYLVSLGVSPQRMKTMSYGKERPVAVCDDISCWNQNRRVVIS
                                                                                                                                                                                     \frac{3}{3}
                                                                                                                                                                                                             70 VYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVR 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 KITLAFLALCVL---AGCNT-------TKRAPQFDGNMNQSEETSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 QIAAAAAALSVLTFMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVD-----NDET--
                                                                                                                                                                                                                                          43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MKDFEKHAGNAVWFAFDSSALSPKAKEELERQACWLSKHPEVKVTVEGHCDERGTKEYNL
                                                                                                                                                        NYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELS 171
                                                                                                                                                                                    VFFSLDSSVIEADAQRILVRQAEWLLLYPHHTIMIEGHADDRGTREYNLALGQRRAIAVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                         Conservative
                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28.2%; Score 242.5; 35.9%; Pred. No. 6.
                                                                                                                                                                                                                                                       27.3%;
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01,
19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25;
                                                                                                                                                                                                                                           26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                       Score 235; DB 2;
Pred. No. 3.9e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Marks K.L., Ihler G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58E05C7E8F027A84 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                               3A156E3F8FF24DBE CRC64;
                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           171
                                                                     179
                                                                                                                                                                                                                                                                                                                                                                                                                  Bartonella bacilliformis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.8e-15;
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                                                                                                                                                                                                                                                                    Length 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                             Indels
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                                                                                                                                        134
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01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

associated lipoprotein precursor (OMP18).

Peptidoglycan

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1092K87
202K87
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 21
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                         gastric pathogen Helicobacter pylori.",
Nature 397:176-180(1999).
EMBL; AE001533; AAD06633.1; -.
                                                                                                                                                                                             Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C. Smith D.R., Noonan B., Gulld B.C., deJonge B.L., Carmel G., Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
                                                                                                           "Genomic sequence comparison of two unrelated isolates
                                                                                                                                                          Trust T.J.;
                                                                                                                                                                       Gibson R., Merberg D., Mills S.D., Jiang Q.,
                                                                                                                                                                                                                                                                                           MEDLINE=99120557; PubMed=9923682;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1999 (TIEMBLIEL 10, Created)
01-MAY-1999 (TIEMBLIEL 10, Last sequence update)
01-JUN-2001 (TIEMBLIEL 17, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Putative outer membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR01021; OMPADOMAIN.
ProDom; PD000930; Bac_OmpA; 1.
Hypothetical protein; Lipoprotein;
SEQUENCE 179 AA; 19978 MW; 5B5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G., Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S., Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M., Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
         InterPro;
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=85963;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9ZK87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q92K87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001145; Bac_OmpA. Pfam; PF00691; OmpA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGR; HP1125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE000619; AAD08169.1; -.
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MEDLINE=97394467; PubMed=9252185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 388:539-547(1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=210;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NQALGVKRTLSVKNALVIKGVEKDMIKTISFGETKPKCAQKTRECYKENRRVDV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAVE -- SGTIIASIYFDFDKYEIKESDQETLDEIVQKAKENH-MQVLLEGNTDEFGSSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ETVKALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREY 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVFSFLVAFLLVAGCSHKMDNKTVAGDVSAKTVQTAPVTTEPAPEKEEPKQEPAPVVEEK 64
IPR001145; Bac_OmpA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 215.5; DB 16; Length 179; Pred. No. 2.8e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sin; Complete proteome.
5B5521E284E27B4C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                    Taylor D.E., Vovis G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63;
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                                                                                                              of the human
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Q8XWU0
ID Q8
AC Q8
DT 01
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Q9ZAW7
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Q9ZAW7;
01-MAY-1999
01-MAY-1999
01-JUN-2001
                                                                   Q8XWU0
                                                                                                                                                                                                                                                                                                                                                                                                   Seo W.Y., Kim J.S., Jang J.H., Yu G.J., Yum J.; submitted (CCT-1996) to the EMBL/GenBank/DDBJ databases. EMBL, U75869; AAD09577.1; ... InterPro; IPR001145; Bac_OmpA. Pfam; PF00691; OmpA; 1.
                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO1021; OMPADOMAIN.
PRODOM; PD000930; Bac_OmpA; 1.
SEQUENCE 179 AA; 20024 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=KCTC0217BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Omp22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OMP22.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helicobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                           122 ERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAEL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 NMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAEL 170
                                                                                                                                                                                                                62 LASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 NQALGVKRTLSVKNALVIKGVEKDMIKTISFGESKPKCVQKTRECYRENRRVDV
                                                                                                                                                                                                                                            10 LVAFLFIAGCKHNMDKETVAGDVSAKAVQSAPVSTEIAQEKQEPKQEPAPVVEEKPAVE-
                                                                                                                                                                                                                                                                      14 LSVLTFMTGCANKSTSQYMVAP-NAPTGYTGVIYTGV-----APLVDNDETVKA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 PAIE--SGTIIASIYFDFDKYEIKESDQETLDEIVQKAKENH-MQVLLEGNTDEFGSSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 ETVKALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 SYLTFM-----TGCANK------STSQVMVAP--NAPTGYTGVIYTGVAPLVDND
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                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                  VKRTLSVKNALVIKGVEKDMIKTISFGETKPKCTQKTRECYKENRRVDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                      -SGTIIASIYFDFDKYEIKESDQETLDEIVQKAKENH-MQVLLEGNTDEFGSSEYNQALG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) (TrEMBLrel. 10,
) (TrEMBLrel. 10,
1 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                        Conservative
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                                                                PRELIMINARY;
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32.8%;
                                                                                                                                                                                                                                                                                                                 24.2%; Score 208.5; DB 30.8%; Pred. No. 1.2e-11
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                            025ADC298F50C5AC CRC64;
                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                209
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                                                                                                                                                                                                                                                                                                                              Length 179;
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Q8XWU0; 01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-JUN-2002 (TrEMBLrel. 21,

Created)

Probable

transmembrane protein.

Last annotation update)

Last sequence update)

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Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Schiex T., Weissenbach J., Boucher C.A., "Genome sequence of the plant pathogen Ralstonia solanacearum."; "Therefore J. (2016) 1.1; "InterPro. IPR001145; Bac_Omph. Pfam; PF00691; OmpA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RSC2380 OR RS01165.
Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21681879; PubMed=11823852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=305;
                                                                                                 "Identification of Helicobacter pylori Antigens.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF181881; AAF04276.1; -
InterPro; IPR001145; Bac_OmpA.
                                                                                                                                                                                                                                                                      Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                      STRAIN-RU-1
                                                                                                                                                                                                                                                                                                                                                                                           Q9RNF4;
                                                                                                                                                                                                                                                                                                                                                                                                         Q9RNF4
                                   PRINTS; PR01021; OMPADOMAIN.
ProDom; PD000930; Bac_OmpA; 1.
SEQUENCE 157 AA; 17536 MW;
                                                                                                                                                                      Kolesnikow T., Gekas S., Lee A.;
                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                 SEQUENCE
                                                                                   Pfam; PF00691; OmpA; 1
                                                                                                                                                                                                                                      NCBI_TaxID=210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173 RMSAEGRGQTQPVGDNATEAGRAQNRRVEI 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 SVEIISFGEERPIAFGTNEEAWSQNRRAEL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53 GGALGAAGGAAVGYNWNAIKSKLTGDTAGTGTQISEQPDGSLKLNIPSQVSFDTDSAVIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 MLHIQIAAAAALSVLTFMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETV--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LISVSLVALLAA-----GCATEQQNQTL----AGTGVGAAVGAGIGALVGNSKGAAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PSFRGPLDSVAETLSQHPELAANVVGHTDSTGNPNYNMSLSQRRAQSVASYLTDRGVARN 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   209 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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27.6%; Pred. No. 2.4
     23.9%;
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Last annotation updat
   Score 205.5;
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                                       E7FB05D3C4E5641C CRC64;
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     Length 157;
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Best Local S
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
PEPTIDOGLYCANE associated lipoprotein precursor (Peptidoglycan associated lipoprotein) (OMP18).
OMP18 OR PAL OR CJ0113.
                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-20150912; PubMed-10688204; Retley J.M., Churcher C., Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C., Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S., Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W., Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Burnens A., Stucki U., Nicolet J., Frey J.;
Burnens A., Stucki U., Nicolet J., Frey J.;
Identification and characterization of an immunogenic outer membrane protein of Campylobacter jejuni.";
J. Clin. Microbiol. 33:2826-2832(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group; Campylobacter.
                                                                                                                                                                                                                         ProDom; PD000930; Bac_OmpA; 1.
Signal; Lipoprotein; Complete proteome.
SIGNAL 1 18 POTENTIAL
                                                                                                                                                                                                                                                                                          reveals hypervariable sequences.";
Nature 403:665-668(2000).
EMBL; X83374; CAA58288.1; -.
EMBL; AL139074; CAB72597.1; -.
Interpro; IPR001145; Bac_OmpA.
Pfam; PF00691; OmpA; 1......
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                                                                                                                                                                                                                                                                                                                                                                                           Whitehead S., Barrell B.G.; "The genome sequence of the food-borne pathogen Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=NCTC 11168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96121222; PubMed=8576327;
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                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                            PRINTS; PR01021; OMPADOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 · APVVEEKPAVE - - SGTIIASIYFDFDKYEIKESDQETLDEIVQKAKENH - MQVLLEGNTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 APLVDNDETVKALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46;
35 NRGSGGSDGWDIDSKISQLNDTLNKVYFDFDKFNIRPDMQNVVSTNANIFNTEVSGVSIT
                                                               4 ILFTSIAALAVVIS-----GCSTKSTS---
                                                                                              2 MLHIQIAAAAAALSVLTEMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVKA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EFGSSEYNQALGVKRTLSVKNALVIKGVEKDMIKTISFGETKPKCAQKTRECYKENRRVD
                                                                                                                                               Similarity
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                                                                                                                                                                                             165 AA; 17829 MW;
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                                                                                                                                Conservative
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                                --LASKLPSL-----VYFDFDSDEIKPQAAAILDEQAQFLTTNQT-ARVL 103
                                                                                                                                               23.8%; Score 204.5; DB 30.1%; Pred. No. 2.6e-11
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5; Mismatches
                                                                                                                                                                                                                  PEPTIDOGLYCANE ASSOCIATED LIPOPROTEIN.
                                                                                                                                                                                                  24CA7928532C2B66 CRC64;
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                                                                                                                                                                Length 165;
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Q9Z7C5
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Best Local :
                                                                                                                                                                                         Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; "Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA."; Nucleic Acids Res. 28:2311-2314(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20150255; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Eisen J., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20330349; PubMed=10871362;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria: Chlamydiales; Chlamydiaceae; Chlamydophila.
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01-MAY-1999 (TrEMBLrel. 10,
01-DEC-2001 (TrEMBLrel. 19,
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09Z7C5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic Acids Res. 28:1397-1406(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptidoglycan-associated lipoprotein. PAL OR CPN0781 OR CP1091.
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                                                                                                                                                        Local
                           111 RGSREYNMSIGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAE 169
                                                                                                                                                                                                                                                                                                 AE001659; AAD18919.1; -. AE002265; AAF38862.1; -. AP002547; BAA98989.1; -.
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                                                                                                                                                                                                                                                                                     CP1091;
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                                                                                                                                       46;
                                                                                                                                                      Similarity
RGAASYNLALGARRANAIKEHLRKQGISADRLSTISYGKEHPLNSGHNELAWQQNRRTE 186
                                                            DSKEEKQYKSSQVAAFRNITFATDSYTIKGEENLAILTNLVHYMKKNPKATLYIEGHTDE 127
                                                                                           DNDETVKALASKLPSL--VYFDFDSDEIK-PQAAAILDEQAQFLTTNQTARVLVAGHTDE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QNRRAE 160
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                                                                                                                                   Conservative
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                                                                                                                                23.8%; Score 204.5; DB 1 38.7%; Pred. No. 3.2e-11; tive 24; Mismatches 46
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Best Local
               Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Tabauchi C., Yamada M., Tabata S.,
                                                                                                                                                                                                                                                       01-OCT-2001 (TrEMBLrel. 18, 01-OCT-2001 (TrEMBLrel. 18, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q92ST9
Q92ST9;
Q92ST9;
Q1-DEC-2001
Q1-DEC-2001
Q1-MAR-2002
                                                                                               STRAIN=MAFF303099;
MEDLINE=21082930; PubMed=11214968;
                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                             Phyllobacteriaceae; Mesorhizobium
                                                                                                                                                                                              Bacteria; Proteobacteria; alpha
                                                                                                                                                                                                          Rhizobium loti (Mesorhizobium loti)
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                                                                                                                                                                                                                               MLR0220.
                                                                                                                                                                                                                                           Hypothetical protein mlr0220
                                                                                                                                                                                                                                                                                                          Q98NA9;
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PROSITE; PS01068; OMPA; UNKNOWN_1.
Hypothetical protein; Complete proteome.
Hypothetical 221 AA; 22852 MW; 3FF7CBA8F69DD396 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sinorhizobium meliloti strain 1021.";
Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
EMBL; AL591783; CAC41711.1; -.
InterPro; IPR001145; Bac_OmpA.
Pfam; PF00691; OmpA; 1.
   "Complete genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TREMBLrel. 19, Created)
01-DEC-2001 (TREMBLrel. 19, Last sequence update)
01-DEC-2002 (TREMBLrel. 20, Last annotation update)
Hypothetical transmembrane protein SMc00354.
R00274 OR SMC00354.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                        210 RVEIS 214
                                                                                                                                                                                                                                                                                                                                                                                                                                      167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HTDERGSREYNMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNR 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGVAPLVDNDETVKALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                      RAELS 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                             HTDSTGSASYNQGLSERRAASVANYLASRGVDQRRMSAVGYGLERPIASNATEVGRAQNR 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGVSVTRAGDRII----LNMPSNITFATDRDQVIPAFYSTLDSVAIVLRKFNKTLIDVDG
                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17;
                                                                                                                                                                                                                                                       Last annotation update)
                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                         Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 204; DB 16;
Pred. No. 4.4e-11;
""matches 57;
                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                       subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                         sequence update)
                                                                                                                                                                                                                                                                                                                        216 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 221;
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                                                                   RESULT 30
Q46099
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Best Local :
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Best Local :
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Q46099;
01-NOV-1996
01-NOV-1996
01-MAR-2002
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ProDom; PD000930; Bac_OmpA; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 216 AA; 22401 MW; 6FC9E5B8BAAC404A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mesorhizobium loti.";
DNA RES. 7:331-338(2000).
EMBL; AP002994; BABA7852.1; -.
Interpro; IPR001145; Bac_OmpA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (TYEMBLrel. 20, Created)
01-MAR-2002 (TYEMBLrel. 20, Last sequence update)
01-JUN-2002 (TYEMBLrel. 21, Last annotation update)
Hypothetical 26.3 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00691; OmpA;
                                                                                                                                                                                                                                                                                                                                                  Submitted (NOV-2001) to the EMBL/GenBank/DDBJ EMBL; AF448145; AAL46989.1; -. InterPro; IPR001145; Bac_OmpA. Pfam; PF00691; OmpA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                            "A Chemosensory System from Myxococcus xanthus Regulates Developmental Gene Expression Rather than Motility.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; delta subdivision; Myxobacteria; Myxococcales; Cystobacterineae; Myxococcaceae; Myxococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Myxococcus xanthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8VR19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8VR19
                                                                                                                                                                                                                                                                                                                        PRINTS; PR01021; OMPADOMAIN. ProDom; PD000930; Bac_Ompa; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                         Q46099
                                                                                                                                                                                                                                                                                                  Hypothetical protein.
SEQUENCE 249 AA; 26335 MW; 170AF8EFAF632855 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167
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                                                                                                                                                                                   146 SPVPFGFNESGLSADAQQRLSDLAQCMKT-APGRVTLAGHADERGTEEYNLQLSNRRAAS
                                                                                                                                205
                                                                                                                                                          128 VRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAE 169
                                                                                                                                                                                                                                                                                                                                                                                                                                         J.R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTDERGSREYNMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNR 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          {\tt TGVSVTRSGDQII----LNMPSDITFNVDQDAVKPGFYPVLNSVALVLKKFKQTTVDVFG}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGVAPLVDNDETVKALASKLPSLYYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RVEI 210
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                                                                                                                              VKRYLTDLGVPASQLGTVGYGETRPVNSASSEDAWSENRRVE
                                                                                                                                                                                                               SLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVA
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  (TrEMBLrel. 01, (TrEMBLrel. 01, (TrEMBLrel. 20,
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Zusman D.R.;
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                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                           OMPADOMAIN.
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Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                        Score 201.5; DB 2
Pred. No. 8.8e-11;
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    update)
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 084605;
01-NOV-1998 (TrEMBLrel. 08,
01-NOV-1998 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmid; Signal.
PROFIENCE 165 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; 047617; AAC35420.1; ...
EMBL; AJ132802; CAA10786.1; ...
Interpro; IPR001145; Bac_OmpA.
pfam; pF00691; OmpA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pawelec D.P., Jagusztyn-Krynicka K.E., submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Konkel M.E., Mead D.J., Cieplak W. Jr.; "Cloning, sequencing, and expression of a gene from Campylobacter jejuni encoding a protein (Omp18) with similarity to peptidoglycan-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-M275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OMP18 protein.
PAL OR CJAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     associated lipoproteins.";
Infect. Immun. 64:1850-1853(1996).
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                                                                      Chlamydia trachomatis.";
Science 282:754-759(1998).
EMBL; AE001330; AAC68202.1;
                                                                                                                                                                                                                                                                                                                                                                                          Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae;
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                     InterPro; IPR001145; Bac_OmpA. Pfam; PF00691; OmpA; 1.
                                                                                                                                                                                                    Stephens R.S., Kalman S., Lammel C.J., Fa
Mitchell W.P., Olinger L., Tatusov R.L.,
                                                                                                                                                                                                                                                             STRAIN-D/UW-3/CX;
MEDLINE-99000809; PubMed=9784136;
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                PAL OR CT600.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptidoglycan-associated lipoprotein
ProDom; PD000930;
                                                                                                                                                                                      Davis
                                                                                                                                                   "Genome sequence of an obligate intracellular pathogen of humans:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109 QALGLKRAKAVKEALIAQGVNSDRIAVKSYGETNPVCTEKTKACDAQNRRAE
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                                                                                                                                                                                      R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 MLHIQIAAAAALSVLTFMTGCANKSTSQVMVAPNAPTGYTGVIY---TGVAPLVDNDET
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  Bac_OmpA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17890 MW; 35E67427864BBC9D CRC64;
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Pred. No. 7.6e-11;
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                                                                                                                                                                                                                                          J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70;
                                                                                                                                                                                                              , Marathe R., Aravind Q., Koonin E.V.,
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RESULT 33
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Q9PJE0
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   Q9xcz6
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20150255; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Eisen J., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9PJEO;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                   Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-MOPN / NIGG;
                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                               PRINTS; PRO1021; OMPADOMAIN.
ProDom; PD000930; Bac_OmpA; 1.
                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001145; Bac_OmpA
Pfam; PF00691; OmpA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chlamydia muridarum.
                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE002355; AAF39684.1; TIGR; TC0889; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=83560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TC0889
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                                                                                                                                                                                                                                                Local Similarity
les 48; Conserv
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                                                                                                      151
                                                                                                                                 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     164 HPVHPGHNELAWQQNRRTE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151
                                                                                                                                                                                        58
                                                                                                                                                                                                                     48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48 GVAPLVDNDETVKALASKLPSL-------VYFDFDSDEIKPQ-AAAILDEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49;
                                                                                                                         VRHLRKSPKTTLYIEGHTDERGAAAYNLALGARRANAVKQYLIKQGIASDRLFTISYGKE 177
                                                                                                                                                   AQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGKGINQASVEIISFGEE 150
                                                                                                                                                                               GFVPFYSDEEIQQAFVEDFDSKEEQLYKTSAQSTSFRNITFATDSYSIKGEDNLTILASL 117
                                                                                                                                                                                                            GVAPLVDNDETVKALASKLPSL--------VYFDFDSDEIKPQ-AAAILDEQ
                                                                                                 RPIAFGTNEEAWSQNRRAE 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                       HPVHSGHNELAWQQNRRTE 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RPIAFGTNEEAWSQNRRAE 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VRHLHKSPKATLYIEGHTDERGAAAYNLALGARRANAVKQYLIKQGIAADRLFTISYGKE 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGKGINQASVEIISFGEE 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GFVPFYSDEEIQOAFVEDFDSKEEQLYKTSAQSTSFRNITFATDSYSIKGEDNLTILASL 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chlamydiales; Chlamydiaceae; Chlamydia
                                                                                                                                                                                                                                                                                                      202 AA;
 PRELIMINARY;
                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                   23208 MW; 02F2F13F6CDF6901 CRC64;
                                                                                                                                                                                                                                                         22.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22.8%; Score 196.5; 35.3%; Pred. No. 1.7
                                                                                                                                                                                                                                            19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19; Mismatches
                                                                                                                                                                                                                                                            Score 196.5; DB Pred. No. 1.9e-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1A999E4AC5C31253 CRC64;
321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            202 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.7e-10;
AA.
                                                                                                                                                                                                                                                                    DB 16; Length 202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 16;
                                                                                                                                                                                                                                         55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 188;
                                                                                                                                                                                                                                          17;
                                                                                                                                                                                                                                         Gaps
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InterPro; IPR001145; Bac_OmpA.
Pfam; PF00591; OmpA; 1.
PRINTS; PR01021; OMPADOMAIN.
PrODOM; PD000930; Bac_OmpA; 1.
PROSITE; PS01068; OMPA; UNKNOWN_1.
                                                                      fixing Pseudomonas stutzeri.";
Syst. Appl. Microbiol. 22:215-224(1999).
EMBL; AF117975; AAD39370.1; -.
                                                                                                                                                                                                                                                                                     Q9XCZ3;
01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
01-DEC-2001 (TrEMBLrel. 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON_TER
SEQUENCE
                                                                                                                           Vermeiren H., Willems A.,
Vanderleyden J.;
                                                                                                                                                                                                                                                                            Outer membrane protein OprF
                                                                                                        "The rice inoculant strain Alcaligenes faecalis A15 is a nitrogen-
                                                                                                                                                     MEDLINE=99319345; PubMed=10390872;
                                                                                                                                                                     STRAIN-ATCC
                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                       Bacteria;
                                                                                                                                                                                                                                                    Pseudomonas stutzeri ZoBell.
                                                                                                                                                                                                                                                                                                                                                 Q9XCZ3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001145; Bac_OmpA.
Pfam; PF00691; OmpA; 1.
PRINTS; PR01021; OMPADOMAIN.
ProDom; PD000930; Bac_OmpA; 1.
PROSITE; PS01068; OMPA; UNKNOWN_1.
NON TEP 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fixing Pseudomonas stutzeri.";
Syst. Appl. Microbiol. 22:215-224(1999).
EMBL; AF117972; AAD39367.1; -
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Outer membrane protein OprF (Fragment).
                                                                                                                                                                                                             NCBI_TaxID=96564;
                                                                                                                                                                                                                          Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=LMG 10652;
MEDLINE=99319345; PubMed=10390872;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vermeiren H., Willems A., Schoofs G., de Mot R., Keijers V., Hai W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The rice inoculant strain Alcaligenes faecalis Al5 is a nitrogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vanderleyden J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=91504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas stutzeri A15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                 320 E 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 ERGSREYNMSLGERRAVAVRNYLLGK-GINQASVEIISFGEERPIAFGTNEEAWSQNRRA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                              169 E 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    260 SYGTDQYNQRLSERRAEAVRNYLYNEYGYQGNRVNSYGYGESRPVADNSTEEGRQINRRV 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       200 APIVDNEPEPAPEVVRVELDVKFDFDKSRVREESYSDIKNLADFMQQYPQTTTVVEGHTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50 APLVDNDETVKALASKLPSLYYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTD 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                  Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      321 AA;
                                                                                                                                                                14405;
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                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34767 MW; 51110919C3E4FDE1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22.5%; Score 193.5; 35.5%; Pred. No. 7e-
                                                                                                                                      Schoofs G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21;
                                                                                                                                                                                                                                                                         (Fragment).
                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                              321 AA
                                                                                                                                    de Mot R., Keijers V., Hai W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . 7e-10;
56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 321;
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RESULT 36
Q9HXU8
ID Q9HXU
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Q9XCZ5
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Best Local Similarity
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Best Local :
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-DSM 4066;
MEDLINE-99319345; PubMed-10390872;
Vermeiren H., Willems A., Schoofs G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOY-1999 (TrEMBLrel. 12, Created)
01-NOY-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Syst. Appl. Microbiol. 22:215-224(1999).
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     дэнхив
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fixing Pseudomonas stutzeri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=91505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas stutzeri CMT.9.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Outer membrane protein OprF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR01021; OMPADOMAIN.
ProDom; PD000930; Bac_OmpA; 1.
PROSTTE; PS01068; OMPA; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00691; OmpA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001145; Bac_OmpA.
InterPro; IPR001035; MotY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF117973; AAD39368.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vanderleyden J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The rice inoculant strain Alcaligenes faecalis A15 is a nitrogen-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200
                                                                                                                                            305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                320 E 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50 APLVDNDETVKALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTD
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                                                                                                                                                                                                                                                                                                                93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 Similarity 47; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E 169
                                                                                                                                                                                                 PIAFGTNEEAWSQNRRAE 169
                                                                                                                                                                                                                                                            FMQQYPQTTTVVEGHTDSVGTDQYNQRLSERRAEAVRNVLVNEYGVQGNRVNSVGYGESR 304
                                                                                                                                                                                                                                                                                                           FLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGK-GINQASVEIISFGEER 151
                                                                                                                                                                                                                                                                                                                                                                        VAPVEPTP-----EPAPAPIVDTEPEPAPEVVRVELDVKFDFDKSRVREESYSDIKNLAD 244
                                                                                                                                                                                                                                                                                                                                                                                                                          VAPNAPTGYTGVIYTGVAPLVDNDETVKALASKLPSLVYFDFDSDEIKPQAAAILDEQAQ 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APIVDNEPEPAPEVVRVELDVKFDFDKSRVREESYSDIKNLADFMQQYPQTTTTVEGHTD
                                                                                                                                            PVADNSTEEGRQINRRVE 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            321
321 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              323
323 AA;
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     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34807 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.2%; Score 191; DB 2; 34.1%; Pred. No. 1.2e-09;
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Pred. No. 1.1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14EEF230B4CDA559 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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     261
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Best Local
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01-MAR-2001 (TrEMBLrel.
01-OCT-2001 (TrEMBLrel.
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EMBL; AE004788; AAG07080.1;
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MEDLINE=20437337; PubMed=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-ATCC
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=21608550; PubMed=11743193;

WOOD D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,

Wood D.W., Setubal J.C., Kaul R., Monks D.E., Almeida N.F. Jr., Woo L.,

Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,

Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,

Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,

Chapman T., Levy R., Li M.-J., McClelland E., Palmieri A.,

Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,

Raymond S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,

Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,

Zhang S., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Agrobacterium tumefaciens (strain C58 / ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OMPA OR ATU2722 OR AGR_C_4934.
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16, Last sequence update)
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Last annotation update)
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RESULT 38
Q8XRS0
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                      WEDLINE=21681879; PubMed=11823852;
Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
AA Arlat M., Billault A., Brottler F., Camus J.C., Cattolico L.,
Catholico L.,
Chandler M., Choisne N., Claudel Renard C., Cunnac S., Demange N.,
Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
Catholico J., Boucher C.A.,
Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
Weissenbach J., Boucher C.A.,
"Genome sequence of the plant pathogen Ralstonia solanacearum.";
Nature 415:497-502(2002).
REMBL; AL646080; CAD17912.1; -.
RINTS; PRO101145; Bac_OmpA.
Pfam; PF00691; OmpA; 1.
PF1am; PF00691; OmpA; 1.
PRINTS; PR01021; OMPANOMAIN.
PRODOM; PD000930; Bac_OmpA; 1.
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       SEQUENCE
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                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                           Ralstonia solanacearum (Pseudomonas solanacearum).
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                                                                                                                                                                                                                                                                                                                                    Plasmid megaplasmid
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                                                                                                                                                                                                                                                                                                                                                                              Probable lipoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21608551; PubMed=11743194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 294:2317-2323(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107 HTDERGSREYNMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSONR 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94 TGVSVTRRGD----SIVLNMPSNITFATDQDQVIPPFYQTLDSVAIVLNKFNRTLIDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47 TGVAPLVDNDETVKALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42;
   Complete proteome.
277 AA; 28898 M
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   28898 MW;
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21,
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Last annotation update)
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D08C29F4498FF525 CRC64;
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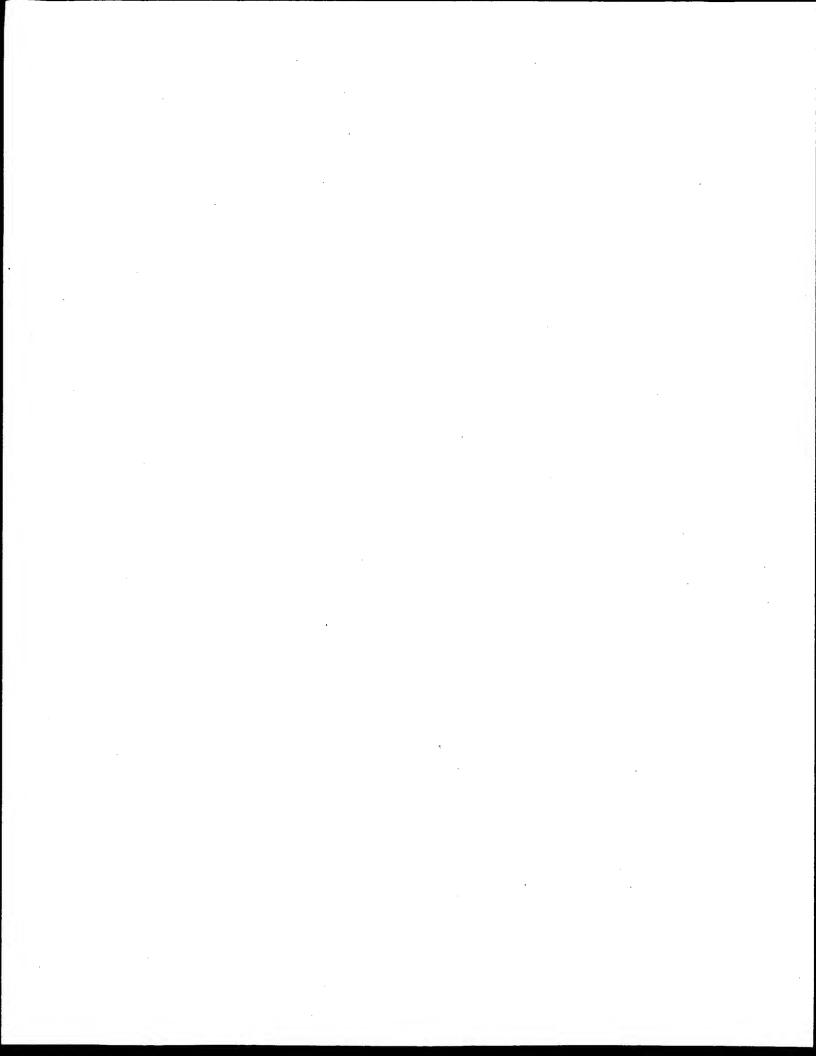
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RESULT 40
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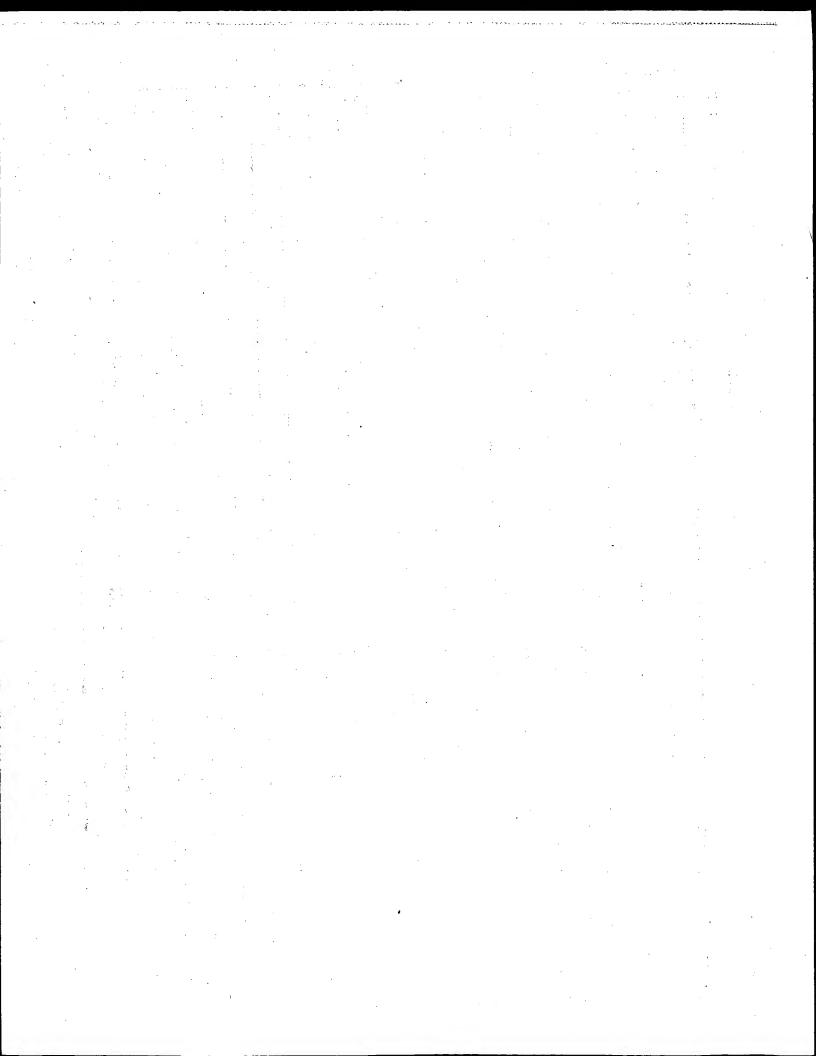
MEDLINE-20020109; PubMed-11756688;

DelVecchio V.G. Kapatral V. Berkkar R.J., Patra G., Mujer C., Los Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G., Ivanova N., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
EMBL; AE009519; AAL51967.1; -
InterPro; IDR0011145; Bac_OmpA.
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR01021; OMPADOMAIN. ProDom; PD000930; Bac_Ompa; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The genome sequence of the facultative intracellular pathogen Brucella melitensis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Selkov E., Elzer P.H., Hagius S., O'Cal
Haselkorn R., Kyrpides N., Overbeek R.,
                                                                                                                                                                                                                                                                                                                                                                                                Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00691; OmpA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brucellaceae; Brucella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brucella melitensis.
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                                                                                                      131 DQVKSQFYPTLNSVAIVLRKFDKTLVDVYGFTDSTGSASYNQALSQRRAASVASYLDSQG
                                       191 IDPRRFAVIGYGASQPIASNATPEGRAQNRRVEI 224
                                                                          137 INQASVEIISFGEERPIAFGTNEEAWSQNRRAEL 170
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                                                                                                                                                                      71 NAVLIGAGIGALGGGLIGNYMDRQEAELRAQLQGTGVSVTRNGDRIILNMPSNITFDTDQ 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 NEAQRQQLASDMATT--LGASYTTKNGLRVAAVSEQSLLDQTLANR---IIEFETGSATL
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                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                      DEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGKG 136
                                                                                                                                                                                                                                                                                                                                                                           232 AA; 24422 MW; 528DE7B4367E73FF CRC64;
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27.1%; Pred. No. 1.6
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31.3%;
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20, Last sequence update)
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Pred. No. 1.5e-09;
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Syst. Appl. Microbiol. 22:215-224(1999).

REMBL; AFR117971; AAD33366.1; -.
RINTERPRO; IPR001145; Bac_OmpA.
RINTERPRO; IPR001035; MotV.
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RPKLNTS; PR01021; OMPADOMAIN.
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STRALN=LMG 111997;
MEDLINE=99319345; PubMed=10390872;
Wermeiren H., Willems A., Schoofs G., de Mot R., Keijers V., Hai W., Vanderleyden J.;
Vanderleyden J.;
"The rice inoculant strain Alcaligenes faecalis Al5 is a nitrogen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Outer membrane protein OprF (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas stutzeri (Pseudomonas perfectomarina).
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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NCBI_TaxID=316;
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                                                                                                                                                  262 SYGTDQYNQRLSERRAEAVRNYLYNEYGYQGNRVNSYGYGESRPVADNSTEEGRQINRRV 321
                                                                                                                                                                                                                        202 APIVDTEPEPAPEVVRVELDVKFDFDKSRVREESYSDIKNLADFMQQYPQTTTVVECHTD 261
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US-08-913-880C-11
US-09-28-913-880C-11
US-09-31-88-91-880C-11
US-09-31-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-88-91-
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5173294-2
;Patent No. 5173294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94120023.0
FILING DATE: 16-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US.
FILING DATE: 14-DEC-19-
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/07/92,948 FILING DATE: 08-OCT-1987 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: MURPHY, TIMOTHY F.; APICELLA, MICHAEL A. TITLE OF INVENTION: DNA PROBE FOR THE IDENTIFICATION
CELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                               NAME: M. Paul Barker
REGISTRATION NUMBER: 32,013
                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 20005-3315
                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                     STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 932,872
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Knapp, Bernhard
Hungerer, Klaus-Dieter
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                                                                                                                                                                        14-DEC-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunogenic Hybrid Protein OprF-OprI
Derived From Pseudomonas aeruginosa Membrane Proteins
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               05552.1395-00000
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; MOLECULE TYPE:
US-09-267-747-13
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                                                                                                      TELEFAX: (202) 408-44
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                                                                                                                                                          REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: APPLICANT:
                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 14-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: 11 MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Immunogenic Hybrid Protein OprF-OprI
TITLE OF INVENTION: Derived From Pseudomonas aeruginosa Membrane Proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                               TYPE: amino acid
TOPOLOGY: linear
                                                                    LENGTH:
                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Washington
                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                 NAME:
                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Finnegan, Henderson, Farabow, ADDRESSEE: Dunner
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                                                                                                                                                                                                            M. Paul Barker
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                                                                  214 amino acids
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                                                                                                                      (202) 408-4400
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                                                                                                                                           (202) 408-4000
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202) 408-4400
                protein
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                                                                                                                                                                            05552.1395-00000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 214;
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Best Local Similarity
                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Zlotnick | TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 07-MAR-1994
                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 201/831-3246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: unl
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Harrington, James J
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
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                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                235 QAQATIDSIYGEMSQVKSAKVAVAGYTDRIGSDAFNVKLSQERADSVANYFVAKGVAADA 294
                                                                                                                                   184 INPNTAIHYNPXIGSINAGISYRFGQGAAP-----VKTFSLNLD--VTFAFGKANLKP 234
                                 142 VEIISFGEERPIAFGTNEEAWSQ-----NRRAELS 171
                                                                                                  82 QAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGKGINQAS 141
                                                                                                                                                                      33 VAPNAPTGY-----TGVIY---TGVAPLVDNDETVKALASKLPSLYYFDFDSDEIKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 DVLVNEYGVEGGRVNAVGYGESRPVADNATAEGRAINRRVESSH 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 NYLLGK-GINQASVEIISFGEERPIAFGTNEEAWSQNRRAELSY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 VKFDFDKSKVKENSYADIKNLADFMKQYPSTSTTVEGHTDSVGTDAYNQKLSERRANAVR 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 VYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVR 129
                                                                                                                                                                                                                   46;
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ISATGYGKANPVTGATXDQVWGRWALIATLAPDRRVEIA 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New Jersey
                                                                                                                                                                                                                                                                                                                                                                         338 amino acids
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                                                                                                                                                                                                                                                                                                                         unknown
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Purified No. 5770213typable Haemophilus
influenzae P5 Protein as a Vaccine for No. 5770213typable
Haemophilus Influenzae Strain
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                                                                                                                                                                                                                            Score 174.5; DB 1; Pred. No. 1e-12;
                                                                                                                                                                                                               Mismatches
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US-08-572-447C-11

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RESULT 6
US-09-267-747-11
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                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Knapp, Bernhard
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                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                          APPLICANT: Domdey, Horst
TITLE OF INVENTION: Immunogenic Hybrid Protein OprF-OprI
TITLE OF INVENTION: Derived From Pseudomonas aeruginosa Membrane Proteins.
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APPLICATION NUMBER: EP 94120023.0
FILING DATE: 16-DEC-1994
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
CORRESPONDENCE ADDRESS:
                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
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ADDRESSEE: Finnegan, Henderson, Farabow,
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APPLICANT: Domdey, Horst
TITLE OF INVENTION: Immunogenic Hybrid Protein OprF-OprI
TITLE OF INVENTION: Derived From Pseudomonas aeruginosa Membrane Proteins.
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ADDRESSEE: Dunner
ADDRESSEE: 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
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                                                                                      Broker, Michael
Von Specht, Ber
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Broker, Michael
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                                                                                      Bernd-Ulrich
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 171.5; DB 2
Pred. No. 7.3e-13;
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15,
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APPLICANT: Knapp, Bernhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (202) 408-44
INFORMATION FOR SEQ ID NO:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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MEDIUM TYPE: Floppy disk
COMPUTER: IHM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                     APPLICANT: Domdey, Horst TITLE OF INVENTION: Immur TITLE OF INVENTION: Deriv NUMBER OF SEQUENCES: 15
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ATTORNEY/AGENT INFORMATION:
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FILING DATE: 14-DEC-1995
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REGISTRATION NUMBER: 32,013
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                                                          ZIP: 20005-3315
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                                                                           COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53 VKFDFDKSKVKENSYADIKNLADFMKQYPSTSTTVEGHTDSVGTDAYNQKLSERRANAVR 112
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                                                                                                              Washington
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amino acid
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                                                                                                                         3: Dunner
1300 I Street, N.W.,
                                                                           USA
                                                                                                                                                                                                                                                                                                               Hungerer, Klaus-Dieter
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                                                                                                                                                                                                                                                                                              Broker, Michael
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                                                                                                                                                                                                       Derived From Pseudomonas aeruginosa Membrane Proteins 15
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37.6%; Pred. No. 7.3e-13;
tive 15; Mismatches 47
                                                                                                                                                                                                                                           Immunogenic Hybrid Protein OprF-OprI
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                                                                                                                                 Suite 700
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                                                                                                                                                                     Garrett &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 226 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Knapp, Bernhard
APPLICANT: Hungerer, Klaus-Dieter
APPLICANT: Broker, Klaus-Dieter
APPLICANT: Broker, Michael
APPLICANT: Von Specht, Bernd-Ulrich
APPLICANT: Domdey, Horst
TITLE OF INVENTION: Immunogenic Hybrid Protein OprF-OprI
TITLE OF INVENTION: Derived From Pseudomonas aeruginosa Membrane Proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
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                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 14-DEC-
                                                                                                                                                            CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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ATTORNEY/AGENT INFORMATION
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REGISTRATION NUMBER: 32
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 16-DE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
                  APPLICATION NUMBER: EP 9
FILING DATE: 16-DEC-1994
                                                                                                                    CLASSIFICATION:
                                                                                                                                           FILING DATE
                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                            STREET: 1300 I St
CITY: Washington
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                                                                                                                                                                                                                                                    TELEPHONE: (216) 622-8458
TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA: APPLICATION NUMBER: US.
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: Otitis Media Vaccine
NUMBER OF SEQUENCES: 6
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REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
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                                                                        Local Similarity tes 47; Conserv
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                           NAME: Golrick, Mary E. REGISTRATION NUMBER: 3
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199 PNTAINYNPWIGCINAGISYRFGQGEAPVVAAPEMVSKTFS-LNSDVTFAFGKANLKPQA 257
                                 35 PNAPTGY-----TGVIY---TGVAPLVDNDETVKALASKLPSLVYFDFDSDEIKPQA 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38;
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amino acid
)GY: linear
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Suite 1800
                                                                                                                                                                                                                359 amino acids
                                                                        Conservative
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29.9%;
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Pred. No. 1.3e-11;
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                                                                     RESULT 11
US-08-836-500A-2
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           Sequence 2, Application US/08836500A Patent No. 6197929
GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/467,722A
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 22 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Golrick, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Kolattukudy, P. E. TITLE OF INVENTION: Otitis Media Vaccine NUMBER OF SEQUENCES: 6
APPLICANT:
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                                                                                                                                                                                                                                                                                                    199 PNTAINYNPWIGCINAGISYRFGQGEAPVVAAPEMVSKTFS-LNSDVTFAFGKANLKPQA 257
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                                                                                                                                                                                                                                                              84 AAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGKGINQASVE 143
                                                                                                                                                                                                                                                                                                                                        35 PNAPTGY-----TGVIY---TGVAPLVDNDETVKALASKLPSLVYFDFDSDEIKPQA 83
                                                                                                                                                                                                                                                                                                                                                                                  47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QATLDSVYGEISQVKSRKVAVAGYTNRIGSDAFNVKLSQERADSVANYFVAKGVAADAIS 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/08467722A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ohio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   359 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Suite 1800 800 Superior Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U.S.A>
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Binz, Hans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (216)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (216) 622-8458
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29.9%;
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                                                                                                                                                                                                                                                                                                                                                                                              Score 165.5; DB 3; Pred. No. 1.3e-11;
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                                                                                                                                                                                     --AWSQNRRAELS 171
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                                                                                                                                                                                                                                                                                                                                                                                  63;
                                                                                                                                                                                                                                                                                                                                                                                                                Length 359;
                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                              21;
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APPLICANT:

Baussant, Thierry

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RESULT 12
US-08-469-260A-605
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                                                                                                                                                                                                                                                                                                     Sequence 605, Application US/08469260A Patent No. 6451578
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Best Local Similarity
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 2:
                                                            APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BÜJJK
APPLICANT: ISA K. MÜSHAHWAR
TITLE OF INVENTION: NON-A, NON-B. NON-C, NON-D, NON-E
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
                                 NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Katz, Martin L.
REGISTRATION NUMBER: 25,011
REFERENCE/DOCKET NUMBER: PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 312 - TD NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/836,500A
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                                                                                                                                                                                                                                                                                                                                                                                                                                       124 RAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNE-----EAWSQNRRAEL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          206 LKSDVLFNFNKATLKPEGQQALDQLYTQLSNMDPKDGSAVVLGYTDRIGSEAYNQQLSEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 LPSLVYFDFDSDEIKPQAAAILDEQAQFLTT--NQTARVLVAGHTDERGSREYNMSLGER 123
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                                                                                                                                                      GEORGE J. DAWSON
GEORGE G. SCHLAUDER
SURESH M. DESAI
THOMAS P. LEARY
ANTHONY SCOTT MUERHOFF
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E: ABBOTT LABORATORIES
100 ABBOTT PARK ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         335 amino acids
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180 N. Stetson, 2 Prudential Plaza, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haeuw, Jean-Francois
                                                                                                                                                                                                                                            JOHN N. SIMONS
TAMI J. PILOT-MATIAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nguyen Ngoc, Thien
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Effect, Immunogenic Complex Containing It, Process for
Their Preparation, Nucleotide Sequence and Vaccines
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                D377/AP6D
                                                                                    NON-D, NON-E HEPATITIS
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US-08-469-260A-83
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                                                                                                                                                                                                                                                                                                                                                        Patent No. 645157
                                                                                                                                                                                                                                                                                                                                                                          Sequence 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,260A
                                                                                                                       TITLE OF INVENTION:
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TELEPHONE: 708-937-6365
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                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                            APPLICANT:
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COUNTRY:
                                    CITY:
                                                     STREET:
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REFERENCE/DOCKET NUMBER: 5527.PC.01
                    STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: ABBOTT PARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   451 HAATILAIIEYCCG 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 RRA--VAVRNYLLG 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 ASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 LHIQIAAAAALSVLTFMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVKAL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 10.2%; Score 87.5; DB
Similarity 28.4%; Pred. No. 0.063;
38; Conservative 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60064-3500
                                  ABBOTT PARK
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                                                                                                                     INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E INVENTION: REAGENTS AND METHODS FOR THEIR USE
                                                                                                                                      SURESH M. DESAI
THOMAS P. LEARY
ANTHONY SCOTT MUERHOFF
JAMES C. ERKER
JAMES C. ERKER
SHERI L. BUIJK
ISA K. MUSHAHWAR
NVENTION: NON-A, NON-B. N
                                                                                                                                                                                                                                                                                                                                                                        Application US/08469260A
                                                 100 ABBOTT PARK ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    507 amino acids
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GEORGE G. SCHLAUI
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TAMI J. PILOT-MATIAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                        716
                                                                                                                                                                                                                                                                   SCHLAUDER
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                                                                     D377/AP6D
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                                                                                                                                          NON-E HEPATITIS
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Best Local Similarity
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                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: POREMBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 527
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
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LENGTH: 1422 amino aci
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                TITLE OF INVENTION:
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ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                     COUNTRY: USA
ZIP: 60064-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: si
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                          CITY: ABBOTT PARK
                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/469,260P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              653 HAATILAIIEYCCG 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 RRA--VAVRNYLLG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    612 ASFIP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     562 LAVGVGVAMAYLAIDTFGATCVRRCWSITSV----PTGAT-----VAPVVDEEEIVEEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 ASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 LHIQIAAAAALSVLTEMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVKAL 62
                                                                                                                                                                        JAMES C. ERKER
SHERI L. BUIJK
ISA K. MUSHAHWAR
INVENTION: NON-A, NON-B. N
INVENTION: REAGENTS AND ME
                                                                                                                                                                                                                                                                    GEORGE J. DAWSON
GEORGE G. SCHLAUDER
SURESH M. DESAI
THOMAS P. LEARY
ANTHONY SCOTT MUERHOFF
                                                                                                         E: ABBOTT LABORATORIES D377/AP6D 100 ABBOTT PARK ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1422 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               708-938-2623
                                                                                                                                                                                                                                                                                                                                                               JOHN N. SIMONS
TAMI J. PILOT-MATIAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.2%; Score 87.5; DB 28.4%; Pred. No. 0.31; tive 17; Mismatches
                                                                                                                                                               716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/08/424,550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --LEAMVAAI-DKLKSTITT-----TSPFTLETALEKLNTFLGP 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5527.PC.01
                                                                                                                                                                                METHODS
                                                                                                                                                                          NON-C, NON-D, NON-E HEPATITIS METHODS FOR THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 1422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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US-08-475-989-41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 5679352
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 41, Application US/08475989 Patent No. 5679352
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APPLICATE: 07-JUN-1...

FILING DATE: 07-JUN-1...

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: POREMBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: CHONG, Pele
APPLICANT: KANDII, Ali
APPLICANT: SIA, Charles
APPLICANT: KLEIN, Michel
TITLE OF INVENTION: Synthetic Haemophilus Influenzae
TITLE OF INVENTION: Conjugate Vaccine
NUMBER OF SEQUENCES: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                   COUNTRY: Canada
ZIP: M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 706-938-2623
                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                       SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1616 ASFIP------LEAMVAAI-DKLKSTITT----TSPFTLETALEKLNTFLGP 1656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1566 LAVGVGVAMAYLAIDTFGATCVRRCWSITSV----PTGAT-----VAPVVDEEEIVEEC 1615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 RRA--VAVRNYLLG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 ASKLPSLYYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 LHIQIAAAAAALSVLTFMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVKAL 62
                                                                                                                                                                                                                                                                                                                  Toronto
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                                                                                                                                                       PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.2%; Score 87.5; DB 28.4%; Pred. No. 0.92;
                                      US 08/256,839
                                                                                                                  US/08/475,989
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FR: 5527.PC.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2864;
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RESULT 16
US-08-475-985-41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: CHONG, Pele
APPLICANT: KANDIL, Ali
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (416) 595-1163 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/CA93/00041
FILING DATE: 03-FEB-1993
                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/256,839
FILING DATE: 03-FEB-1993
                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: GB 9202219.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Synthetic Haemophilus Influenzae TITLE OF INVENTION: Conjugate Vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                              APPLICATION NUMBER: US/01 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                            COUNTRY: Canada
ZIP: M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 30 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: GB 9 FILING DATE: 03-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
 FILING DATE:
              APPLICATION NUMBER: GB 9202219.3
                                                                                                                         CLASSIFICATION: 424
                                                                                                                                                                                               CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 24,973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145 ISFGEERPIAFGTNEEAWSQNRRAELSY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15;
                                                                                                                                                                                                                                                                                                                                                                                                              Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VSYGEEKPAVLGHDEAAYSKNRRAVLAY 30
                                                                                                                                                                                                                                                                                                                                                                                               Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                               Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KLEIN, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIA, Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                                                                        Floppy disk
03-FEB-1992
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53.6%;
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Pred. No. 0.0021;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-475-985-41
                                                                                                                TELEFAX: (416) 595-1155;
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 6018019
GENERAL INFORMATION:
    Matches
                   Best Local Similarity
                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                         NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-373 MIS:jb
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                        CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,839
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Synthetic Haemophilus Influenzae TITLE OF INVENTION: Conjugate Vaccine NUMBER OF SEQUENCES: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                               TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
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   15;
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M5G 1R7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08256839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Sim & McBurney
Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHONG, Pele
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KLEIN, Michel
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SIA, Charles
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7; Mismatches
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Pred. No. 0.0021;
                   Score 84; DB 3;
Pred. No. 0.0021;
                   0.0021;
                                  Length 30;
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145 ISFGEERPIAFGTNEEAWSQNRRAELSY 172

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VSYGEEKPAVLGHDEAAYSKNRRAVLAY 30

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RESULT 19
US-09-620-412C-177
: Sequence 177, Application US/09620412C
: Patent No. 6448234
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US-09-556-877-177
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; TYPE: PRT
; ORGANISM: Chlamydia
US-09-556-877-177
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                                                                                                                                                                                                                                                                   US-09-620-412C-177
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Steven p. Fling
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.46907
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SOFTWARE: FastSEQ for Windows Version 3.0/4.0
SEQ ID NO 177
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SEQ ID NO 177
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Best Local Similarity
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CURRENT FILING DATE: 2000-04-19
NUMBER OF SEQ ID NOS: 305
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APPLICANT: Maisonneuve, Jeff
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C5
FILE REFERENCE: 210121.469C5
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APPLICANT: Bhatia, Ajay
APPLICANT: Skeiky, Yasir
                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/620,412C
                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Chlamydia
                                                                                                                                                                                                                                                                                                                                  LENGTH: 964
                                                                                                                                                                                             Match 9.4%;
Local Similarity 23.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                277 ASDGGAIKVTTRLDVTGNR--GRIFFSDNITKNYGGAIYAPVVTLVDNGPTYFINNIANN 334
                                                                                   277 ASDGGAIKVTTRLDVTGNR--GRIFFSDNITKNYGGAIYAPVVTLVDNGPTYFINNIANN 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 LPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRA 125
                                         66 LPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRA 125
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                                                                                                                               8 AAAAAALSVLTFMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDET---VKALASK 65
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Skeiky, Yasir
Fling, Steve
KGGAIYIDGTSN-----SKISADRHAIIFNENIVTNVTNANGTSTSANPP-----RRNA 383
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23.6%;
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Pred. No. 1;
                                                                                                                                                                                           Score 81; DB 4; Length 964; Pred. No. 1;
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US-09-620-412C-191
Sequence 191, Application US/09620412C
Patent No. 6448234
GENERAL INFORMATION:
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US-09-556-877-191
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SEQ ID NO 191
LENGTH: 977
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SOFTWARE: FASTSEQ for Windows Version 3.0/4.0
SEQ ID NO 191
LENGTH: 977
TYPE: PRT
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Patent No. 64329
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Best Local S
                                                                                           Matches
                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                  APPLICANT: Steven P. Fling
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C7
CURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT FILING DATE: 2000-07-20
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CURRENT FILING DATE: 2000-04-19
NUMBER OF SEQ ID NOS: 305
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APPLICANT: Skeiky, Yasir
APPLICANT: Filng, Steve
APPLICANT: Maisonneuve, Jeff
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                                                                                                                                                                                                     ORGANISM: Chlamydia
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290 ASDGGAIKVTTRLDVTGNR--GRIFFSDNITKNYGGAIYAPVVTLVDNGPTYFINNIANN 347
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                                                                                           39;
                                           8 AAAAAALSVLTFMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDET--VKALASK 65
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                                                                                      9.4%; Score 81; DB 4; Length 977; 23.6%; Pred. No. 1.1; rative 23; Mismatches 75; Indels
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363
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US-08-475-989-39
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                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                               TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PC
FILING DATE: 03-FEB-19
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRETT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 08/256,839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: CHONG, Pele APPLICANT: KANDIL, Ali
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                                                                                                                                                                                                                           LENGTH: 24 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 01 FILING DATE: 03-FEB-1993 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/475,989 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                           NAME: STEWART, MICHAEL REGISTRATION NUMBER: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: GB 9202219.3 FILING DATE: 03-FEB-1992
                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: Canada
ZIP: M5G 1R7
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                                                                             111 RGSREYNMSLGERRAVAVRNYLLG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                397 ITVASSSGEILLGAGSSQNLIFYDPIEVSNAG----VSVSFNKEA 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 VAVRN----YLLGKGINQ-----ASVEIISFGEERPIAFGTNEEA 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         348 KGGAIYIDGTSN-----SKISADRHAIIFNENIVTNVTNANGTSTSANPP-----RRNA 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 LPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Toronto
                                          RGTPEYNIALGQRRADAVKGYLAG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ontario
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Suite 701, 330 University Avenue
                                                                                                                   Conservative
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                                                                                                                                                                                                              linear
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                                                                                                                                 9.2%;
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                                                                                                                                                                                                                                                                                                                                                                                           24,973
                                                                                                               5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                          1038-505 MIS:vg
                                                                                                                                 Score 79; DB 1;
Pred. No. 0.0059;
                                                                                                                                                  Length 24;
                                                                                                               0
                                                                                                            Gaps
                                                                                                               0,
                                      / Sequence 39, Application.
/ Sequence 39, Application.
/ Patent No. 6018019
/ GENERAL INFORMATION:
/ POT TOANT: CHONG, Pele
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                                                                                                                             US-08-256-839-39
                                                                                                                                                RESULT 24
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Best Local Similarity
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Patent No. 59
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INFORMATION FOR SEQ ID NO:
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               APPLICANT:
APPLICANT:
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LENGTH: 24 amino acids
TYPE: amino acid
STRANDEDNESS: single
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: PCT/CA93/00041
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/256,839
FILING DATE: 03-FEB-1993
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CORRESPONDENCE ADDRESS:
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APPLICANT: SIA, Charles
APPLICANT: KLEIN, Michel
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STREET: Su_
Ontario
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REFERENCE/DOCKET NUMBER: 1038-506 MIS:vg
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/
FILING DATE: 03-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 07-JUI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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                                                                                                                                                                                                                                         111 RGSREYNMSLGERRAVAVRNYLLG 134
                                                                                                                                                                                                    1 RGTPEYNIALGQRRADAVKGYLAG 24
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5972349
                                                                                                            Application US/08256839
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                 KANDIL, Ali
SIA, Charles
                                                                                                                                                                                                                                                                               Conservative
KLEIN, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (416) 595-1163
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                                                                                                                                                                                                                                                                                                                                                                        linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (416) 595-1155
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Pred. No. 0.0059;
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Gaps

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                                                                                                                                                                                                                                                                                   SEQ ID NO:3:
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INFORMATION FOR SEQ ID NO: 3
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ZIP: M5G lk/
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 331,037
FILING DATE: 29-MAR-1989
APPLICATION NUMBER: 752,981
FILING DATE: 08-JUL-1985
                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/550,816
FILING DATE: 06-JUL-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: RENARD, ANDRE; DINA, DINO; MARTIAL, JOSEPH TITLE OF INVENTION: DNA ENCODING BOVINE DIARRHEA
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ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I
REGISTRATION NUMBER: 24,9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 3
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TYPE: amino acid
STRANDEDNESS: single
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REFERENCE/DOCKET NUMBER: 1038-373 MIS:jb
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Local Similarity 62.5%;
es 15; Conservation
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1729 TLADE---IHSRDERPFYLYLGSRSSMSNRAKTARNINCTQKRPQEIRDLMAQGRMLYVA 1785
                                                                                1675 TSEVGI---TLVGRAALMTTGITPVVEKTE---PNADGSPSSIKIGLDEGCYDGPRPQDH 1728
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                                        85 AILDEQAQFLTTNQTARVLVAGHTDERGSREYN------MSLGERRAVA 127
                                                                                                                    28 TSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVKALASKLPSLVYFDFDS----DEIKPQAA 84
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                                                                                                                                                               Conservative
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                                                                                                                                                            9.2%; Score 79; DB
21.8%; Pred. No. 8.5;
7ative 28; Mismatches
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Conjugate Vaccine
56
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                                                                                                                                                                                                     DB 6; Length 2616;
                                                                                                                                                               68; Indels 40;
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US-09-074-579-5
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; LIBRARY: GENEBAN
; CLONE: gi288563
US-09-074-579-5
                                                                                                                                                                                                                                                                                   RESULT 27
US-09-388-774-5
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; Patent No. 6228991
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GENERAL INFORMATION:
APPLICANT: Hillman,
APPLICANT: Guegler,
APPLICANT: Pattersor
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 8.8%; Score 76; DB 3; Length 885, Best Local Similarity 25.5%; Pred. No. 3.7;
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MEDIUM TYPE: Diskett
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SOSTWARE: Word Perfect 6.1/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
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REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1786 LRSFNPELSELVDFKGTFLDRVALEALSLGPGRPKQVTTATVKELLEQEEQVEI 1839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 VRNY------LLGKGINQASVEIISFGEERP--IAFGTNEEAWSQNRRAEL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                          177 HFEIEVDIFEPQGISMLDAEASFITNDLLGSALTKSFSGKKGHVSFKPSLDQQRS 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 YFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       885 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patterson, Chandra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hillman, Jennifer L. Guegler, Karl J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                   Hillman, Jennifer L.
Guegler, Karl J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENEBANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Incyte Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            650-855-0555
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PATTERSON, CHANGI'A
VENTION: GROWTH-ASSOCIATED TRYPSIN-TYPE

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Gaps

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RESULT 28
US-08-762-106-9
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Patent No. 5948677
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                      SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                               MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                APPLICANT: Jarvik, Jonathan W.
TITLE OF INVENTION: READING FRAME INDEPENDENT EPITOPE
TITLE OF INVENTION: TAGGING
NUMBER OF SEQUENCES: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE:
LIBRARY: GENEB
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LENGTH: 885 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/388,774
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CORRESPONDENCE ADDRESS:
                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                           APPLICATION NUMBER:
                                                                                                                                                                      COUNTRY:
              FILING DATE:
                                                                                                                                                                                                                                        ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Word Perfect 6.1/MS-DOS 6.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
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                                                                                                                                                        92037
                                                                                                                                                                                   SSEE: Harris Brotman
P: 202 Coast Blvd., Suite 111
La Jolla
California
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              09-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.8%; Score 76; DB / 25.5%; Pred. No. 3.7; ative 16; Mismatches
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                         US/08/762,106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
; MOLECULE TYPE: ; FRAGMENT TYPE: US-09-320-774-9
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US-09-320-774-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/09320774 Patent No. 6265545
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Best Local Similarity 21.2%; Pred. No. 3.3;
                                                                                                                       INFORMATION FOR SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL
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                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                  REGISTRATION NUMBER: 35,461
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION: NAME: Brotman, Harris F.
                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Jarvik, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: FRAGMENT TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                TYPE: amino acid
                                                     TOPOLOGY:
                                                                                    LENGTH:
                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: La Jolla
STATE: California
                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/320,774
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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REGISTRATION NUMBER: 35,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 KVLEQGLMEVLE--EEELAAMRAHQEHFEQIRNAEL 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135 KGINQASVEIISFGEERPIAFGTNEEAWSQNRRAEL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 TQTDAFLDRPPTPLFVPQKTGTDAITQITDRQTDRQTGIENGDLFDFDFEVEPILEVLVG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 PQAAAILDE-QAQFLTTNQTARVLYAGHTDERGSREYNMSLGER-----RAVAVRNYLLG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 PADATQTQTKGPSPASTKKRTTRTLPPRTPEAVDGRRHIDIQTDVYLEELTDTVPEADTS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38 PTGYTGVIYTGVAPLVDNDETVKALASKLPSLV----YFDFDSD------EIK 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33;
                                                                                                                                                                                       Brotman, Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                  527 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       202 Coast Blvd., Suite 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jarvik, Jonathan W.
                                                   linear
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                                                                                                                         ID NO:
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TAGGING
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STATE: STREET: Matches Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/345,882
CURRENT FILING DATE: 1999-06-30
CURRENT FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/091,315
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/111,909
PRIOR FILING DATE: 1998-12-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 140
SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Bouqueleret, Lydie TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7) TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID. FILE REFERENCE: GENSET.031A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1312
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: CARBOHYD
755..757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CARBOHYD
LOCATION: 294..296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                  NAME/KEY: CARBOHYD
LOCATION: 1151..1153
OTHER INFORMATION: potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 432..434 OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                           LOCATION: 1226..1228
OTHER INFORMATION: potential
                                                                                           NAME/KEY: CARBOHYD
                                                                                                                                                                                                                                OTHER INFORMATION: potential
                                                                                                                                                                                                                                                        NAME/KEY: CARBOHYD
LOCATION: 910..912
                                                                                                                                                                                                                                                                                                                       LOCATION: 859..861
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CARBOHYD
LOCATION: 859..861
                                                                                                                                                                                                                                                                                                                                                                                                                 OCATION: 856..858
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                 EATURE:
NAME/KEY: PHOSPHORYLATION
                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                y Match 8.5%; Score 73.5; DB 4; Length 527; Local Similarity 21.2%; Pred. No. 3.3; hes 33; Conservative 21; Mismatches 77; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 TQTDAFLDRPPTPLFVPQKTGTDAITQITDRQTDRQTGIENGDLFDFDFEVEPILEVLVG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 KVLEQGLMEVLE - - EEELAAMRAHQEHFEQIRNAEL 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 PQAAAILDE-QAQFLTTNQTARVLVAGHTDERGSREYNMSLGER-----RAVAVRNYLLG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 PADATOTOTKGPSPASTKKRTTRTLPPRTPEAVDGRRHIDIOTDVYLEELTDTVPEADTS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38 PTGYTGVIYTGVAPLVDNDETVKALASKLPSLV----YFDFDSD------EIK 80
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NAME/KEY: PHOSPHORYLATION LOCATION: 663..666 LOCATION: 102..105
OTHER INFORMATION: potential NAME/KEY: PHOSPHORYLATION LOCATION: 17..19
OTHER INFORMATION: potential NAME/KEY: PHOSPHORYLATION OTHER INFORMATION: potential OTHER INFORMATION: potential FEATURE: OTHER INFORMATION: potential FEATURE: NAME/KEY: PHOSPHORYLATION LOCATION: 41..43 LOCATION: 31..33
OTHER INFORMATION: potential NAME/KEY: PHOSPHORYLATION LOCATION: LOCATION: 507..509
OTHER INFORMATION: potential LOCATION: 471..473
OTHER INFORMATION: potential LOCATION: 216..218
OTHER INFORMATION: potential OTHER INFORMATION: potential NAME/KEY: PHOSPHORYLATION LOCATION: 100..102
OTHER INFORMATION: potential NAME/KEY: PHOSPHORYLATION OTHER INFORMATION: potential NAME/KEY: PHOSPHORYLATION EATURE: COCATION: NAME/KEY: PHOSPHORYLATION LOCATION: 531..533 NAME/KEY: PHOSPHORYLATION NAME/KEY: PHOSPHORYLATION NAME/KEY: PHOSPHORYLATION LOCATION: 815..817
OTHER INFORMATION: potential NAME/KEY: PHOSPHORYLATION NAME/KEY: PHOSPHORYLATION LOCATION: 812..814 LOCATION: 656..658
OTHER INFORMATION: potential LOCATION: 591..593 OTHER INFORMATION: potential FEATURE: OTHER INFORMATION: potential OTHER INFORMATION: potential LOCATION: 801..803
OTHER INFORMATION: potential NAME/KEY: PHOSPHORYLATION FEATURE: NAME/KEY: PHOSPHORYLATION FEATURE: NAME/KEY: PHOSPHORYLATION NAME/KEY: PHOSPHORYLATION LOCATION: 876..878 FEATURE 656.

OTHER INFORMATION: potential

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LOCATION: 295..298
OTHER INFORMATION: potential
                                                                       LOCATION: 276..279
OTHER INFORMATION: potential
                                                                                                                                          LOCATION: 274..277
OTHER INFORMATION: potential
                                         NAME/KEY: PHOSPHORYLATION
                                                                                                          NAME/KEY: PHOSPHORYLATION
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OTHER INFORMATION: potential
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OTHER INFORMATION: potential
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OTHER INFORMATION: potential
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OTHER INFORMATION: potential
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OTHER INFORMATION: potential
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OTHER INFORMATION: potential
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US-08-790-912-3
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                                                                                      Matches
                                                                                                                        Query Match
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Best Local :
                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1964 amino aci
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                                                                                                                                                                                                                                                                                                                                             NAME: Leary Kathryn
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 76
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 567-2020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 23-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Weiser, Jeffrey N.
APPLICANT: Plaut, Andrew G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT
TITLE OF INVENTION: OF STREPTOCOCCUS PNEUMONIAE INFECTION
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: APPLICANT:
                                                                              Local Similarity 23.6%; Score 73; DB Local Similarity 23.6%; Pred. No. 29; es 42; Conservative 10. ...
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                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                        TYPE:
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CITY: Philadelphia
STATE: Pennsylvani
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1195 LKYQTDFAN-----LPEYNLGNTGLLYTPNQFLYDRDSIVKEV---LPELQKLDYQS 1243
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                                   17 LTFMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVKALASKLPSLYYFDFDS 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 YNMSLGERRAVAVRNYLLGKGINQASVEIISFGE 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 DEIKP-----QAAAILDEQAQFLTTNQ------TARVLV----AGHTDERGSRE 115
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                                                                                                                                                                                                                                                    1964 amino acids
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                                                                                                                                                                                                                                                                                                                               (215) 567-2991
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22.1%; Pred. No.
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                                                                            19; Mismatches
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                                                                                                                  DB 2; Length 1964;
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                                                                              57; Indels
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                                                                            60;
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US-08-790-912-2
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RESULT 33
US-08-960-756-2
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                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Leary, Kathryn
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 7600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 567-2020
TELEFAX: (215) 567-2991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,939
FILING DATE: 23-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                              ocal Similarity
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                                                                                1376 IKNNKEALLLGLTYLERWYNFNYGQ---VNYKDLVMYHPDFFGKGNTSPLDTLIELGK 1430
                                                                                                                                                                   1317 DAIR-KTLGISPEVKLTELYLEDQFSKTKQNLGDSLKKLLSADAGLASDNSVTRGYLVDK 1375
                                                                                                                                                                                                                                                      1268 LKYQTDFAN-----LPEYNLGNTGLLYTPNQFLYDRDSIVKEV---LPELQKLDYQS 1316
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                                                                                                                                                                                                                                                                                                                                     tch 8.5%; Score 73; al Similarity 23.6%; Pred. No. 42; Conservative 19; Mismatcl
                                                                                                                                                                                                                                                                                             17 LTFMTGCANKSTSOVMVAPNAPTGYTGVIYTGVAPLVDNDETVKALASKLPSLVYFDFDS 76
                                                                                                                                                                                                            77 DEIKPQAAAILDE------QAQFLTTNQTA------RVLVAGHTDERG----- 112
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1601 Market Street, 36th Floor
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                                                                                                                           --SREYNMSLGERRAVAVRNYLL-----GKGINQASVEIISFGE 149
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                                                                                                  Sequence 2, Application US/07920281C patent No. 5739026 GENERAL INFORMATION:
                                                                                                                                                           US-07-920-281C-2
                                                                                                                                                                           RESULT 34
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APPLICANT: WAYNE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: METHOD FOR CLONING AND TITLE OF INVENTION: PRODUCING THE TSP45I RESTRICTION ENDONUCLEASE IN E. COLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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CURRENT APPLICATION DATA:
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APPLICANT: Garoff, Henrik
APPLICANT: Liljestrom, Peter
APPLICANT: Liljestrom, Peter
TITLE OF INVENTION: DNA Expression Systems Based on
TITLE OF INVENTION: Alphaviruses
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
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REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: N
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                                                                                                                                                                                                                                                             145 ISFGEERPIAF --- GTNEEAWSQN 165
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                                                                                                                                                                                                                                                                                                                                                                                                 38 PTGYTG---VIY-----TGVAPLVDNDETVKALASKLPSLYYFDFDSDEIKPQAAAILD 88
                                                                                                                                                                                                                                                                                                                             89 EQAQFLTTNQTARVLVAGHTDERGSREYNMSL----GERRAVAVRNYLLGKGINQASVEI 144
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US-08-466-277-2
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GENERAL INFORMATION:
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TELEX: 248345
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2431 amino acids
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NAME: MUTPBY Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 828-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
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TOPOLOGY: linear
MOLECULE TYPE: prot
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MEDIUM TYPE: Floppy disk
                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Birch, STREET: P.O. Box 7/CITY: Falls Church
                                        PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: DNA Expression Systems Based on
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Garoff, Henrik
Liljestrom, Peter
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                                              APPLICATION NUMBER: US/08/466,277
FILLING DATE: 06-Jun-1995
CLASSIFICATION: <Unknown>
APPLICATION NUMBER: 07/920,281 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                     CITY: Falls Church
                                                                                                                                                                                                                                                                                                     ADDRESSEE: Birch, Stewart, Kolasch & Birch STREET: P.O. Box 747
                                                                                                                                                                                                                                                    COUNTRY: USA
                                                                                                                                                                                                                                                                     STATE: Virginia
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O. Box 747
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23.0%; Pred. No. 46;
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INFORMATION FOR SEQ ID NO:
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APPLICANT: FAIRWE,
APPLICANT: MAKOFF
                                                                     REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                                                                  APPLICATION NUMBER: GB 8914122.0 FILING DATE: 20 June 1989 ATTORNEY_AGENT INFORMATION: NAME: MAIY J. Wilson
                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                              FILING DATE: 29-NOV-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/110
FILING DATE: 23-AUG-1993 1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: FAIRWEATHER, Neil Fraser
APPLICANT: MAKOFF, Andrew Joseph
TITLE OF INVENTION: Expression of tetanus toxin fragment C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                  TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
                                                TELEPHONE:
                                                                                                                REGISTRATION NUMBER:
                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A.
ZIP: 22201-4714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1799 SGITFGDFDDVLRLGRAGAYIFSSDTG----SGHLQQKSVRQHNLQCAQLDAV 1847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1756 ASRAAERPVPAPRKPT-----PAPRT----AFRNKLP-LTFGDFDEHEVDALA 1798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 703-241-1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 AAI-----LDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 ANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVKALASKLPSLVYFDFDSDEIKPQA 83
                                                                                                                                Mary J. Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              % 8.4%;
Similarity 23.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 828-103P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 2431 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 248345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Nixon & Vanderhye p.C.
1100 No. 5443966th Glebe Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 703-241-2848
                                                       (703)
                                                                                                                                                                                                                                20-JUN-1990
                                                                                                                                                                                                                                                                                       29-NOV-1991
                                                                                                                                                                                                                                                                                                         US 07/777,337
                                                                                                                                                                                                                                              PCT/GB90/00943
                                                                                                                                                                                                                                                                                                                                                                                  US/08/110,786A
                                                                                                           32,955
                                                                                         117-134
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Pred. No. 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 2431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36; Indels 31;
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US-08-306-871-47
                                                                 US-08-306-871-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 47, Application US/08306871 Patent No. 5712118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                       TELEPHONE: (716) 856-4000
TELEFAX: (716) 849-0349
INFORMATION FOR SEQ ID NO: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/129,719 FILING DATE: September 29, 1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                   FEATURE:
                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (716) 856-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                    ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
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nes 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                         NAME: Nelson, M. Bud
REGISTRATION NUMBER: 35
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: MS-DOS/ Microsol SOFTWARE: Wordperfect for Windows
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/306,871 FILING DATE: 20-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Buffalo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
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                                                                                                                 STRAIN:
                                                                                                                                   ORGANISM:
                                                                                                                                                                      TOPOLOGY:
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                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 GWSVSL-----KGNNLIWTLKDSAGEVRQITF 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 RRAVAVRNYLLGKGINQASVEIISFGEERPIAF 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 SSEVIVHKAMDIEYNDMFNNFTVSFWLRVPKVSASHLEQYGTNEYSINSSMKKHSLSIGS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53 VDNDETVKALASKLPSLVYFDFDSDEIK------PQAAAI--LDEQAQFLTTNQ 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99 TARVLV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         œ
19;
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                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New York
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                                                                                                                     25240
                                                                                                                                                                                                    59 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1800 One M&T Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Timothy F. Murphy
Conservative
                                                                                 CD amino acid positions 332-390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IBM Compatible
                                                                                                                                                                      linear
                                                                                                                                   Branhamella catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.3%; but
20.9%; Pred
25;
              8.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MS-DOS/ Microsoft Windows 3.1 fect for Windows 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaccine For Branhamella catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52
                                                                                                                                                                                                                                                                                                                          35,300
                                                                                                                                                                                                                                            47:
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Pred. No. 4.5;
5; Mismatches 39; Indels 5
8;
                                                                                                                                                                                                                                                                                                             11520.0053
              Score 70; I
Pred. No. 0
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----AGHTDERGSREY----NMSLGE 122
                DB 1; Length 59; 0.29;
 26;
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57;
4;
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US-08-569-959-47
                                                                                                                                                                                                                                                                                       밁
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US-08-569-959-47
                                                                                                                                                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                   US-08-854-585-2
                                                                                                                                                                                                                                  RESULT 39
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Patent No. 5725862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No.
                                                                                                                                                                             Sequence 2, Application US/08854585 Patent No. 6114140
                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Tonks, Nicholas K. and stman, Arne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (716) 849-03
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: September 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Nelson. M D. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: MS-DOS/ Microsoft Windows 3.1 SOFTWARE: Wordperfect for Windows 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 35,300
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 59 residues
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STREET: Z...
STREET: Z...
CITY: Chicago
TTD: Illinois
                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                            TITLE OF INVENTION:
                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/569,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                   ADDRESSEE: Marshall, O'TOUTE, COLLEGE 6300 STREET: 233 South Wacker Drive, Suite 6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 ARVLVAGHTDE----RGSREYNMSLGERRAVAVRNYLLGK-GINQASVEIISFGEERP 152
                                                                                                                                                                                                                                                                                                                         100 ARVLVAGHTDE---RGSREYNMSLGERRAVAVRNYLLGK-GINQASVEIISFGEERP 152
                                                                                                                                                                                                                                                                                                                                                              19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 ATATIEGHASRDSARSSARYNORLSEARANAVKSMLSNEFGIAPNRLNAVGYGFDRP 59
                                                                                                                                                                                                                                                                                       3 ATATIEGHASRDSARSSARYNQRLSEARANAVKSMLSNEFGIAPNRLNAVGYGFDRP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14203-2391
                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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7: United States
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Timothy F. Murphy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (716)
                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CD amino acid positions 332-390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Branhamella catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hodgson, Russ, Andrews, Woods & Goodyear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (716) 856-4000
                                                                     Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   849-0349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        435
                                                                                                                                                                                                                                                                                                                                                                          8.1%;
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                                                                                                                          Density Enhanced Protein Tyrosine Phosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08/129,719
                                                                                                                                                                                                                                                                                                                                                              8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11520.0053
                                                                                                                                                                                                                                                                                                                                                                               Score 70; DB 1
Pred. No. 0.29;
                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 59.
                                                                                                                                                                                                                                                                                                                                                                26;
                                                                                                                                                                                                                                                                                                                                                                Indels
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COMPUTER READABLE FORM:

COUNTRY:

United States of America

60606

MEDIUM TYPE:

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PCT-US95-05512-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-08-854-585-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application PC/TUS9505512
GENERAL INFORMATION:
APPLICANT: Toolks, Nicholas K. and stman, Arne
TITLE OF INVENTION: Density Enhanced Protein Tyrosine
TITLE OF INVENTION: Phosphatase
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1337 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 312-474-6300
                                                                         NAME: Borun, Michael F. REGISTRATION NUMBER: 25,447 REFERENCE/DOCKET NUMBER: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                         STREET: 233 Sout
CITY: Chicago
STATE: Illinois
                  TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                          COUNTRY: UI
ZIP: 60606
                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 8.0%;
Local Similarity 21.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         321 SGQQSRDTEVLLVGLEPGTRYNATVYSQAANGTEGQP--QAIEFRTNAIQVFDVTAVNIS 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 TGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVKALASKLPSLVYFDFDSDEIK 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24;
                                                                                                                                                                                                                                                                                                                                                                                               233 South Wacker Drive, Suite 6300
                                                                                                                                                                                                                                                                                                                                           United States of America
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                                                                           27866/31954
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Pred. No. 49;
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                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1337 amino acids
                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                            379 ATSLTLIWKVSDNES---SSNYTYKIHVAGETDSS----NLNVSEPRAV 420
                                                                                                                                             321 SGQQSRDTEVLLVGLEPGTRYNATVYSQAANGTEGOP--QAIEFRTNAIQVFDVTAVNIS 378
                                                                                   21 TGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVKALASKLPSLVYFDFDSDEIK 80
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6, 2003, 14:08:12
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Gaps

Search completed: July Job time: 39 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries
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Perfect score:
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    re greater than or equal to the score of the result being is derived by analysis of the total score distribution.
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Match
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1: /cgn2_6/ptodata/2/pubpaa/U
2: /cgn2_6/ptodata/2/pubpaa/U
3: /cgn2_6/ptodata/2/pubpaa/U
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   /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
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US-10-129-342-9
US-10-156-761-10782
US-09-998-279-26
US-09-998-279-26
US-09-998-279-26
US-08-424-5508-605
US-08-424-5508-394
US-08-424-5508-394
US-09-742-659-6
US-09-742-659-6
US-09-86-468-132-17
0 US-09-841-132-191
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Compugen
Sequence 2, Appli
Sequence 10782, A
Sequence 10782, A
Sequence 26, Appli
Sequence 24, Appl
Sequence 24, Appl
Sequence 12, Appl
Sequence 39, Appl
Sequence 39, Appl
Sequence 6, Appli
Sequence 17, Appl
                                                                                                                                                                                                                  Description
    0 US-09-828-423-5
0 US-10-156-761-13516
0 US-09-815-242-5567
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0 US-09-815-242-13314
0 US-09-815-
         Sequence 5, Appli Sequence 10510, A Sequence 10510, A Sequence 10510, A Sequence 10510, A Sequence 6179, Ap Sequence 10417, Ap Sequence 10417, Ap Sequence 1262, Appli Sequence 13680, Ap Sequence 1313, App Sequence 1313, App Sequence 1313, Ap Sequence 12949, A Sequence 11949, Ap Sequence 141, Appli Sequence 141, Appli Sequence 141, Appli Sequence 141, Appli Sequence 13113, Ap Sequence 13114, Ap Sequence 13124, Ap Sequence 13124, Ap Sequence 13124, Ap Sequence 13124, Ap Sequence 10029, Appli Sequence 10029, Appli Sequence 10044, Appli Sequence 10079, Appli Sequence 13748, Ap Sequence 13748, Ap Sequence 23, Appli Sequence 24, Appli Sequence 21, Appli Sequence 23, Appli Sequence 21, Appli Sequence 31, Appli Seq
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Gaps

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; ORGANISM: Haemophilus influenzae US-10-203-942-9
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US-09-747-348-2
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                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9, Application US/10203942 Publication No. US20030096370A1 GENERAL INFORMATION:
       Query Match
                                                                                                 SEQ ID NO 9
LENGTH: 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/203,942
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: PCT/EP01/01556
PRIOR FILING DATE: 2001-02-13
PRIOR APPLICATION NUMBER: GB 0003502.2
PRIOR APPLICATION NUMBER: GB 0003502.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                      APPLICANT: BERTHET, FRANCOIS-XAVIER APPLICANT: DENOEL, PHILIPPE APPLICANT: POOLMAN, JAN APPLICANT: THONNARD, JOELLE
                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: HAEMODHILUS INFLUENCA OUTER MEMBRANE TITLE OF INVENTION: PROTEIN AND USE THEREOF IN VACCINATION FILE REFERENCE: B45210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/171,525
PRIOR FILING DATE: 1999-12-22
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Andrew D. MURDIN, Raymond P. OOMEN, Joe WANG, Pamela DUNN
TITLE OF INVENTION: Chlamydia antigens and corresponding DNA fragments and uses there
FILE REFERENCE: 77813-37
                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                     PRIOR FILING DATE: 2000-02-15
NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/747,348
CURRENT FILING DATE: 2000-12-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54 DNDETVKALASKLPSL--VYFDFDSDEIK-PQAAAILDEQAQFLTTNQTARVLVAGHTDE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RGAASYNLALGARRANAIKEHLRKQGISADRLSTISYGKEHPLNSGHNELAWQQNRRTE 186
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US-10-156-761-14808

US-09-738-626-6891

US-10-156-761-10274

US-10-156-761-10912

US-10-156-761-12273
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Pred. No. 6.2e-14;
     Score 176.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-815-242-5603
US-09-815-242-12181
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Sequence 14808, A
Sequence 6891, Ap
Sequence 10274, A
Sequence 10912, A
Sequence 12273, Ap
Sequence 5603, Ap
Sequence 12181, A
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               Sequence 2, Application US/10169953
Publication No. US20030044915A1
GENERAL INFORMATION:
APPLICANT: Phierry BAUSSANT
APPLICANT: Pascale JEANNIN
APPLICANT: Yves DELNESTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 10782
LENGTH: 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIKA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: OMURA, SATOSHI APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                             148
                                                                                                                                                                                                                                                                                 127 AIADEIKKQNATNVRVFGFTDNLGSYAHGLTLSKKRAEAVHDQLASALGSQDVTFEVRGY 186
                                                                                                                                                                                                        187 SEDYPIADNTSEQGRRKNRRVEVTF 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          312 ATGYGKANPVTGATCDQVKGRKALIACFAPDRRVEIA 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144 IISFGEERPIAFGTNEE-----AWSQNRRAELS 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193 PNTALNYNPWIGSINAGISYRFGQGAAPVVAAPEVVSKTFS-LNSDVTFAFGKANLKPQA 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  252 QATLDSIYGEMSQVKSAKVAVAGYTDRIGSDAFNVKLSQERADSVANYFVAKGVAADAIS 311
                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                         67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 AAILDEQAQFLITNQTARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGKGINQASVE 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35 PNAPTGY-----TGVIY---TGVAPLVDNDETVKALASKLPSLVYFDFDSDEIKPQA 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 AAAAALSVLTFMTGCANKSTSQVMVAPNA-----PTGYTGVIYTGVAPLVD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                             GEERPIAFGINEEAWSQNRRAELSY 172
                                                                                                                                                                                                                                                                                                                    EQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGK-GINQASVEIISF 147
                                                                                                                                                                                                                                                                                                                                                         ADGATLAPAKVLDIKSVVEDLGGEERREDTNADVTFALQAEVLFPKDSPKLNPEARSRIN 126
                                                                                                                                                                                                                                                                                                                                                                                                                                 ATATATATTITALAVLATLTLTV-PSAVADDGDPSAPPGSVTTSPPPDVDANSPGLKL 66
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HORIKAWA, HIROSHI
SHIBA, TADAYOSHI
FranOois LAWNY
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                                                                                                                                                                                                                                                                                                                                                                                            ------NDETVKALASKLPSLVYFDFDSDEIKPQAAAILD 88
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Gaps

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Query Match
Best Local Similarity
Watches 35; Conserva
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LENGTH: 344
TYPE: PRT
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SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 380
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: BURGESS, NICOLA A.
APPLICANT: GARCIA, MIGUES M.
APPLICANT: KIRKE, DAVID F.
APPLICANT: MEYERS, NICHOLAS L.
APPLICANT: WILLIAMS, PAUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/998,279
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 60/250,288
PRIOR FILING DATE: 2000-11-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2000-01-04
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/169,953
CURRENT FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: FR 00 00070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: ginS FILE REFERENCE: GM50081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Jean-Yves BONNEFOY
TITLE OF INVENTION: METHOD FOR PREPARING A POLYPEPTIDE SOLUBLE IN AN AQUEOUS SOLVENT
TITLE OF INVENTION: IN THE ABSENCE OF DETERGENT
FILE REFERENCE: D18390
                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Porphyromonas gingivalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Klebsiella pneumoniae
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                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  215 LKSDVLENENKATLKPEGQQALDQLYTQLSNMDPKDGSAVVLGYTDRIGSEAYNQQLSEK 274
                                       154 AFGTNEEAWSQ 164
                                                                                                                                                                  267 PTQPT-VTRVV-----VDN-------VVYFRINSAKIDRNQEINVYNTAEYA 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 RAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNE-----
                                                                                                                     95 TINQTARVLVAGHTDER-GSREYNMSLGERRAVAVRNYLLGKGINQASVEIISFGEERPI 153
                                                                                                                                                                                                          35 PNAPTGYTGVIYTGVAPLVDNDETVKALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFL 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 LPSLVYFDFDSDEIKPQAAAILDEQAQFLTT--NQTARVLVAGHTDERGSREYNMSLGER 123
                                                                                                                                                                                                                                                        40;
---YEENAWNR 372
                                                                               KTN-NAPIKVVGYADEKTGTAAYNMKLSERRAKAVAKMLEKYGVSADRITIEWKGSSEQI 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEI 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/09998279
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                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                      12.4%; Score 107; DB 9; 30.5%; Pred. No. 0.0041;
                                                                                                                                                                                                                                                    16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 9;
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                                                                                                                                                                                                                                                                                              Length 380;
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; LENGTH: 237
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-10-010-160-12
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; SEQ ID NO 24
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                                                                                                                                                                                                                                       SOFTWARE: F
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                                                                             Matches
                                                                                                Query Match
Best Local Similarity
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Good, Robert T,
APPLICANT: King, Kendall W.
TITLE OF INVENTION: NOVEL THERAPEUTIC COMPOSITIONS FOR
TITLE OF INVENTION: TREATING INFECTION BY LAWSONIA SEF
FILE REFERENCE: DAVIIIO.001AUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/998,279
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 60/250,288
PRIOR FILING DATE: 2000-11-30
                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/010,160 CURRENT FILING DATE: 2001-11-09 PRIOR APPLICATION NUMBER: AU PRI381 PRIOR FILING DATE: 2000-11-10
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                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/249,596 PRIOR FILING DATE: 2000-11-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rosey, Everett L. APPLICANT: Strugnell, Richard A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 38
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: gins FILE REFERENCE: GM50081
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                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          272 PTQPT-VTRVV-----VDN-------VVYFRINSAKIDRNQEINVYNTAEYA 310
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86 ANK-LKKMLMADAIPQSATGISADDVGVLL----RVNSNSTFFPGTATLTPEGKKVMGTV 140
                                     24 ANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVKALASKLPSLVYFDFDSDEIKPQA 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35 PNAPTGYTGVIYTGVAPLVDNDETVKALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFL
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MEYERS, NICHOLAS L.
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                                                                             Conservative
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                                                                                              10.9%;
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                                                                             29; Mismatches
                                                                                              Score 93.5; DB 9; Pred. No. 0.058;
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                                                                                                                 Length 237;
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US-08-424-550B-605

APPLICANT: APPLICANT: APPLICANT:

APPLICANT: APPLICANT: APPLICANT:

CITY:

ADDRESSEE:

COUNTRY:

USA

FILING DATE:

APPLICANT: APPLICANT: APPLICANT: RESULT 8

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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-424-550B-605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NON-A, NON-B. NON-C, NON-D, NON-E HEPATITIS TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: /vo -- TELEPHONE: /vo -- 708-938-2623
                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 33 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                            360 LAVGVGVAMAYLAIDTFGATCVRRCWSITSV----PTGAT-----VAPVVDEEEIVEEC 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            193 ASRIRSVGYADTRPLE-PSSPEGSTKNRRIEFYF 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 LAVLREYNLYL-----VIRGHADIGEITKGSPFASNWELSGARAAAAAQYLVEHGIK 192
                                                                                                            63 ASKLPSLYYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGE 122
                                                                                                                                                                                                                            3 LHIQIAAAAAALSVLTFMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVKAL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60064-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABBOTT PARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POREMBSKI, PRISCILLA E.
      RRA--VAVRNYLLG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QASVEIISFGEERPIAFGTNEEAWSQNRRAELSY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAILDEQAQFLTTNQTARVLVAGHTD----ERGSR-EYNMSLGERRAVAVRNYLLGKGIN 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JAMES C. ERKER
SHERI L. BUIJK
ISA K. MUSHAHWAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             507 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3: ABBOTT LABORATORIES 100 ABBOTT PARK ROAD
                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SURESH M. DESAI
THOMAS P. LEARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GEORGE J. DAWSON
GEORGE G. SCHLAUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOHN N. SIMONS
TAMI J. PILOT-MATIAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTHONY SCOTT MUERHOFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                708-937-6365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            435435
                                                                                                                                                                                                                                                                                                                             10.2%;
28.4%;
                                                            -----LEAMVAAI-DKLKSTITT-----TSPFTLETALEKLNTFLGP 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/08/424,550B
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ເສນ. 55
                                                                                                                                                                                                                                                                                                  17;
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                                                                                                                                                                                                                                                                                                                          Score 87.5; DB Pred. No. 0.75;
                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D377/AP6D
                                                                                                                                                                                                                                                                                                                                                  DB 8;
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                                                                                                                                                                                                                                                                                                                                                  Length 507;
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RESULT 10
US-08-424-550B-394
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US-08-424-550B-83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-424-550B-83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 708-938-2623 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 708-937-6365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: ABBOTT PARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: ABBOTT LABORATORIES STREET: 100 ABBOTT PARK ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME:
                                                                                                                  653 HAATILAIIEYCCG 666
                                                                                                                                                                         123 RRA--VAVRNYLLG 134
                                                                                                                                                                                                                                  612 ASFIP------LEAMVAAI-DKLKSTITT-----TSPFTLETALEKLNTFLGP 652
                                                                                                                                                                                                                                                                                                                                                     562 LAVGVGVAMAYLAIDTFGATCVRRCWSITSV----PTGAT-----VAPVVDEEEIVEEC 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     451 HAATILAIIEYCCG 464
                                                                                                                                                                                                                                                                                         63 ASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGE 122
                                                                                                                                                                                                                                                                                                                                                                                    3 LHIQIAAAAAALSVLTFMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVKAL 62 | ; ; | | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INVENTION: REAGENTS AND METHODS FOR THEIR USE SEQUENCES: 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1422 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GEORGE J. DAWSON
GEORGE G. SCHLAUDER
SURESH M. DESAI
THOMAS P. LEARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTHONY SCOTT MUERHOFF
JAMES C. ERKER
SHERI L. BUIJK
ISA K. MUSHAHMAR
VENTION: NON-A, NON-B. NON-C, NON-D, NON-E HEPATITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Release #1.0, Version #1.25
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Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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Š 밁 Ş Дb

Matches Query Match

38;

STRANDEDNESS:

LENGTH:

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Sequence 2, Application US/09742659; Patent No. US20010034019A1; GENERAL INFORMATION:
APPLICANT: Hong, Zhi
APPLICANT: Butkiewicz, Nancy J.; APPLICANT: Bong, Weidong; APPLICANT: Ingravallo, Paul
                                                                                                                                     RESULT 11
US-09-742-659-2
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 394:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUJJK
APPLICANT: ISA K. MUSHAHWAR
TITLE OF INVENTION: NON-A, NON-B. NON-C, NON-D, NON-E |
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: 11 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 55:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: ABBOTT PARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                  1657 HAATILAIIEYCCG 1670
                                                                                                                                                                                                                                                                                         1616 ASFIP------LEAMVAAI-DKLKSTITT-----TSPFTLETALEKLNTFLGP 1656
                                                                                                                                                                                                                                                                                                                                                                  1566 LAVGVGVAMAYLAIDTFGATCVRRCWSITSV----PTGAT-----VAPVVDEEEIVEEC 1615
                                                                                                                                                                                                                                                       123 RRA--VAVRNYLLG 134
                                                                                                                                                                                                                                                                                                                          63 ASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           3 LHIQIAAAAAALSVLTFMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVKAL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                     38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GEORGE J. DAWSON
GEORGE G. SCHLAUDER
SCRESH M. DESAI
THOMAS P. LEARY
ANTHONY SCOTT MUERHOFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 ABBOTT PARK ROAD
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TAMI J. PILOT-MATIAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.2%; Score 87.5; D 28.4%; Pred. No. 8.8;
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1566 LAVGVGVAMAYLAIDTFGATCVRRCWSITSV----PTGAT-----VAPVVDEEEIVEEC 1615

63 ASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGE 122

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; TYPE: PRT
; ORGANISM: GB virus-B
US-09-742-659-2
                                                                                                           US-09-742-659-6
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US-09-742-659-6
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                                        Best Loc
Matches
                                                                      Query Match
                                                                                                                                                                                                                                                SEQ ID NO 6
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Best Local Similarity
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SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                           LENGTH: 2865
TYPE: PRT
ORGANISM: GBV-B/HCV
FEATURE:
                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/742,659
CURRENT FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: US 60/171,469
PRIOR FILING DATE: 1999-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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CURRENT FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: US 60/171,469
PRIOR FILING DATE: 1999-12-22
                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE:
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TITLE OF INVENTION: Chimeric HCV/GBV-B viruses
FILE REFERENCE: ID01116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                      NAME/KEY: SITE
LOCATION: (2275)..(2865)
OTHER INFORMATION: chimeric region
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                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 ASKLPSLYYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38;
3 LHIQIAAAAAALSVLTFMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVKAL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 LHIQIAAAAAALSVLTFMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVKAL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                  PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                      Lemon, Stanley M.
VENTION: Chimeric HCV/GBV-B viruses
                                                                                                                                                                                                                                                                                                                                                                                                                           Lau, Johnson Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Butkiewicz, Nancy J.
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                                        Conservative
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28.4%; Pred. No. 8.8;
ative 17; Mismatches
                                                      10.2%; Score 87.5; Di 28.4%; Pred. No. 8.8;
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                                    17; Mismatches
                                                                      DB 10;
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                                Indels
                                                                     Length 2865;
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                                    31;
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RESULT 14
US-09-841-132-177
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US-09-886-468-21
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APPLICANT: AventLs Pasteur Limited
APPLICANT: INVENTION: Chlamydia antigens and corresponding DNA fragments and uses there
Sequence 177, Application US/09841132 Patent No. US20020061848A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: POSEQ ID NO 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/114,061
PRIOR FILING DATE: 1998-12-28
NUMBER OF SEQ ID NOS: 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENGTH: 871
                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1998-12-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 1998-12-28
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                                                                                                                       532 TNLLFSGNKATGPSNSSANQEGCGGAILSFLESASVS--TKKGLWIEDNENVSLS 584
                                                                                                                                                                                                    477 ----LTFDGNTAGTSGGAIYTETEDFTLTGSTGTVTFSTNTAKTGGALYSKGNNSLSGN
                                                                                                                                                                                                                                                                                 426 AILAFIDSGSVSDKTGLSIANNQEVSLTSNAATVSGGAIYATKCTLTGNGS-----
                                                                                                                                                          123 RRAVAVRNYLLGKGINQASVE-----IISFGEERPIAFGTNEEAW-SQNRRAELS 171
                                                                                                                                                                                                                                       67 PSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREY---NMSL-GE 122
                                                                                                                                                                                                                                                                                                                       15 SVLTFM-----TGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVKALASKL 66
                                                                                                                                                                                                                                                                                                                                                            42;
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    RESULT 16
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RESULT 15
US-09-841-132-191
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SOFTWARE: FastSEQ for Windows Version 3.0/4.0
SEQ ID NO 191
LENGTH: 977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 191, Application US/09841132 Patent No. US20020061848A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 3.0/4.0 SEQ ID NO 177 LENGTH: 964
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APPLICANT: Bhatia, Ajay
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                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REPERENCE: 210121.469C8
CURRENT APPLICATION NUMBER: US/09/841,132
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APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C8
CURRENT APPLICATION NUMBER: US/09/841,132
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NUMBER OF SEQ ID NOS: 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Chlamydia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     277 ASDGGAIKVTTRLDVTGNR--GRIFFSDNITKNYGGAIYAPVVTLVDNGPTYFINNIANN 334
                                                126 VAVRN----YLLGKGINQ-----ASVEITSFGEERPIAFGTNEEA 161
                                                                                                      348 KGGAIYIDGTSN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 VAVRN----YLLGKGINQ-----ASVEIISFGEERPIAFGTNEEA 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   335 KGGAIYIDGTSN-----SKISADRHAIIFNENIVTNVTNANGTSTSANPP------RRNA 383
397 ITVASSSGEILLGAGSSQNLIFYDPIEVSNAG----VSVSFNKEA 437
                                                                                                                                                                                                           290 ASDGGAIKVTTRLDVTGNR--GRIFFSDNITKNYGGAIYAPVVTLVDNGPTYFINNIANN 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 LPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRA 125
                                                                                                                                                     66 LPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRA 125
                                                                                                                                                                                                                                                                                                            39;
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                                                                                                                                                                                                                                                         8 AAAAAALSVLTFMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDET--VKALASK 65
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Similarity 23.6%;
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                                                                                                                                                                                                                                                                                                                                     9.4%; Score 81; DB 10; Length 977; 23.6%; Pred. No. 9.4;
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                                                                                                    ---SKISADRHAIIFNENIVTNVTNANGTSTSANPP
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      В
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CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9543
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SEQ ID NO 74
LENGTH: 361
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                                                                                                                                                                                                     Query Match
Best Local :
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APPLICANT: Bhatia, Ajay
APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT
TITLE OF INVENTION: AND DIAGNOSIS OF CHLAMYDIAL INFECTIFILE REFERENCE: 210121.515C2
CURRENT APPLICATION NUMBER: US/10/007,693
CURRENT FILING DATE: 2001-12-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
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                                                                                                                                                                                                                                                                                                            LENGTH: 420
TYPE: PRT
                                                                                                                                                                                                   Local Similarity
                                                                                 172 EIAAKGVGLTIDTLGLVPNSKLSKQLSCIAEA----TGGTYTSVEHKEDLTDKVNQLVDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 AVRN----YLLGKGINQASVEIISFGEERP 152
228 AADKVVTPVAVDGAADCAKAPTLKSGLFTDRAEFAOHRWYRVDVKPGQELRASVSLSADR 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245 DLGGSEKPCYVVGKNIEENSIYIVR-GEDHP 274
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                                           63 -ASKLPSLVYFDFDSDEIKPQA--AAILDEQAQF-----LTTNQTARVLVAGHTDE 110
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                                                                                                                               6 QIAAAAAALSVLTEMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVKAL---
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HORIKAWA, HIROSHI
                                                                                                                                                                               Conservative
                                                                                                                                                                        9.3%; Score 80; DB
23.4%; Pred. No. 3.6;
7ative 33; Mismatches
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US-10-156-761-13758
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Best Local S
Matches 53
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LENGTH: 877
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APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                           APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L. APPLICANT: Zyskind, Judith W. APPLICANT: Wall, Daniel
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PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identificat
TITLE OF INVENTION: Prokaryote
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APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90 QAQFLT-----TNQTARVLV------AGHTDERGSREYNMSLGERRAVAVRNYLL 133
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53; Conserv
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                                                                                     Carr, Grant J.
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HORIKAWA, HIROSHI
                                                                                                           Trawick, John D.
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                      Identification of Essential Genes
Prokaryotes
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24.1%; Pred. No. 19;
tive 23; Mismatches
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RESULT 20
US-09-828-423-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/09828423 Patent No. US20020099178A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 14076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Salmonella typhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH: 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 8.98;
Local Similarity 22.28;
                 OPERATING SYSTEM: DOS
SOFTWARE: Word Perfect 6.1/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/828,423
FILING DATE: 05-Apr-2001
                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                            Patterson, Chandra
TITLE OF INVENTION: GROWTH-ASSOCIATED TRYPSIN-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hillman, Jennifer L. Guegler, Karl J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              239 HLNRQ 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 SQNRR 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 VTEDHMDR-YPFGLQQYRAAKLRVYEKAKVCVVNADDALTMPVRGADERCVSFGVNMGDY 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135 -GVGGNIG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 MLHIQIAAAAA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTDERGSREYNMSLGERRAVAVRNYLLGK----GINQASVEIISFGEERPIAFGTNEEAW 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGVAPLVDNDETVKALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAG 106
                                                                                                                      COMPUTER: IBM Compatible
                                                                                                                                                                                                                                 STATE: CA
  CLASSIFICATION:
                                                                                                                                              MEDIUM TYPE: Diskette
                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                    CITY: Palo Alto
                                                                                                                                                                                         ZIP:
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<Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --LPALMLLDADRELYVLELSSF---QLETTSSLQAAAATVLN 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29;
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Pred. No. 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-156-761-13516
                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 13516
LENGTH: 155
                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, WA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: JP 2001-272697 PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: OMURA, SATOSHI APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: JP 2001-204089
                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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                                                                                                                                                                                                                                                    Local
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NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0505
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE:
127 AVRNYLLGKGINQASVEIISFGEERPIAF-----GTNEEAWS 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177 HFEIEVDIFEPQGISMLDAEASFITNDLLGSALTKSFSGKKGHVSFKPSLDQQRS 231
                                                           52 -----KCKPDIQTDADEIRQAVCKSTSRKFILATFATDRGQREW---LNEAKDY 97
                                                                                                  67 PSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71 YFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14;
                                                                                                                                           9 VAGAAVALLAL---TGCGGSSGSDDGAAKAVPATATG--
                                                                                                                                                                                     7 IAAAAAALSVLTFMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVKALASKL 66
                                                                                                                                                                                                                                 38;
                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 09/388,774 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 650-845-4166
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                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                8.8%;
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25.5%; Pred. No.
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                                                                                                                                                                                                                                                Score 75.5; D
Pred. No. 2.6;
                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                      Length 155;
                                                                                                                                                                                                                                 Indels
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0;

Gaps

0;

45;

Gaps

-SLEDLAAEV 51

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RESULT 22
US-09-815-242-5697
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                                                                                                                                                                                                              US-09-815-242-12668
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SOFTWARE: FASE
; SEQ ID NO 5697
FENGTH: 794
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                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                          Sequence 12668, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Identification of Essential Genes TITLE OF INVENTION: Prokaryotes
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                                                           APPLICANT:
                                                                               APPLICANT:
                                                                                               APPLICANT:
                                                                                                                    APPLICANT:
                                                                                                                                  APPLICANT: Haselbeck, Robert
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PRIOR APPLICATION NUMBER: 60/257,931
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
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                                       APPLICANT:
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     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
nes 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION
                                                                                                                                                                                                                                                                                                                                                                    499 TITNGRPVVTDYHGDDQTLQLLATA---
                                                                                                                                                                                                                                                                                                                                                                                                                                           439 ALVASISVLVIACPCALGLATPTSIMVGTGRAAENGILFKGGEFVERTHQIDTIVLDKTG
                                                                                                                                                                                                                                                                                         550 TTFKAVPGHGIEATIDHHHILVGNRKLMADNDISLPKHIS 589
                                                                                                                                                                                                                                                                                                                                                                                                    44 VIYTGVAPLVD---NDETVKALASKLPSLVYFDFDSDEIKPQAAAILD--EQAQFLTINQ 98
                                                                                                                                                                                                                                                                                                                           99 TARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGKGIN 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 AAAAALSVLTEMTGCA--NKSTSQVMVAPN--APTGY------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xu, H. Howard
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Zyskind, Judith W.
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Yamamoto, Robert T
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                   Carr, Grant J.
Yamamoto, Robert T.
                                                       Trawick, John D.
                                                                           Wall, Daniel
                                                                                               Ohlsen, Kari L.
Zyskind, Judith W.
   Xu, H. Howard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-02-16
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23.8%; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                ---EKDSEHPLAEAIVNYAKEKQLTLTET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10;
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                                                                                                            SEQ ID NO 10510
LENGTH: 1330
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 80
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38;
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; TYPE: PRT ; ORGANISM: Streptomyces avermitilis US-10-156-761-10510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version SEQ ID NO 12668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10510, Application US/10156761 Publication No. US20030119018A1
                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILLING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: OMURA, SATOSHI APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
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CURRENT FILING DATE: 2001-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 14110
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PRIOR APPLICATION NUMBER: 60/206,848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 8.8%;
Local Similarity 23.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               550 TTFKAVPGHGIEATIDHHHILVGNRKLMADNDISLPKHIS 589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 439 ALVASISVLVIACPCALGLATPTSIMVGTGRAAENGILFKGGEFVERTHQIDTIVLDKTG 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99 TARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGKGIN 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44 VIYTGVAPLVD----NDETVKALASKLPSLVYFDFDSDEIKPQAAAILD--EQAQFLTTNQ 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 AAAAALSVLTFMTGCA--NKSTSQVMVAPN--APTGY------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISHIKAWA, JUN
HORIKAWA, HIROSHI
SHIBA, TADAYOSHI
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8.7%;
25.0%;
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Pred. No. 27;
Score 74.5;
Pred. No. 72;
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                        DB
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                        9;
                           Length 1330;
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: Sequence 8493, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
                                                                                                                      RESULT 26
US-10-128-714-8493
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APPLICANT: Hu, Wengi
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
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US-10-128-714-3493
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Best Local (
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SEQ ID NO 3493
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             APPLICANT:
         APPLICANT: Jiang, Bo APPLICANT: Hu, Wenqi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/316,362 PRIOR FILING DATE: 2001-08-31
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CURRENT FILING DATE: 2002-04-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 10182-018-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1177
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                139
                                                                                                                                                                                                                                                     127 AVRNYLLGKG-----INQASVEIISFGEERPIAFGT 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     690 PLLLDQTAGWL-----
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                                                                                                                                                                                                                                                                                                                                          72 FDFDSDEIKPQAAAILDEQAQFLTTNQ-----TARVLVAGHTDERGSREYNMSLGERRAV 126
                                                                                                                                                                                                                                                                                                                                                                                  42 LDAICEVLGITNMSTVRAQNLQDLIYKRGQAGVTKASVTIVFDNRDTAKSPIG-----
                                                                                                                                                                                                                                                                                                                                                                                                                              14 LSYLTEMTGCANKSTSQVMVAPNA--PTGYTGVIYTGVAPLVDNDETVKALASKLPSLVY 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84 AAILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGKGINQASVE 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38 PTGYTGVIYTG------VAPLVDNDETVKALASKLPSLVYFDFDS-DEIKPQA 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PatentIn version 3.1
                                                                                                                                                                                                         NNPNFLIMQGRITKVLNMKPVEILSMIEE---AAGT 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.6%; ilarity 23.1%; Conservative 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                              ---FEEYATISVTRQIVLGGTSKYLINGHRAQQQTVQ-NLFQSVQLNI 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23;
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 9; Length 1177;
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                                                                                                                                                                                                                                                                                                                                                                                      94
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US-09-738-626-6179
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PRIOR FILING DATE: 2001-04-23
PRIOR PELICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR PELICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN VET. 3.0
SEQ ID NO 6179
LENGTH: 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6179, Application US/09738626
Publication No. US20020197605A1
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Best Local (
                                                                                                                                   PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: NAKAGAWA, SATOSHI APPLICANT: MIZOGUCHI, HIROS
                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: JP 99/377484
                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
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CURRENT FILING DATE: 2002-04-23
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APPLICANT: Zamudio, Carios
APPLICANT: Excentian, Alexey M
APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/316,362 PRIOR FILING DATE: 2001-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 8.6%; Score 74;
Local Similarity 23.1%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139 NNPNFLIMQGRITKVLNMKPVEILSMIEE --- AAGT 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        127 AVRNYLLGKG-----INQASVEIISFGEERPIAFGT 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 FDFDSDEIKPQAAAILDEQAQFLTTNQ-----TARVLVAGHTDERGSREYNMSLGERRAV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42 LDAICFYLGITNMSTYRAQNLQDLIYKRGQAGYTKASYTIYFDNRDTAKSPIG------ 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 LSVLTFMTGCANKSTSQVMVAPNA--PTGYTGVIYTGVAPLVDNDETVKALASKLPSLVY 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36;
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                                                                                                                                                                                                                                                                                                                   IKEDA, MASATO
OZAKI, AKIO
                                                                                                                                                                                                                                                                                                                                                           SENOH, AKIHIRO
                                                                                                                                                                                                                                                                                                                                                                               YOKOI, HARUHIKO
TATEISHI, NAOKO
                                                                                                                                                                                                                                                                                                                                                                                                                           OCHIAI, KEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAYASHI, MIKIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANDO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIZOGUCHI, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -FEEYATISVTRQIVLGGTSKYLINGHRAQQQTVQ-NLFQSVQLNI 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59;
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US-09-815-242-10417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-815-242-10417
                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 10417
LENGTH: 928
                                                                                                                                                                    Matches
                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 8.5%;
Best Local Similarity 23.6%;
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APPLICANT:
APPLICANT:
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PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA 011A
                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/206,848
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PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/269,308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2000-05-26
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                                                                                                                                                                                    Local Similarity
  369 VGLSFAIEPGVAAYIPVAHDYLDAPDQISR-----
                                                                           310 ETSVADEAPEVTATVISYDNYVTILD-EETLKAWIAKLEKAPVFAFDTETDSLDNISANL 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 GDQDRRLTISEQ----ITNYDHGEVVDEDTVR-FHFSEPAP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 GSREYNMSLGERRAVAVRNYLLGKGINQASVEIISFGEERP 152
                                                                                                               30 QVMVAPNAPTGYTGVI-YTGVAPLVDNDETVKALASKLPSLVYFDFDSD-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 SLVYFDFDSDEIKPQAAAIL---DEQAQFLTTNQTARVLVAGHTD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 AAAATLAGLAVLSGCTAQPSQAEDNTLTYLEPQFFRTLYPPSAGFYPNGSVVNNIADR-- 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 AAAAALSVLTEMTGC-ANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVKALASKLP 67
                                     -----EIKPQAAAILDEQAQFL-TTNQTARVLVAGHTDERGSREYNMSLGERRAVAV-RN 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -LLYQDPETLELKPWIATELPEVNEDATEFTFNIRTDVTYSDGTPLTAENVVKNFDLYGL 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carr, Grant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yamamoto, Robert T
                                                                                                                                                                 Conservative
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                                                                                                                                                                              8.5%; Score 73.5; DB 10; 26.3%; Pred. No. 55;
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Pred. No. 27;
                                                                                                                                                               Mismatches
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--ERALELLKPLLEDEKALKVGQN 420
                                                                                                                                                                                                   Length 928;
                                                                                                                                                             Indels
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RESULT 29
US-10-071-179-29
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LENGTH: 1312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/111,909 PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/345,882
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/091,315
PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/071,179
CURRENT FILING DATE: 2002-02-07
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TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-
TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
FILE REFERENCE: GENSET.031A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
             LOCATION: 808..811
OTHER INFORMATION: potential
                                                       NAME/KEY: PHOSPHORYLATION
                                                                                                   OTHER INFORMATION: potential
                                                                                                                            NAME/KEY: PHOSPHORYLATION LOCATION: 663..666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 755..757
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CARBOHYD
LOCATION: 294..296
OTHER INFORMATION: potential
FEATURE:
                                                                                FEATURE:
                                                                                                                                                                                        OTHER INFORMATION: potential
                                                                                                                                                                                                                                  NAME/KEY: PHOSPHORYLATION
                                                                                                                                                                                                                                                                            LOCATION: 1226..1228
OTHER INFORMATION: potential
                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: potential
                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CARBOHYD
LOCATION: 1151..1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 910..912
OTHER INFORMATION: potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CARBOHYD LOCATION: 859..861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CARBOHYD LOCATION: 856..858 OTHER INFORMATION:
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                                                                                                                                                                        FEATURE:
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NAME/KEY: PHOSPHORYLATION LOCATION: 885..888 OTHER INFORMATION: potential
                                                                                                                                                                                             NAME/KEY: PHOSPHORYLATION LOCATION: 876..878 OTHER INFORMATION: potential
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OTHER INFORMATION: potential
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OTHER INFORMATION: potential
                      FEATURE
                                     OTHER INFORMATION: potential
                                                                                                                   OTHER INFORMATION: potential
                                                                                                                                     NAME/KEY: PHOSPHORYLATION LOCATION: 888..890
                                                                                                                                                                                                                                                                           NAME/KEY: PHOSPHORYLATION
LOCATION: 815..817
OTHER INFORMATION: potential
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OTHER INFORMATION: potential
NAME/KEY: PHOSPHORYLATION
                                                                                                  FEATURE:
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OTHER INFORMATION: potential
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OTHER INFORMATION: potential
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OCATION: 656..658
THER INFORMATION: potential
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THER INFORMATION: potential
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THER INFORMATION: potential
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OCATION: 507..509
THER INFORMATION: potential
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OTHER INFORMATION: potential
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AME/KEY: PHOSPHORYLATION
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                                                           PHOSPHORYLATION 939..941
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Query Match
Best Local S
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OTHER INFORMATION: potential
                                                                             NAME/KEY: PHOSPHORYLATION LOCATION: 295..298
                                                                                                                                        NAME/KEY: PHOSPHORYLATION LOCATION: 276..279
OTHER INFORMATION: potential
                                                                                                                                                                                                                                        FEATURE: PHOSPHORYLATION LOCATION: 274..277
                                                                                                                                                                                                                                                                                                                      NAME/KEY: PHOSPHORYLATION LOCATION: 216..219
                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: PHOSPHORYLATION LOCATION: 159..162
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OTHER INFORMATION: potential
FEATURE:
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OTHER INFORMATION: potential
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OTHER INFORMATION: potential
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OTHER INFORMATION: potential
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OTHER INFORMATION: potential
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                    Similarity
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1208..1210
8.5%; Score 73;
22.1%; Pred. No.
tive 22; Mismatc
                    DB 9;
1e+02;
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1076 GELQDLQSEGNSSPAGFDASYSSSSSNQPEPEHPEKACTGQKRVKDAQGGGSSSSKKQKRS 1135

27 STSQVMVAPNAPTGYTGVIYTGVA------PLVDNDETVKALASKLPSLVYFDFDS

Mismatches

60;

38;

Gaps

76

Length 1312; Indels

Matches

Conservative

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US-09-815-242-12162

Sequence 12162, Application US/09815242

Patent No. US20020061569A1

; GENERAL INFORMATION:
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
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Best Local
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           APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT:
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NUMBER OF SEQ ID NOS: 14110
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PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/253,625 FILING DATE: 2000-11-27
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                                                                                                                                                                                                                                                   495 SLFNY 499
                                                                                                                                                                                                                                                                                          127 AVRNY 131
                                                                                                                                                                                                                                                                                                                            435 NIQYQDSQWKDETLFKLQRQFAYTKEEIHKYIQELVEGKKDPIGAMGYDAPIAVLNERPE 494
                                                                                                                                                                                                                                                                                                                                                                                                             375 VVDVPESNVAFKGQLNPGKLLLVDFKQNKVIENNDLKGAIAGELPYKAWIDNHKVDFDFE 434
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Yamamoto, Robert T.
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25.6%;
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SEQ ID NO 12162
                                                                           CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
                                                                                                                                                             APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
                 PRIOR APPLICATION NUMBER: JP 00/159162 PRIOR FILING DATE: 2000-04-07 PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
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PRIOR FILING DATE: 2000-05-3
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
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CURRENT FILING DATE: 2001-03-21
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YOKOI, HARUHIKO
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                                                                                                                                                                                                                                           SENOH, AKIHIRO
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Yamamoto, Robert T.
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25.6%; Pred. No.
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NUMBER OF SEQ ID NOS: 7059

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               ; Sequence 2, Application US/09901106
; Patent No. US20020151067A1
                                                    RESULT 34
US-09-901-106-2
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US-10-156-761-9933
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LENGTH: 851
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: HATTORI, MASAHIRA TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
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CURRENT FILING DATE: 2002-05-29
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                538 CAGSVGVRPLVDRPEDADVDMPVGDHMALALSGRVLPA-----SDRRVLAAFAAQAAV 590
                                                                                                                                                                                                                                                                                                                                                      483 QAARLRAESEILSFLAGSVLRGETSLDALLERVRETFGMESVALLERESDVAP-----WT 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                368 GSVSKDERATTETMLKEGRLRAV-ISTSSLELGIDMGAVDLVIQVESPPSVASG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 ----TDERGSREYNMSLGERRAVAVRNYLLGKGINQASVEIISFGEERP-IAFG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        311 VNSRRSAERLTSRLNEIWAMEHDPESLSPQ---LRRDPAQIMSSADVAGKAPQVIARAHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 VDNDETVKALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTA----RVLVAGH-
                                                                                                                                                                                                                                           86 ILDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGKGINQASVEII 145
                                                                                                                                                                                                                                                                                                               43 GVIYTGVAPLVD-----IKPQAAA 85
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                                                                                                                                                               SFGEERPIA-----FGTNEEAWSQNRRAEL 170
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HORIKAWA, HIROSHI
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SAKAKI, YOSHIYUKI
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21.1%; Pred. No. 62;
vative 19; Mismatches
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Pred. No. 1.3e+02;
Pred. No. 1.3e+04;
                                                                                                                                                                                                      ------QREADQARTLAEGNSIRTALLAAV 621
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US-10-156-761-13680
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
 PRIOR FILING DATE: 2001-09 PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Garoff, Henrik
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Sequence 13680, Application US/10156761 Publication No. US20030119018A1
                                                                                                          APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-252
                                     CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
                                                                                                                                                                                                                                                                                                      APPLICANT: OMURA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2431 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 828-103P TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/07/920,281C FILING DATE: 11-AUG-1992 ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M. REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/901,106
FILING DATE: 10-Jul-2001
CLASSIFICATION: -Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1799 SGITFGDFDDVLRLGRAGAYIFSSDTG----SGHLQQKSVRQHNLQCAQLDAV 1847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1756 ASRAAERPVPAPRKPT------PAPRT-----AFRNKLP-LTFGDFDEHEVDALA 1798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 AAI------LDEQAQFLTTNQTARVLVAGHTDERGSREYNMSLGERRAV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 ANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVKALASKLPSLVYFDFDSDEIKPQA 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Falls Church
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Birch, Stewart, Kolasch & Birch STREET: P.O. Box 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 703-241-1300
TELEFAX: 703-241-2848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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HORIKAWA, HIROSHI
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                      2001-05-30
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23.0%;
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JP 2001-272697
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Pred. No. 2.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36;
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Gaps

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; PRIOR FILING DATE: 2001-08-02; NUMBER OF SEQ ID NOS: 15109; SEQ ID NO 13680; LENGTH: 441; TYPE: PRT TYPE: PRT ORGANISM: Streptomyces avermitilis US-10-156-761-13680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROS
APPLICANT: SHIBA, TADAYOSH
ADDITCANT: SHIBA, TADAYOSH
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US-10-156-761-14476
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Best Local Similarity
Matches 46; Conserv
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LENGTH: 507
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                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                             Query Match
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CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                         Local
                                 137 INQASVEIISFGEERP 152
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362 LDEGAV--LRCGGRRP 375
                                                                          305 AGARLLVEDSLHDRFVDEVVRRAAEIRLGGPFDERAQTGALISAAHRAKVEA---YVAKG
                                                                                                                                                     245 FTGGLHTGRRLMAAAAGTVKKVALELGGKNPNIVFADADFDTAVDMALTAVFLHSGQVCS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     186 EVYAAGGATAVAMFAYGTESCAPADMVTGPGNIWVAAAKRYFTGKIGIDAEAGPTEIAVL
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                                                                                                           82 QAAAILDEQA---QFL--TTNQTARVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGKG 136
                                                                                                                                                                                      41 YTGVIYTGVAPLVDNDETVKALASKL----PSLYYFDFDSD-----
                                                                                                                                                                                                                                      l Similarity
32; Conserv
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HORIKAWA, HIROSHI
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23.5%; Pred. No. 3
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24.1%; Pred. No. 31;
tive 21; Mismatches
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; ORGANISM: Homo sapiens US-09-925-301-908
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                                                            SOFTWARE: Pat
SEQ ID NO 908
LENGTH: 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 5
LENGTH: 2862
TYPE: PRT
ORGANISM: GBV-B/HCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/09742659 Patent No. US20010034019A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  Sequence 908, Application US/09925301 Patent No. US20020052308A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                 APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PA106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/742,659
CURRENT FILING DATE: 2000-12-21
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PRIOR FILING DATE: 1999-12-22
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APPLICANT:
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                                                                                                                              NUMBER OF SEQ ID NOS: 1694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 1 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lemon, Stanley M. TITLE OF INVENTION: Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: SITE
LOCATION: (945)..(1129)
OTHER INFORMATION: chimeric region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: SITE
LOCATION: (1579)..(1593)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: chimeric region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 8.3%; Score 71.5; DB 10; Local Similarity 27.5%; Pred. No. 4.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1651 FLGPHAATILAIIEYCCG 1668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1566 LAVGVGVAMAYLA----STGCV-----VIVGRIVLSGKPTGAT-----VAPVVDEEEI 1609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1610 VEECASFIP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 SLGERRA--VAVRNYLLG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 VKALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNM 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 LHIQIAAAAAALSVLTFMTGCANKSTSQVMVA----PNAPTGYTGVIYTGVAPLVDNDET 58
                                                                                                          PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wright-Minogue, Jacquelyn Lau, Johnson Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhong, Weidong
Ingravallo, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Butkiewicz, Nancy J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hong,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2862;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 41;
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Query Match

8.2%;

Score 71;

DB 10;

Length 248;

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US-09-997-181-133; Sequence 133, Application US/09997181; Publication No. US20030049269A1; GEMERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                       Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Mycobacterium tuberculosis US-09-996-634-133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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                                                                                                                                                                                                                                                                                                                           RESULT 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-996-634-133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 09/447,135
PRIOR FILING DATE: 2000-01-03
PRIOR APPLICATION NUMBER: 08/990,823
PRIOR FILING DATE: 1997-12-15
PRIOR APPLICATION NUMBER: US 96/10375
PRIOR FILING DATE: 1996-06-14
PRIOR APPLICATION NUMBER: 60/000,254
PRIOR FILING DATE: 1995-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 133, Application US/09996634 Patent No. US20020172684A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local
Matches
                                                    CURRENT APPLICATION NUMBER: US/09/997,181
CURRENT FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: 09/447,135
PRIOR FILING DATE: 2000-01-03
PRIOR APPLICATION NUMBER: 08/990,823
                                                                                                                                                          APPLICANT: Nano, Francis
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
TITLE OF INVENTION: immunostimulatory Peptides
FILE REFERENCE: 61257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/996,634
CURRENT FILING DATE: 2001-11-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Nano, Francis
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
TITLE OF INVENTION: immunostimulatory Peptides
FILE REFERENCE: 61260
                                         PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
FILING DATE: 1997-12-15
APPLICATION NUMBER: US 96/10375
FILING DATE: 1996-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               156 FGEAK 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147 FGEER 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 -----KLPSLVYFDFDSD-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40 ETVPATEQELPQPQAETGSGTESDSDESVPE----LEEQDSTQATTQQAQLAAAAEIDEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57 ETVKALASKLPSLVY-----FDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTD-- 109
                                                                                                                                                                                                                                                                                                                                                                               75 VVVTVNNLSTLPFESVDADVTNQPQGNGQAVGNAKVRMKPNTPVVATE---FLVTNKT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96 PVSKAKQSRSEKKARKAMSKLGLRQVTGVTRVTIRKSKNILFVITKPDVYKSPASDTYIV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 IAAAAAALSVLTFMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVKALAS-- 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                               VAILIAATLFATVVAGCGKKPTTASSPSPGSPSPEAQQI-----LQDSSKATKGLHSVH 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 71;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; DB 9;
. 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                       ----EIKPQAAAILDEQAQFLTTNQT 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34;
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                                                                                                                                                       Дb
                                                                                                                                                                                                                                                                                                              ; ORGANISM: Mycobacterium tuberculosis US-09-997-181-133
Search completed: July Job time : 308 secs
                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 133
                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                    Query Match 8.2%; Best Local Similarity 23.7%;
                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/000,254
PRIOR FILING DATE: 1995-06-15
NUMBER OF SEQ ID NOS: 169
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                  LENGTH: 25
TYPE: PRT
                                                                                                                65 -----KLPSLVYFDFDSD-----
                                                                                                                                                       21 VAILIAATLFATVVAGCGKKPTTASSPSPGSPSPEAQQI-----LQDSSKATKGLHSVH 74
                                                                            75 VVVTVNNLSTLPFESVDADVTNQPQGNGQAVGNAKVRMKPNTPVVATE---FLVTNKT 129
                                                                                                                                                                                                                                                                                                                                                                     259
                                                                                                                                                                                                                                    28;
                                                                                                                                                                                           7 IAAAAAALSVLTEMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETVKALAS-- 64
                                                                                                                                                                                                                                    Conservative
                6, 2003, 14:19:27
                                                                                                                                                                                                                                 14; Mismatches
                                                                                                                                                                                                                                                      Score 71;
Pred. No.
                                                                                                                                                                                                                                                      DB 9; Length 259;
16;
                                                                                                                ---EIKPQAAAILDEQAQFLTTNQT 99
                                                                                                                                                                                                                                 42;
                                                                                                                                                                                                                                    Indels
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Gaps

4;

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Command line parameters:

MODEL-frame+_pln.model -DEV=xlp
-0=/cgn2_1/USPTO_spool/US9674779/runat_06072003_121614_9825/app_query.fasta_1.327
-0B=ISSUE_Paramets_NA -QFMT=fastap -SUFFIX=pln.rn1 -MINMATCH_01 -LOOPCL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=100 -DCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=40
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-USER=US09674779_@CGN_1_1_36_@runat_06072003_121614_9825 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                       Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OM protein - nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                                     No
                                                         110
110
110
                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being part and is derived by analysis of the total score distribution.
                                     264
264
264
176.5
175.5
177.5
171.5
171.5
                                                                                                                                                                                                                                                                                   Score
                                                                                                                                                                                                                                                                                                                                                                                                                                               Issued_Patents_NA:*

1: /cgn2_5/ptodata/1

2: /cgn2_6/ptodata/1

3: /cgn2_6/ptodata/1

4: /cgn2_6/ptodata/1

5: /cgn2_6/ptodata/1

6: /cgn2_6/ptodata/1
                                                                                                                                                                                                                                                                               Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                                                                                                                                                                                                                   Query
                                   30.7
30.7
30.7
30.7
30.7
20.5
20.4
20.4
19.9
19.9
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861
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Listing first 100 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MMLHIQIAAAAAALSVLTFM.....IAFGTNEEAWSQNRRAELSY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                       /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
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867
1019
1059
645
645
486
486
681
1720
                                                                                                                                                                                                                                                                               DB
                       US-07-807-049-1
US-08-476-102A-3
US-08-572-447C-12
US-09-267-747-12
US-09-267-747-10
US-08-572-447C-14
US-08-572-447C-14
US-08-572-447C-14
US-08-457-997B-1
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5173294-3
5173294-1
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850.781 Million cell updates/sec
                                   Sequence 178, App
Patent No. 5173294
Patent No. 5173294
Sequence 1, Appli
Sequence 2, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 14, Appli
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           9.0 80161
9.0 403765
8.6 38155
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8.6 1290
8.5 1581
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8.5 6202
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8.4 11517
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2 US-08-721-979A-1
3 US-08-256-840B-11
4 US-08-836-80A-1
4 US-08-836-871-14
1 US-08-469-250A-1
1 US-08-469-250A-39
4 US-09-620-412C-113
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US-09-221-017B-786
Sequence 1, Appli Sequence 786, App Sequence 78, Appli Sequence 1, Appli Sequence 1, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 12, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 180, Appli Sequence 191, Appli Se
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RESULT 1
US-08-743-637B-178
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Score:
                           Alignment Scores:
                                                     US-08-743-637B-178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 178:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: OUELLETTE, MARC
APPLICANT: ROY, PAUL H.
APPLICANT: ROY, PAUL H.
TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/526,840
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REGISTRATION NUMBER: 850886 00
                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 85
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                 MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 411 EAST
CITY: MILWAUKEE
STATE: WISCONSIN
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                            TOPOLOGY:
                                                                                                                         STRANDEDNESS:
                                                                     ORGANISM:
                                                                                                                                                  LENGTH: 462 base pairs
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PCT-US95-13662A-9
US-07-618-312A-3
US-08-110-786A-7
US-08-280-228-3
US-08-668-381A-6
US-09-453-702B-39
US-08-784-582-57
US-08-784-582-57
US-08-784-582-72
US-09-221-017B-314
US-09-453-702B-242
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US-08-854-585-1
PCT-US95-05512-1
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    Length: Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: MURPHY, TIMOTHY F.; APPICELLA, MICHAEL A.
TITLE OF INVENTION: DNA PROBE FOR THE IDENTIFICATION
OF HAEMPHILUS INFLUENCAE:
NUMBER OF SEQUENCES: 3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/92,948
FILING DATE: 08-0CT-1987
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 932,872
                                                                                                                                                                                                                                                                                                                              No.:
                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 18-NOV-1986
                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              331 GGTTATTTAGCAGGTAAAGGTGTTGATGCTGGTAAATTAGGCACAGTATCTTACGGTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 AsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGluIleIleSerPheGlyGlu 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   211 CACGCAGCATATTTAAATGCAACGCCAGCTGCTAAAGTATTAGTAGAAGGTAATACTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151 GTATATTTTGGTTTTGATAAATACGACATCACCGGTGAATACGTTCAAATCTTAGATGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          271 GAACGTGGTACACCAGAATACAACATCGCATTAGGACAACGTCGTGCAGATGCAGTTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        150 GluArgProlleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArgArgAlaGlu 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       451 TTAGCGTAC 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170 LeuSerTyr 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90 GlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAsp 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 valTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAspGlu 89
                                                                                                                                                                            151 GTATATTTTGGTTTTGATAAATACGACATCACCGGTGAATACGTTCAAATCTTAGATGCG
                           130 AsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGluIleIleSerPheGlyGlu 149
                                                                              110 GluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaValAlarg
          331 GGTTATTTAGCAGGTAAAGGTGTTGATGCTGGTAAATTAGGCACAGTATCTTACGGTGAA 390
                                                                                                                      211 CACGCAGCATATTTAAATGCAACGCCAGCTGCTAAAGTATTAGTAGAAGGTAATACTGAT
                                                                                                                                                                                                    70 ValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAspGlu 89
                                                                                                                                               90 GlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAsp 109
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                                                                 GAACGTGGTACACCAGAATACAACATCGCATTAGGACAACGTCGTGCAGATGCAGTTAAA
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US-07-807-049-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
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NUMBER OF SEQUENCES: 3

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/92,948

FILING DATE: 08-OCT-1987
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; APPLICANT: MURRHY,TIMOTHY F.;APICELLA, MICHAEL A.
; TITLE OF INVENTION: DNA PROBE FOR THE IDENTIFICATION
                                                                                                                                                                                                                                                                                       Sequence 1, Application US/07807049 Patent No. 5300632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO:
                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                       APPLICANT: Murphy, Timothy F
APPLICANT: Apicella, Michael A
TITLE OF INVENTION: A Method for Purifying an Outer Membrane
TITLE OF INVENTION: Protein of Haemophilus Influenzae
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
LENGTH: 867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 932,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        458 GAAAAACCTGCAGTATTAGGTCACGATGAAGCTGCATATTCTAAAAACCGTCGTGCAGTG 517
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                                                     Alan S. Korman, Esq
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.
FILING DATE: 08-OCT-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.
                                                                                                          DOCUMENT NUMBER: US 4,474,758
FILING DATE: 02-OCT-1984
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                 PUBLICATION INFORMATION:
DOCUMENT NUMBER: US 4,427,782
FILING DATE: 24-JAN-1984
           PUBLICATION INFORMATION:
                                                                                                                                                                                                PUBLICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 853-8100
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ATTORNEY/AGENT INFORMATION:
NAME: KORMAN ESQ., ALAN S
REGISTRATION NUMBER: 32,932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
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HYPOTHETICAL: NO
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APPLICATION NUMBER: US 0
FILING DATE: 29-MAR-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS:
AUTHORS:
AUTHORS:
                             DOCUMENT NUMBER: US J.CLIN.INVEST.V.78
PUBLICATION DATE: 01-OCT-1986
RELEVANT RESIDUES IN SEQ ID NO: 1: FRO
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DATE:
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                                                                                      DOCUMENT NUMBER:
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HAPLOTYPE: N/A
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STATE: NY
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JRS: Apicella, M A
JRS: Murphy, T F
JRS: VanKeulen, H
JRS: VanKeulen, H
JRS: Spotila, L D
JRS: Spotila, L D
JRS: Rekosh, D M
DRS: Rekosh, D 
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Best Local Similarity:
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US-08-476-102A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08476102A Patent No. 6355450 GENERAL INFORMATION:
TELEPHONE: 301-309-8504
TELEX: 301-309-8439
INFORMATION FOR SEQ ID NO: 3:
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                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS: 9
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No. 6355450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Fleischmann, et al. TITLE OF INVENTION: Nucleotide Sequence of the Haemphilus
                                                                                                                            APPLICATION NUMBER: US/08/476,102A
FILING DATE: 07-Jun-1995
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        370 GTATATTTTGGTTTTGATAAATACGACATCACCGGTGAATACGTTCAAATCTTAGATGCG 429
                                                    REFERENCE/DOCKET NUMBER: PB186P2
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                              STATE: MD
                                                                                                                                                                                                                                                                                                                                                                 CITY: Rockville
                                                                                          NAME: Marks, Michelle S. REGISTRATION NUMBER: 41,971
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                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                              ZIP: 20850
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01-SEP-1985
                                                                                                                                                                                                                      PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                      influenzae Rd Genome, Fragments Thereof, and Uses Thereof
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCOLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
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                                                                                                                                                                                                                                                                                                                                                                         US-08-572-447C-12
                                                                                                                                                                                                                                                                                                                                                                                            RESULT 6
                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                        APPLICANT: Domdey, Horst
TITLE OF INVENTION: Immur
TITLE OF INVENTION: Deriv
               COMPUTER READABLE FORM:
                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                 CITY: Washington STATE: D.C.
                                 COUNTRY: USA
ZIP: 20005-3315
                                                                                                     STREET:
                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1059 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                               994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161
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                                                                                                       1300 I Street, N.W.,
                                                                                                                                                                                                                                                                                                   Knapp, Bernhard
                                                                                                                                                                                                                                                                   Broker, Michael
                                                                                                                        Dunner
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176.50
47.77%
30.57%
20.50%
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US-09-674-779B-2 (1-172) x US-08-476-102A-3 (1-1059)
                                                                                                                                                                                                                                                                                                                                                 Sequence 12, Application US/08572447C Patent No. 5955090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  577 CCAAATACCGCACTTAACTACAACCCTTGGATTGGTTCTATCAATGCGGGTATTTCTTAC 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       637 CGTTTTGGTCAAGGCGCAGCACCAGTTGTTGCAGCACCTGAAGTTGTAAGCAAAACTTTC 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  814 GTTGCTGGTTACACTGACCGTATTGGTTCTGACGCGTTCAACGTAAAACTTTCTCAAGAA 873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                697 AGC---TTAAACTCTGATGTAACTTTCGCATTTGGTAAAGCAAACTTAAAACCTCAAGCA 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104 ValAlaGlyHisThrAspGluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArg 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         754 CAAGCAACATTAGACAGCATCTATGGCGAAATGTCACAAGTTAAAAGTGCAAAAGTAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 AlaAlaIleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeu 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47 -----ThrGlyValAlaProLeuValAspAsnAspGluThrValLysAlaLeuAla 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 SerLysLeuProSerLeuValTyrPheAspPheAspSerAspGluIleLysProGlnAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35 ProAsnAlaProThrGlyTyr------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGTAAAGCGCTTATCGCTTGTTTTGCTCCAGACCGTCGTGTAGAAATCGCG 1044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IleIleSerPheGlyGluGluArgProIleAlaPheGlyThrAsnGluGlu------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGTGCAGATTCAGTAGCTAACTTCGTTGCTAAAGGTGTTGCAGCAGACGCAATCTCT 933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGlu 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----AlaTrpSerGlnAsnArgArgAlaGluLeuSer 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCAACTGGCTACGGTAAAGCAAACCCAGTAACTGGTGCAACTTGTGACCAAGTTAAGGGT 993
                                                                                                                                                                                      Von Specht, Bernd-Ulrich
                                                                                                                                                                                                                                                 Hungerer, Klaus-Dieter
Finnegan, Henderson, Farabow,
                                                                                         Immunogenic Hybrid Protein OprF-OprI
Derived From Pseudomonas aeruginosa Membrane Proteins.
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US-09-674-779B-2 (1-172) x US-08-572-447C-12 (1-645)
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-572-447C-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION:
Patent No. 5955090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (202) 408-4400 INFORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS: LENGTH: 645 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94120023.0
FILING DATE: 16-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: M. Paul Barker
REGISTRATION NUMBER: 32,013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Pseudomonas aeruginosa
TISSUE TYPE: Serotype 6; ATCC 33354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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147 PheGlyGluGluArgProIleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArg 166
                                          325 GTTCGTGACGTACTGGTCAACGAGTACGGTGTGGAAGGTGGTCGCGTGAACGCTGTCGGT 384
                                                                                                                                                                    108 ThrAspGluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAla 127
                                                                                   128 ValArgAsnTyrLeuLeuGlyLys---GlyIleAsnGlnAlaSerValGluIleIleSer 146
                                                                                                                              265 ACCGACTCCGTCGGTACCGACGCTTACAACCAGAAGCTGTCCGAGCGTCGTGCCAACGCC 324
                                                                                                                                                                                                                 205 AAGAACCTGGCCGACTTCATGAAGCAGTACCCGTCCACTTCCACCACCGTTGAAGGTCAT
                                                                                                                                                                                                                                                                                                  145 CTGGACGTGAAGTTCGACTTCGACAAGTCCAAAGGTCAAAGAGAACAGCTACGCTGACATC 204
                                                                                                                                                                                                                                                                                                                                                                                                                                57 GluThrValLysAlaLeuAlaSerLysLeuProSerLeu--
                                                                                                                                                                                                                                                                                                                                                                                        85 GCCAACGTCACCGTTGACGCCAACGGCTGCCCGGCTGTCGCCGAAGTCGTACGCGTACAG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 GCTCCGACTCCGACAACGACGGCGTCTGCGACAAC-GTCGACAAGTGCCCCGGACACCCCG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37 AlaProThrGlyTyrThrGlyValIleTyrThrGlyValAlaProLeuValAspAsnAsp
                                                                                                                                                                                                                                                          AspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHis 107
                                                                                                                                                                                                                                                                                                                                           ----ValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeu 87
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Alignment Scores: Pred. No.:
                                                                                          . OTHER INFORMATION: C-terminus and oprI without signal sequence ^{\circ} US-09-267-747-12
     Percent Similarity:
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                                                                                                                             Patent No. 6300102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/572,
FILING DATE: 14-DEC-1995
APPLICATION NUMBER: EP 941200:
FILING DATE: 16-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: M. Paul Barker
REGISTRATION NUMBER: 32,013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                     HYPOTHETICAL: NO ANTI-SENSE: YES
                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 645 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                         OTHER INFORMATION:
                                                                                                                                                                              NAME/KEY: CDS
                                                                                                                                                                 LOCATION:
                                                                                                                                                                                                                 TISSUE TYPE:
                                                                                                                                                                                                                                   ORGANISM:
                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Finnegam, nonversal ADDRESSEE: Dunner STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            385 TACGGCGAGTCCCGGCGGTTGCCGACAACGCCACCGCTGAAGGCCGCGCTGTCAACCGT 444
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                                                                                                                                                                                                                                                                                                                                                                       645 base pairs
                                                                                                                                                                                                               Pseudomonas aeruginosa
E: Serotype 6; ATCC 33354
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Broker, Michael
                                                                                                                                                                                                                                                                                                                     linear
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16-DEC-1994
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                    1.41e-14
175.50
     46.58%
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                                                                                                                                     /note= "Sequence is coding for oprF
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Conservative:
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL
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APPLICANT:
                                                                                                     CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Von Specht, Bernd-Ulrich
APPLICANT: Domdey, Horst
TITLE OF INVENTION: Immunogenic Hybrid Protein OprF-OprI
TITLE OF INVENTION: Derived From Pseudomonas aeruginosa Membrane Proteins.
      PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94120023.0
FILING DATE: 16-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                     STREET:
CITY: W
                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                   ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner STREET: 1300 I Street, N.W., Suite 700
                                                                                          FILING DATE:
                                                                                                                                                                                                                                       COUNTRY:
                                                                         CLASSIFICATION: 424
                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGGACGTGAAGTTCGACTTCGACAAGTCCAAGGTCAAAGAGAACAGCTACGCTGACATC
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Best Local Similarity:
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                                                                US-09-267-747-10
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           Sequence 10, Application US/09267747
Patent No. 6300102
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (202) 408-4400 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 05:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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HYPOTHETICAL:
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APPLICANT:
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LOCATION:
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US-09-674-779B-2 (1-172) x US-08-572-447C-10 (1-486)
                                               147 PheGlyGluGluArgProIleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArg
                                                                                                  331 GTTCGTGACGTACTGGTCAACGAGTACGGTGTGGAAGGTGGTCGCGTGAACGCTGTCGGT
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TACGGCGAGTCCCGCCCGGTTGCCGACAACGCCACCGCTGAAGGCCCGCGCTATCAACCGT
                                                                                                                                               ValArgAsnTyrLeuLeuGlyLys----GlyIleAsnGlnAlaSerValGluIleIleSer 146
                                                                                                                                                                                                     ACCGACTCCGTCGGTACCGACGCTTACAACCAGAAGCTGTCCGAGCGTCGTGCCAACGCC
                                                                                                                                                                                                                             ThraspGluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAla 127
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                                                                                                                                                                                                                                                                                                                                                       AspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHis 107
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E: Serotype 6; ATCC 33
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171.50
46.15%
33.57%
19.92%
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                                                                                                                                                                                               Query Match:
                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: US-09-267-747-10
                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Patent No. 6300102
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APPLICATION NUMBER: US/08/5/2/2.

FILING DATE: 14-DEC-1995

APPLICATION NUMBER: EP 94120023.0

FILING DATE: 16-DEC-1994

ATTORNEY/AGENT INFORMATION:
NAME: M. Paul Barker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 05:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                               No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Immunogenic Hybrid Protein OprF-OprI
TITLE OF INVENTION: Derived From Pseudomonas aeruginosa Membrane Proteins.
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: (
HYPOTHETICAL: NO
ANTI-SENSE: YES
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                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner STREET: 1300 I Street, N.W., Suite 700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: double
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91 GCCAACGTCACCGTTGACGCCAACGGCTGCCCGGCTGTCGCCGAAGTCGTACGCGTACAG 150
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                                  GluThrValLysAlaLeuAlaSerLysLeuProSerLeu----
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E: Serotype 6; ATCC 33354
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Broker, Michael
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171.50
46.15%
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Matches:
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Indels:
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US-08-572-447C-14
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                                                                                                                          TELEFAX: (202) 408-440 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Von Spech
APPLICANT: Domdey, H
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94120023.0
FILING DATE: 16-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 14-DEC-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MOLECULE TYPE: HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                  FILING DATE: 16-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                             TOPOLOGY:
                                                             STRANDEDNESS: double
                                                                               TYPE: nucleic acid
                                                                                                                                                                                                                                                            REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
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ADDRESSEE: Dunner
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                                                                                                                                                                                                                                                   M. Paul Barker
M. Paul Barker
32,013
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Derived From Pseudomonas aeruginosa Membrane Proteins.
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                                                                                                                                                                                                                                                                                                        RESULT 11
US-09-267-747-14
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OTHER INFORMATION:
                                                                                                                                                                                                                                                    Patent No. GENERAL II
                                                                                                                                                                                                                                                                                       Sequence 14,
                                                                                                                                                                                                              APPLICANT:
APPLICANT:
                                                                                   APPLICANT: Domdey, Horst
TITLE OF INVENTION: Immunogenic Hybrid Protein OprF-OprI
TITLE OF INVENTION: Derived From Pseudomonas aeruginosa |
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
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STREET:
CITY: W
STATE:
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LOCATION: 1..678
                                 ADDRESSEE: Finnegan, Henderson, Farabow, Garrett ADDRESSEE: Dunner STREET: 1300 I Street, N.W., Suite 700
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 Washington D.C.
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E: Serotype 6; ATCC 33354
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; OTHER INFORMATION:
US-09-267-747-14
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Best Local Similarity:
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TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: N
HYPOTHETICAL: N
ANTI-SENSE: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 16-DEC-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NO . .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Pseudomonas aeruginosa
TISSUE TYPE: Serotype 6; ATCC 33354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 32,013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/O FILING DATE: 14-DEC-1995 APPLICATION NUMBER: EP 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
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                                                                                         406
                                                                                                                                                              346
                                                    108 ThrAspGluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAla
                                                                                                                                                                                                                                                                                                          227 GCTCCGACTCCGACAACGACGGCGTCTGCGACAAC-GTCGACAAGTGCCCGGACACCCCG
                                                                                                                                                                                                                                     286 GCCAACGTCACCGTTGACGCCAACGGCTGCCCGGCTGTCGCCGAAGTCGTACGCGTACAG
                                                                                                                                                                                                 70
                                                                                                                                                                                                                                                                                                                                           37 AlaProThrGlyTyrThrGlyValIleTyrThrGlyValAlaProLeuValAspAsnAsp
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                  AspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHis 107
                                                                                                                                                              CTGGACGTGAAGTTCGACTTCGACAAGTCCAAGGTCAAAGAGAACAGCTACGCTGACATC
                                                                                                                                                                                                                                                                     GluThrValLysAlaLeuAlaSerLysLeuProSerLeu---
                                                                                       AAGAACCTGGCCGACTTCATGAAGCAGTACCCGTCCACTTCCACCACCGTTGAAGGTCAT
                                                                                                                                                                                              -----ValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeu 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                681 base pairs
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1.678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UMBER: EP 94120023.0
16-DEC-1994
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46.15%
33.57%
19.92%
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US-09-674-779B-2 (1-172) x US-08-457-997B-1 (1-1720)
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                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                US-08-457-997B-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 522-8458
                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
                                                                                                                                                                                                                                           No.
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ANTI-SENSE: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kolattukudy, P. E. TITLE OF INVENTION: Otitis Media Vaccine
                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: no
STRAIN: 1128
                                                                                                                                                                                                                                                                                                                  LOCATION:
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                     1001 CCAAATACCGCAATTAACTACAACCCTTGGATTGGTTGTATCAATGCGGGTATTTCTTAC 1060
                                                              35 ProAsnAlaProThrGlyTyr-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 586 TACGGCGAGTCCCGCCCGGTTGCCGACACGCCACCGCTGAAGGCCGCGCGCTATCAACCGT 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147 PheGlyGluGluArgProIleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArg 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         526 GTTCGTGACGTACTGGTCAACGAGTACGGTGTGGAAGGTGGTCGCGTGAACGCTGTCGGT 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 ValArgAsnTyrLeuLeuGlyLys---GlyIleAsnGlnAlaSerValGluIleIleSer 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ohio
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Suite 1800 800 Superior Avenue
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29.94%
19.22%
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                                                                                                                                                                           Mismatches:
                                                                                                                                                                                               Conservative:
                                                                                                                                                           Indels:
                                                          ----ThrGlyVallleTyr 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-467-722A-1
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                                                                                                                                                                                                                                      TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: GOLTICK, Mary E.
                                      FEATURE:
                                                                      ORIGINAL SOURCE:
ORGANISM: non
                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                             ANTI-SENSE:
                                                                                                                            MOLECULE TYPE:
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 NAME/KEY:
LOCATION:
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                                                      STRAIN:
                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 34, REFERENCE/DOCKET NUMBER:
                                                                                                                                                  TOPOLOGY:
                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/467,722A
                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1298 CGTGCAGATTCAGTAGCTAACTACTTTGTTGCTAAAGGTGTTGCAGCAGACGCAATCTCA 1357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104 ValAlaGlyHisThrAspGluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArg 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Calfee, Halter and Griswold Suite 1800 800 Superior Avenue
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CDS
407..1483
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VENTION: Otitis Media Vaccine
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                                                                                                                                            circular
                                                                  non-typable Haemophilus influenzae
                                                                                                                                                                                                                                                                            (216) 622-8458
                                                                                                                        DNA (genomic)
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                                                                                                                                                               double
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP11:
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP15
                                                                                                                                                   OPERATING SYSTEM: Windows SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
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                                                                                            APPLICATION NUMBER: FILING DATE: 23-DE CLASSIFICATION:
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SOFTWARE: FastSE(
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SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: PP291
APPLICATION DATE: 09-APR-1998
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ORIGINAL SOURCE:
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REGISTRATION NUMBER: 32
REFERENCE/DOCKET NUMBER:
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                               2090 GCGCTGACGAAGTTTGCTGCAAACATGAACAAAAACCCCCGACACGGATATTCGTATCGTA 2031
                                                                106 GlyHisThrAspGluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAla 125
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Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
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OTHER INFORMATION: "n" bases at various positions throughout the sequence OTHER INFORMATION: represent a, t, c or g
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                                   1003411 GGACCCCCGGCCTCCGGCCCATGTGCCGACCTGCAATCAGCCATCAATGCCCGTGACGGGT 1003470
                                                                                                  1003291 ACCTTGACCGGAACTGCCCCTTCATCCGAGCACAAGGACGCAGTGAAGCGCGCGGCGACCC 1003350
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                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.:
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64 SerLysLeuProSerLeu---
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US-09-674-779B-2 (1-172) x US-09-103-840A-1 (1-4411529)
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APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
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ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
1003290 ACCTTGACCGGAACTGCCCCTTCATCCGAGCACAAGGACGCAGTGAAGCGGCGGCGGCGACC 1003349
                                                                                                           1003230 GTTTTCACCGCCAGCGTGCCGATTCCTGATTTTGGCCTCAAAGTCGAAAGGGACACCGTC 1003289
                                                                                                                                                                                                                      1003170 ATCGACCAGATTCACGTCGATCCCGTTGTGCGATCACTTGATTTCTCAAGTGCGGAACCA 1003229
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                                                  45 IleTyrThrGlyValAlaProLeuValAspAsnAspGluThrValLys---AlaLeuAla 63
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APPLICATION NUMBER: US/0:
FILING DATE: 23-DEC-1998
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                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PP11
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
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                                                                                                FILING DATE: 10-DEC-1998 ATTORNEY/AGENT INFORMATION:
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REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
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US-08-743-637B-11
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INFORMATION FOR SEQ ID NO:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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                              ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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OPERATING SYSTEM:
                                                                              COUNTRY:
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OUELLETTE, Marc
ROY Danny
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32.538
16.498
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                                                                                                                                                                                       SPECIES-SPECIFIC AND UNIVERSAL DNA PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ....
   PC-DOS/MS-DOS
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Indels:
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Matches:
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CURRENT APPLICATION DATA:

CLASSIFICATION: APPLICATION NUMBER: FILING DATE: 04-NO

04-NOV-1996

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US-09-674-779B-2 (1-172) x US-08-743-637B-11 (1-730)
                                                                                                                                                                                                Sequence 11, Application US/08526840B Patent No. 6001564
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APPLICATION NUMBER: US 08/526,840
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REGISTRATION NUMBER: 35,433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                     608 GCTCGCGGCATGGGTGAATCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCT 667
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             SPECIFIC AND UNIVERSAL PROBES AND
ANPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
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US-08-836-500A-1
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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ORIGINAL SOURCE:
ORGANISM: Kle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 85
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414)_277-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 12-SEP-1994
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: QUARLES & BRADY
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                                                                                    160 ------GluAlaTrpSerGlnAsnArgArgAlaGluLeu 170
                                                                                                                           608 GCTCGCGGCATGGGTGAATCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCT 667
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Query Match:

Best Local Similarity:

Percent Similarity:

3.18e-09 136.50 47.41% 30.17% 15.85%

Alignment Scores: US-08-743-637B-11

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ORIGINAL SOURCE: MOLECULE TYPE:

ORGANISM:

STRANDEDNESS:

TOPOLOGY:

linear

double

DNA (genomic)

TELEFAX: (414)277-5591 INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH:

nucleic acid

REFERENCE/DOCKET NUMBER: 85
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000

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488

US-08-526-840B-11 RESULT 19

GENERAL INFORMATION:

APPLICANT: APPLICANT:

ROY, Paul H. BERGERON, Michel G. OUELLETTE, Marc

APPLICANT: ROY, Paul
TITLE OF INVENTION: S
TITLE OF INVENTION: I
TITLE OF INVENTION: I
TITLE OF INVENTION: I
NUMBER OF SEQUENCES:

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INFORMATION FOR SEQ ID NO: 1:
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APPLICANT: Nguyen Ngoc, Tihen
TITLE OF INVENTION: Carrier Prot
TITLE OF INVENTION: Effect, Immu
TITLE OF INVENTION: Their Prepan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1007 base pairs
TYPE: nucleic acid
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                            NO. :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 180 N. Stetson, 2 Prudential Plaza, Suite STREET: 4700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Katz, Martin L. REGISTRATION NUMBER: 25,011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/836,500A
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796 CGTGCTCAGTCCGTTGTTGACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCC 855
                                    124 ArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGlu 143
                                                                            736 GTTCTGGGCTACACCGACCGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAA
                                                                                                              104 ValAlaGlyHisThrAspGluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArg 123
                                                                                                                                                                                        86 IleLeuAspGluGlnAlaGlnPheLeuThrThr-----AsnGlnThrAlaArgValLeu 103
                                                                                                                                                                                                                                                              66 LeuProSerLeuValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAla 85
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Effect, Immunogenic Complex Containing It, Process i
Their Preparation, Nucleotide Sequence and Vaccines
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US-09-674-779B-2 (1-172) x US-08-721-979A-13 (1-1008)
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                                                                                                        Query Match:
                                                                                                                                            Best Local Similarity:
                                                                                                                                                                         Percent Similarity:
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patent No. 6113911
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INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: US
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
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STREET: 715 The "H" Bldg., 310 East Michigan
STREET: Avenue
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LOCATION: 1..1008
OTHER INFORMATION:
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SYNCYTIAL VIRUS PROTEIN G, IMMUNOGENIC AGENT, PHARMACEUTICAL
COMPOSITION CONTAINING IT AND PREPARATION PROCESS
175
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RESULT 22
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                                                                                              TELEFAX: 616-382-2030
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                    NAME: Hueschen, Gordon W.
REGIZHON NUMBER: 16,157
REFERENCE/DOCKET NUMBER: PETELECOMMUNICATION INFORMATION:
TELEPHONE: 616-382-0030
               MOLECULE TYPE:
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CURRENT APPLICATION DATA:
FEATURE:
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TITLE OF INVENTION:
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STREET: Avenue
CITY: Kalamazoo
STATE: MI
                            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                               LENGTH:
                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kalamazoo
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                                                                             1008 base pairs
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Trudel, Michel
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       peptide
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SYNCTIAL VIRUS PROTEIN G, IMMUNOGENIC AGENT, PHARMACEUTICAL
COMPOSITION CONTAINING IT AND PREPARATION PROCESS
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RESULT 23
US-08-129-719-14
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14, Application US/08129719 Patent No. 5556755 GENERAL INFORMATION:
                                TELEFAX: (716) 849-0349 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                    REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 856-4000
                                                                                                                                                                        FILING DATE: September 29
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                  SOFTWARE: Wordperfect for Windows 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Timothy TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                               COMPUTER: IBM Com
OPERATING SYSTEM:
                                                                                                                                          NAME: Nelson, M. Buc
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                   LENGTH:
                                                                                                                                                                                                                 APPLICATION NUMBER:
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LOCATION: 1..1008
OTHER INFORMATION:
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: 1727 nucleotides
nucleic acid
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                                                                                                                                                                                                                                                                              IBM Compatible
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                                                                                                                                                                                                                                                                                                     Diskette, 3.5 inch, 720 Kb storage
                                                                                                                                                                                              September 29,
                                                                                                                                                             M. Bud
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                                                                                                                                                                                                                                       Sequence 14, Application US/08306871
Patent No. 5712118
GENERAL INFORMATION:
APPLICANT: Timothy F. Murphy
TITLE OF INVENTION: Vaccine For Branhamella catarrhalis
NUMBER OF SEQUENCES: 52
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LIBRARY: genom
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                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
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COMPUTER: IBM Compatible operating SYSTEM: MS-DOS/ Microsoft Windows 3.1 SOFTWARE: Wordperfect for Windows 5.1 URRENT APPLICATION DATA:
                                                                                                                                                    STATE:
                                                                                                                                                                      CITY: Buffalo
                                                                                                                                                                                      STREET:
                                                                                                                                COUNTRY:
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EMBL3 clone 5
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                                                                                                                                                  New York
                                                                                                                                                                                        1800 One M&T Plaza
                                                                                                                                United States
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US-08-569-959-14
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Best Local Similarity:
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             Sequence 14, Application US/08569959
Patent No. 5725862
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (716) 849-0349
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0)
FILING DATE: September 2:
ATTORNEY/AGENT INFORMATION:
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HYPOTHETICAL: Y
ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1727 nucleotides
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APPLICANT:
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: signal sequence of encoded LOCATION: -26 to -1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLONE: EMBL3 clone 5; SUBCLONE: pCD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIBRARY:
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                                                                                                                                                            TrpSerGlnAsnArgArgAlaGlu 169
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Timothy F. Murphy
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September 29, 1993
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Conservative:
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US-09-674-779B-2 (1-172) x US-08-569-959-14 (1-1727)
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                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (716) 849-0349
INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                                                    No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
LOCATION: CD gene region
IDENTIFICATION METHOD: b.
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LENGTH: 1727 nucleotides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Vaccine For Branhamella catarrhalis NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLONE: EMBL3 clone 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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                                                1183 GGTCACGCATCACGCGATTCAGCACGCTCAAGTGCACGCTACAACCAGCGTCTATCTGAA 1242
                                                                                                                  1135 GTTGCTGCGCAAATGCGTGAATTC-----CCAAATGCAACTGCA-----ACCATTGAA 1182
                                                                                                                                                                                  1075 GTATTCTTTGATTATGATAAATCAATCATCAAACCACAATACCGTGAAGAAGTTGCTAAG 1134
123 ArgArgAlaValAlaValArgAsnTyrLeuLeuGlyLys---GlyTleAsnGlnAlaSer 141
                                                                              106 GlyHisThrAspGlu------ArgGlySerArgGluTyrAsnMetSerLeuGlyGlu 122
                                                                                                                                                86 IleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAla 105
                                                                                                                                                                                                        70 ValTyrPheAspPheAspSerAspGluIleLysProGln-----AlaAlaAla 85
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Indels:
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     US-09-674-779B-2 (1-172) x US-08-469-260A-80 (1-4268)
                                                                           Percent Similarity:
Best Local Similarity:
                                                                Query Match:
                                                                                                                  Score
                                                                                                                                Pred. No.:
                                                                                                                                               Alignment Scores:
                                                                                                                                                                                 US-08-469-260A-80
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                                                                                                                                                                                                                                                                            TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                               MOLECULE TYPE:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 708-937-6365
                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION: NAME: POREMBSKI, PRISCIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
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TELEPHONE: 708-938-2623
TO TO NO:
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                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 33, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/469, 260A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
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THOWAS P. LEARY
ANTHONY SCOTT MUERHOFF
JAMES C. ERKER
SHERI L. BUIJK
ISA K. MUSHAHWAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 ABBOTT PARK ROAD
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GEORGE G. SCHLAUI
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TAMI J. PILOT-MATIAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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US-08-469-260A-1
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TELEFAX: 708-938-2623 INFORMATION FOR SEQ ID NO:
                                REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 55;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: NON-A, NON-B. NON-C, TITLE OF INVENTION: REAGENTS AND METHODS
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83 AlaAlaAlaIleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgVal 102
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                                                                                                                           POREMBSKI,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SURESH M. DESAI
THOMAS P. LEARY
ANTHONY SCOTT MUERHOFF
JAMES C. ERKER
SHERI L. BUIJK
                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISA K. MUSHAHWAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GEORGE J. DAWSON
GEORGE G. SCHLAUDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAMI J. PILOT-MATIAS
                   708-938-2623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABBOTT LABORATORIES D377/AP6D
                                                                                                                      PRISCILLA E.
                                                                                                                                                                                        US/08/424,550
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-639-857-32
                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 32,
                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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LENGTH: 8912 base pairs
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                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR CONTROLLING TITLE OF INVENTION: TRANSLATION OF HEPATITIS GB PROTEINS
                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
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                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                CITY: Abbott Park
                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                   ADDRESSEE:
FILING DATE:
                  APPLICATION NUMBER:
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                                                                                                                                                                                                                                 100 Abbott Park Rd
                                                                                                                                                                                                                                                                                                                                                   Mushahwar,
                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                      Simons, J. N. Desai, S. M
                                                                                                                                                                                                                                                       Abbott Laboratories
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ATTORNEY/AGENT INFORMATION:

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                                                                                                                                                                                                                                                                                   Sequence 390, Application US/08469260A Patent No. 6451578
                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: GEORGE J. DANSON

APPLICANT: GEORGE G. SCHLAUDER

APPLICANT: SURESH M. DESAI

APPLICANT: THOMAS P. LEARY

APPLICANT: THOMAS P. LEARY

APPLICANT: JAMES C. ERKER

APPLICANT: JAMES C. ERKER

APPLICANT: SHERI L. BUJJK

APPLICANT: SHERI L. BUJJK

APPLICANT: ISA K. MUSHAHWAR

TITLE OF INVENTION: RON-A, NON-B. NON-C, NON-E HEPATITIS

TITLE OF INVENTION: REACENTS AND METHODS FOR THEIR USE

NUMBER OF SEQUENCES: 716

CORRESPONDENCE ADDRESS:
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LENGTH: 9143 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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TOPOLOGY: lir
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                                                                                                                                                                                                                             JOHN N. SIMONS
TAMI J. PILOT-MATIAS
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TELEPHONE: 708-937-6365
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MEDIUM TYPE: Floppy disk
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TOPOLOGY: lin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/469,260A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                        5414 CATGCAGCTACAATCCTTGCTATCATAGAGTATTGCTGTGGC 5455
                                                                                            5357 ---ACTAGTCCTTTCACATTGGAAACCGCCCTTGAAAAACTTAACACCTTTCTTGGGCCT 5413
                                                                                                                                                                                                                                           5291 GCATCATTCCCC-----------------TTGGAGGCCATG 5317
                                                                                                                                                                      5318 GTTGCTGCAATC---GATAAGCTGAAGAGTACAATAACCACA---
                                                                                                                                                                                                                                                                                                                                                                                     5201 TGTGTGCGGCGTTGCTGGTCTATTACATCAGTC------CCTACCGGTGCTACT 5248
                                                                                                                                                                                                                                                                                                                                                                                                                                                              5141 CTCGCTGTTGGCGTTGGAGTGGCTATGGCTTATCTAGCCATTGACACTTTTGGCGCCACT 5200
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                                                         123 ArgArgAla-----ValAlaValArgAsnTyrLeuLeuGly 134
                                                                                                                                           103
                                                                                                                                                                                                     83 AlaAlaAlaIleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgVal 102
                                                                                                                                                                                                                                                                          63 AlaSerLysLeuProSerLeuValTyrPheAspPheAspSerAspGluIleLysProGln 82
                                                                                                                                                                                                                                                                                                                                                   43 GlyValIleTyrThrGlyValAlaProLeuValAspAsnAspGluThrValLysAlaLeu 62
                                                                                                                                                                                                                                                                                                                                                                                                                        23 CysalaAsnLysSerThrSerGlnValMetValAlaProAsnAlaProThrGlyTyrThr 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 LeuHisIleGlnIleAlaAlaAlaAlaAlaAlaLeuSerValLeuThrPheMetThrGly 22
                                                                                                                              LeuValAlaGlyHisThrAspGluArgGlySerArgGluTyrAsnMetSerLeuGlyGlu 122
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|-GTCGCCCCAGTGGTTGACGAAGAAGAATCGTGGAGGAGTGT 5290
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US-08-469-260A-393
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; LOCATION: 9038..9143
US-08-469-260A-393
                                                                  Best Local Similarity:
Query Match:
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                          US-09-674-779B-2 (1-172) x US-08-469-260A-393 (1-9143)
                                                                                                 Percent Similarity:
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REFERENCE/DOCKET NUMBER: 55
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
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LENGTH: 9143 base pair
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NAME: POREMBSKI, PRISCILLA E.
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APPLICATION NUMBER:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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 3 LeuHisIleGlnIleAlaAlaAlaAlaAlaLeuSerValLeuThrPheMetThrGly
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JAMES C. ERKER
SHERI L. BUIJK
ISA K. MUSHAHWAR
                                                                                                                                                                                                                                                                                                                                                                9143 base pairs
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THOMAS P. LEARY
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GEORGE G. SCHLAU
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                     Pred. No.:
                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Chlamydia
US-09-556-877-171
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APPLICANT:
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SOFTWARE: FastSEQ for
SEQ ID NO 171
LENGTH: 2895
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C5
CURRENT APPLICATION NUMBER: US/09/556,877
CURRENT FILING DATE: 2000-04-19
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                                                                                                                                                                                                                                                                 829 GCTTCTGATGGAGGAGCAATTAAAGTAACTACTCGCCTAGATGTTACAGGCAATCGT---
                                                                                                                                                            886 ---GGTAGGATCTTTTTAGTGACAATATCACAAAAAATTATGGCGGAGCTATTTACGCT 942
66 LeuProSerLeuValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAla 85
                                                                                                        48 GlyValAlaProLeuValAspAsnAspGluThr-----ValLysAlaLeuAlaSerLys
                                                                                                                                                                                                             28 ThrSerGlnValMetValAlaProAsnAlaProThrGlyTyrThrGlyValIleTyrThr 47
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Skeiky, Yasir
Fling, Steve
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                                                         CCTGTAGTTACCCTAGTGGATAATGGCCCTACCTACTTATAAACAATATCGCCAATAAT 1002
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10 9 8		1210 ATTITTATGATCCTATTGAAGTTAGCAATGCAGGG	Db 1003 AAGGGGGGCGCTATCTATATAGACGGAACCAGTAACTCCAAAATT 1047  Qy 86 IleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValala 105
Qy 48 GlyvalAlaProLeuValAspAsnAspGluThrValLysAlaLeuAlaSerLys 65	rcent Similar rent Similar rent Similar rent Similar rent Similar rent Match: :: :: :: :: :: :: :: :: :: :: :: :: :	J-556-877-183 J-566-877-183 J-566-877-183 J-596-877-183 J-5921CANT: Bhatla, PPLICANT: Skeiky, PPLICANT: Skeiky, PPLICANT: Fling, S PPLICANT: Fling S PPLICANT: Fling Date: The PPLICATION: LE REFRENCE: JO RRENT APPLICATION RRENT FILING DATE: MBER OF SEQ ID NOS SFTWARE: FastSEQ fi J NO 183 J D NO 183 JENGT: 2934 YPE: DNA NRGANISM: Chlamydia -556-877-183 Mment Scores:	Db 1108 AATGGTACCAGTACGTCAGCTAATCCTCCTAGAAGAAATGCA 1149  Qy 126 ValalavalargasnTyrLeuLeuGlyLysGlyIleAsnGln 139  :::

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APPLICANT: Steven P. Fling
APPLICANT: Steven P. Fling
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C7
CURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT FILING DATE: 2000-07-20
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ORGANISM: Chlamydia
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                                                          1249 ATTTTTATGATCCTATTGAAGTTAGCAATGCAGGG------GTCTCTGTGTCC 1296
                                                                                                                                                                                                                                                                         106 GlyHisThrAspGluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAla 125
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             ThrAsnGluGluAla 161
                                                                                                                                             ATAACAGTAGCAAGCTCCTCTGGTGAAATTCTATTAGGAGCAGGGAGTAGCCAAAATTTA 1248
                                                                                                                                                                                    ValAlaValArgAsn-----TyrLeuLeuGlyLysGlyIleAsnGln-----
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Best Local Similarity:
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, Sequence 1, Application US/09036987A
; Patent No. 6143526
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CURRENT FILING DATE: 1998-08-14
NUMBER OF SEQ ID NOS: 30
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 80161 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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CITY: Indianapolis
STATE: Indiana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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6014 ATGGGCAGGATAGAAGCTGACCGTTGTCAGGTCGCCGAAGGTTCCGGTCAGCCGTCCCCG 6073
                                                                                                                       5948 -----
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                                                                                   GluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThr 108
                                                                                                                                           LeuValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAsp 88
                                 AspGluArg-----
                                                        GATGCGAGCCAATTCCAGGCTGCCGGTCAACACGCAGCCACCCTCGCCGCTGGTGATGTG 6013
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Treadway, Patti J.
Turner, Jan R.
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Crawford, Kathryn P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dow AgroSciences LLC Patent Department
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US-09-674-779B-2 (1-172) x US-09-370-700-1 (1-80161)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EARLIER FILING DATE: 1998-03-09 NUMBER OF SEQ ID NOS: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/370,700 CURRENT FILING DATE: 1999-08-09 EARLIER APPLICATION NUMBER: US 09/36987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Turner, Jan R
APPLICANT: Waldron, Clive
TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
FILE REFERENCE: 50489 DIV1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Madduri, Krishnamurthy APPLICANT: Treadway, Patti J APPLICANT: Turner, Jan R
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APPLICANT: Broughton, Mary C
APPLICANT: Crawford, Kathryn P
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ORGANISM: Saccharopolyspora spinosa
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6074 GTAGGTGGATCCCACCGCATCACAGTTGTCTTCGACGAGGAACAGCTCGTGTTCTTTGC 613:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5864 ACCGAGGTGGTAGTCGAACCTCTTGCG-------GCAGGTGTTGTCCACGCCGGG 5911
                                           112 -----GlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaVal-----
                                                                                                    6014 ATGGGCAGGATAGAAGCTGACCGTTGTCAGGTCGCCGAAGGTTCCGGTCAGCCGTCCCCG 607:
                                                                                                                                                                                                     5954 GATGCGAGCCAATTCCAGGCTGCCGGTCAACACGCAGCCACCCTCGCCGCTGGTGATGTG 6013
                                                                                                                                                                                                                                                                                                                                                                                                                5912 CTCGCACCAGCAATCCCGTCCCCAGTCACGCAGCGA---
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                                                                                                                                                                                                                                                   89 GluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThr 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                        49 ValAlaProLeuValAspAsnAspGluThrValLysAlaLeuAlaSerLysLeuProSer
                                                                                                                                                                                                                                                                                                                                                            69 LeuValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29 SerGlnValMetValAlaProAsnAlaProThrGlyTyrThrGlyValIleTyrThrGly 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patentin Ver. 2.0
                                                                                                                                                          AspGluArg----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATGATGGCTCGCGTCCGTTCCGTGACGGCGCCTTGATGCGGTCTGG 6232
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; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
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Best Local Similarity:
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FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                       3914957 CTGGGATCCCACCGAGCTCACCGCGACGCTGCGGGACTACTTTGCTGGTCGGGATCCGGA 3914898
                                                                                                                     3915014 GTGACGCTGGTGTCACCGCCGCACATGGAGCGCCGGTTCAGCGCGGAC---GGCACGTCG 3914958
                                                                                                                                                                                                                        3915071 GCGTCCCCGGCTGCCGCGAAGTCAACGGTCAGGTG---TTCATCGTCTACGGTCCGCAG 3915015
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                                                                                                                                                                    AlaArgValLeuValAlaGlyHisThrAspGluArgGlySerArgGluTyrAsnMetSer 119
                                                                                                                                                                                                                                                                                                                         CCGCTGTCGCCGCAGCATGTGGTAAGCCTGGTCCAGTTT---
                                                                                                                                                                                                                                                                                                                                                                     LysAlaLeuAlaSerLysLeuProSerLeuValTyrPheAspPheAspSerAspGluIle 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlyTyrThrGlyValIleTyrThrGlyValAlaProLeuValAspAsnAspGluThrVal 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------CysAlaAsnLysSerThrSerGlnValMetValAlaProAsnAlaProThr 39
                                                                                                                                                                                                                                                                       LysProGlnAlaAlaAlaIleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGlnThr 99
                                                    LeuGlyGluArgArgAla-ValAla---ValArgAsnTyrLeuLeuGlyLysGlyIleAs 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WHITE, Owen R.
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Sequence 79, Application US/09453702B
Patent No. 6365723
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                          Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
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35256 GGACTGGTGATGCTGGGGGCTGCAGCATGGTACACGCTGTACCAGAATCAGGAGCAGGCC 35315
                                                                                                                                                                                                   35145 CTGAACAGAATATTGCTGCCAGAAGCGCCCAGCAATGCGCTGAACAGTACAACGGCG 35204
                                                                                                   35205 GTGGGCTCACGTCTGATGAGCGGTGCGCTG------GGGCTGGTTGGTGGCGTACCC 35255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible operating SYSTEM: PC-DOS/MS-DOS SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: mEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: No. 6365723el Sequences of E. coli 0157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: line MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                               43 GlyValIleTyrThrGlyValAla------ProLeuValAspAsnAspGlu-----
                                                                                                                                             23 CysAlaAsnLysSerThrSerGlnValMetValAlaProAsnAlaProThrGlyTyrThr 42
                                                                                                                                                                                                                                                  3 LeuHisIleGlnIleAlaAlaAlaAlaAlaLeuSerValLeuThrPheMetThrGly 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 03-Dec-1999 CLASSIFICATION: <Unknown>
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ZIP: 53701-2113
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REFERENCE/DOCKET NUMBER: 960296.95017
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TH: 48908 : nucleic acid :NDEDNESS: double LOGY: linear TYPE: DNA (genomic) DESCRIPTION: SEQ ID NO: 137:	LENGTH: 48908  TYPE: nucleic STRANDEDNESS: TOPOLOGY: lin MOLECULE TYPE: DNA SEQUENCE DESCRIPTI US-09-453-7028-137	_
PHONE: (608) 251-5000  PEAX: (608) 251-9166  PR SEQ ID NO: 137:  CHARACTERISTICS:	INFORMATION FOR SEQ SEQUENCE CHARAC	
	NAME: SE REGISTRA REFERENCE	
APPLICATION NUMBER: 60/110,955 FILING DATE: 04-DEC-1998 NEY/AGENT INFORMATION:	; APPLICATI ; FILING DA ; ATTORNEY/AGENT	
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INVENTION: NO. 6365723el Sequences of E. coli 0157 SEQUENCES: 265 DENCE ADDRESS.	TITLE OF INVENT	
Nicole tt, Guy	Pe P1	
tner, Frederic	APPLICANT: Bl	
ation US/09453702B	RESULT 40 US-09-453-702B-137/c ; Sequence 137, Application ; Patent No. 6365733 ; Patent No. 6365733	
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G11G11377F777731-51-51-51-51-51-51-51-51-51-51-51-51-51	149	
ArgAsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGluIleIleSerPheGly 148 :::::: CHI	Db 35499 Caccamom	
CAGGAAAAAGCGCAGTCCATT	35448	
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ATGTCTTTGCCTGAAGCCTCAGATAATGAAGGACGACACGCGGCGGCGGCGCGCGC	35376	
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Search	Db	Qy	Дb	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qу	DЬ	Qy	Db	Qy	Db	Qy	us-09-	DB:	Query	Percen	Pred.	
Search completed: July 6, 2003, 13:40:31	11	149	11471 CAGGATGTGCCGGGCTG	129	Db 11522 GATGAACAGGCCAGTCGGGTGAAATCCCTGCAGGAAAAAGCGCAGTCCATT	109	11540	89	Db 11594 ATGTCTTTGCCTGAAGCCTCAGATAATGAAGGACGAACACGGGCGGCGCTGACA 11541	69	11654 AGGGAGTCTGC	58	11714	43	Db 11765 GTGGGCTCACGTCTGATGAGCGGTGCGCTGGGGCTGGTTGGTGGCGTACCC 11715	Qy 23 CysAlaAsnLysSerThrSerGlnValMetValAlaProAsnAlaProThrGlyTyrThr	Db 11825 CTGAACAGAATATTGCTGCCAGAAGCGCCGCCCAGAATGCGCTGAACAGTACAACGGCG 11766	ω	US-09-674-779B-2 (1-172) x US-09-453-702B-137 (1-48908)	4 Gaps:		39.89% Conservative:	Length:	
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Command line parameters:

-MODEL=frame+_p2n.model -DEV=x1p
-V=/Cgn2_1/USPFO_spool/USO9674779/runat_06072003_121615_9891/app_query.fasta_1.327
-DB=Published_Applications_NA -QEMY=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-COOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-THR.MS=human40.cdi -LIST=100 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=40 -MODE=LOCAL -OUTFMT=tto -NORM-ext -HEAPSIZE=500 -MINLEN-0
-MAXLEN-2000000000 -USER-US09674779_@CGN_1_1_122_@runat_06072003_121615_9891
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-CONGIGG -DEV_TIMEOUT=120 -WANT -TIMEOUT=30 -THREADS=1 -KGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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9 US-10-098-841-330

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10 US-09-815-242-8064

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11 US-10-002-600-80

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10 US-09-070-927A-121
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9 US-10-156-761-1993
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US-09-974-300-1889
Sequence 1, Appli Sequence 25, Appl Sequence 110, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 29, Appl Sequence 29, Appl Sequence 21, Appli Sequence 11, Appl Sequence 21, Appli Sequence 21, Appli Sequence 113, Appl Sequence 113, Appl Sequence 113, Appl Sequence 114, Appl Sequence 21, Appli Sequence 22, Appli Sequence 24, Appli Sequence 25, Appli Sequence 25, Appli Sequence 24, Appli Sequence 25, Appli Sequence 21, Appli Sequence 25, Appli Sequence 21, Appli Sequence 25, Appli Sequence 25, Appli Sequence 21, Appli Sequence 25, Appli Seq
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Sequence 1, Appl
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US-10-329-960-1/c
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CURRENT FILING DATE: 2003-01-02
PRIOR APPLICATION NUMBER: US 09/643,990
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: US 08/487,429
PRIOR APPLICATION NUMBER: US 08/426,787
PRIOR APPLICATION NUMBER: US 08/426,787
PRIOR APPLICATION NUMBER: US 08/426,787
PRIOR FILING DATE: 1995-04-21
NUMBER OF SEQ ID NOS: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/10329960 Publication No. US20030099277A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd Genome, Frag
TITLE OF INVENTION: Thereof, and Uses Thereof
FILE REFERENCE: PB186P1
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LOCATION: (4747)..(4747)
OTHER INFORMATION: n equals a,
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LOCATION: (29298)..(29298)
OTHER INFORMATION: n equals
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LOCATION: (10150)...(10150)
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LOCATION: (36543)..(36543)
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LOCATION: (36551)..(36551)
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OTHER INFORMATION: n equals
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LOCATION: (40808)..(40810)
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LOCATION: (51786)..(51786)
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LOCATION: (51602)..(51602)
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LOCATION: (102696)..(102696)
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LOCATION: (145171)..(145171)
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SOFTWARE: PatentIn Ver.
SEQ ID NO 1
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                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/747,348
CURRENT FILLING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 60/171,525
PRIOR FILING DATE: 1999-12-22
                                                                                                                                                                                                                                                                                                                                   APPLICANT: Andrew D. MURDIN, Raymond P. OOMEN, Joe WANG, Pamela DUNN TITLE OF INVENTION: Chlamydia antigens and corresponding DNA fragments and FILE REFERENCE: 77813-37
                                                                                                                                                        LENGTH: 779
TYPE: DNA
ORGANISM: Chlamydia pneumoniae
                                                                                                                       NAME/KEY: CDS
LOCATION: (10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO
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PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: US 08/487,429
PRIOR FILING DATE: 1995-06-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd Genome, TITLE OF INVENTION: Thereof, and Uses Thereof
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LOCATION: (10150)..(10150)
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LOCATION: (9921)...(9921)
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LOCATION: (29298)..(29298)
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LOCATION: (4747)..(4747)
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LOCATION: (36543)..(36543)
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LOCATION: (145058)..(145058)
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LOCATION: (139910)..(139910)
OTHER INFORMATION: n equals
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LOCATION: (131360)..(131360)
OTHER_INFORMATION: n equals
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LOCATION: (131340)..(131340)
OTHER_INFORMATION: n equals a,
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LOCATION: (122336)..(122336)
OTHER INFORMATION: n equals a,
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LOCATION: (142750)..(142750)
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OTHER INFORMATION: n equals
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LOCATION: (121344)...(121344)
OTHER INFORMATION: n equals a, t,
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LOCATION: (120038)..(120038)
OTHER_INFORMATION: n equals
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LOCATION: (107248)..(107248)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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LOCATION: (117136)..(117136)
OTHER INFORMATION: n equals a,
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LOCATION: (119924)..(119924)
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LOCATION: (119750)..(119750)
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OTHER INFORMATION: n equals a, t, g or c
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                        SEQ ID NO 5
LENGTH: 984
TYPE: DNA
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                                                                                                                                                                                                                                                                                                Sequence 5, Application US/10216338A Publication No. US20030113757A1 GENERAL INFORMATION:
                                                                                   CURRENT APPLICATION NUMBER: US/10/216,338A CURRENT FILING DATE: 2003-01-14 PRIOR APPLICATION NUMBER: 60/310,882 PRIOR FILING DATE: 2001-08-08 NUMBER OF SEQ ID NOS: 8 SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                             APPLICANT: Czajka, John
TITLE OF INVENTION: Rapid and Specific Detection of Campylobacter
FILE REFERENCE: MD1083USNA
TOTAL STREET STREET
ORGANISM: Campylobacter coli
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NAME/KEY: misc_feature
LOCATION: (152500)...(152500)
OTHER INFORMATION: n equals
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LOCATION: (150841)..(150841)
OTHER INFORMATION: n equals
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LOCATION: (152530)..(152530)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104 ValAlaGlyHisThrAspGluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArg 123
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CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 3232
LENGTH: 678
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Query Match:
DB:
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                                                                                                       Alignment Scores:
                                                                                                                                       ; LOCATION: (1).
US-10-156-761-3232
                                                 Percent Similarity:
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APPLICANT:
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                                                                                                                                                                                                             TYPE: DNA ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                              FEATURE:
                                                                                                                                                                          NAME/KEY: CDS
                                                                                      No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           664 CATTTTGGTTTTGATAAGGTAGATATCAATCCAGCCTTTGAAGAAAAAATCAAAGAAATT 723
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                                                                                                                                                                                                                                                                                                                                                                                                                                       SHIBA, TADAYOSHI
SAKAKI, YOSHIYUKI
HATTORI, MASAHIRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISHIKAWA, JUN
HORIKAWA, HIROSHI
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                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
                                                                           SEQ ID NO
                                                                                                               CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                    APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: OMURA, SATOSHI APPLICANT: IKEDA, HARUO
                                                                                              NUMBER OF SEQ ID NOS: 15109
                ORGANISM: Streptomyces avermitilis
FEATURE:
                                       TYPE: DNA
                                                        LENGTH:
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                                                                                                                                                                                                                                                                                                                    SHIBA, TADAYOSHI
                                                                                                                                                                                                                                                                                                                                         ISHIKAWA, JUN
HORIKAWA, HIROSHI
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US-10-216-338A-7
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                                                                                                                                                                                       Sequence 7, Application US/10216338A Publication No. US20030113757A1 GENERAL INFORMATION:
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                                    TITLE OF INVENTION: Rapid and Specific Detection of Campylobacter FILE REFERENCE: MD1083USNA CURRENT APPLICATION NUMBER: US/10/216,338A CURRENT FILING DATE: 2003-01-14 PRIOR APPLICATION NUMBER: 60/310,882 PRIOR APPLICATION NUMBER: 60/310,882 PRIOR FILING DATE: 2001-08-08
                                                                                                                                                                       APPLICANT: Czajka, John
      SOFTWARE: Microsoft Office 97
                           NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: (4187715)
OTHER INFORMATION: a, t, c,
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US-09-674-779B-2 (1-172) x US-09-452-599-11 (1-730)
                                                                    Query Match:
                                                                                          Best Local Similarity:
                                                                                                           Percent Similarity:
                                                                                                                                                                                                                     ; ORGANISM: Klebsiella pneumoniae US-09-452-599-11
                                                                                                                                                                                                                                                                          ; SOFTWARE: Pat
; SEQ ID NO 11
; LENGTH: 730
                                                                                                                                       Score:
                                                                                                                                                        Pred. No.:
                                                                                                                                                                          Alignment Scores:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 11, Application US/09452599 Patent No. US20020055101A1
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LENGTH: 861
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                                                                                                                                                                                                                                                           TYPE: DNA
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Roy, Paul H.
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US-09-674-779B-2 (1-172) x US-10-216-338A-7 (1-861)
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FILE REFERENCE: 12287.31
CURRENT APPLICATION NUMBER: US/09/452,599
CURRENT FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: 08/526,840
PRIOR APPLICATION NUMBER: 08/526,840
PRIOR APPLICATION NUMBER: 08/526,840
PRIOR FILING DATE: 1994-09-12
PRIOR FILING DATE: 1994-09-12
NUMBER OF SEQ ID NOS: 177
NUMBER OF SEQ ID NOS: 177
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                            Indels:
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RESULT 9
US-10-169-953-1
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: METHOD FOR PREPARING A POLYPEPTIDE SOLUBLE IN AN AQUEOUS SOLVENT TITLE OF INVENTION: IN THE ABSENCE OF DETERGENT FILE REFERENCE: D18390
CURRENT APPLICATION NUMBER: US/10/169,953
CURRENT FILING DATE: 2002-07-03
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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                                        703 GCTCTGGATCAGCTGTACACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTT 762
                                                                                                                              643 CTGAAGTCTGACGTTCTGTTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAG
104 ValAlaGlyHisThrAspGluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArg 123
                                                                                 86 IleLeuAspGluGlnAlaGlnPheLeuThrThr-----AsnGlnThrAlaArgValLeu 103
                                                                                                                                                                  66 LeuProSerLeuValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAla 85
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Best Local Similarity:
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LENGTH: 640681
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CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: JP2000-107160
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: SAKAKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILE REFERENCE: 081356/0159
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                                                                                                                                                                                                                                                                                                                                                                                                  365403 TTTAATAGTACGGAATTAAAACCTAGTTCTTATGATAAACTTAATAAATTAGACGATGAT 365344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   365463 GATGATTCTGAACCATTAAACGAACAATATAGCGTATTAAATGAAAATATAAATTTTCCC 365404
                                                                                                                                       365226 TACTTAGCCTCTCGAGGTTTTTCTAGAGATAAAATAACCGTAAAAGGTATGGGAAAATTA 365167
                                                      365166 TATCCGTTA-----ACTAATCAA 365149
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                                                                                                                                                                                    131
                                                                                                                                                                                                                                                               111 ArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArgAsn 130
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                                                                                                                                                                                TyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGluIleIleSerPheGlyGluGlu 150
                                                                                              ArgProIleAlaPheGlyThrAsnGlu 159
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US-09-998-279-25

Sequence 25, Application US/09998279
Publication No. US20030083287A1
GENERAL INFORMATION:
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Best Local Similarity:
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                                                        APPLICANT: BURGESS, NICOLA A.
APPLICANT: GARCIA, MIGUES M.
APPLICANT: KIRKE, DAVID F.
APPLICANT: MEYERS, NICHOLAS L.
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TITLE OF INVENTION: ginS FILE REFERENCE: GM50081
                                         APPLICANT:
APPLICANT:
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APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
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NUMBER OF SEQ ID NOS: 8481
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                                                                                                                                                                                                                                                            510 GTTGAAATC 518
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                                                                                                                                                                                                                                                                                                                                                                                                                                              129 ArgAsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSerVal---GluIleIleSerPhe 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 ---ArgGlySerArg----GluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaVal 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     270 CTTCTCGTATTGAACCCGCCCCGCAATATCGTAATCAGCGGGCATACGGACAATGTGCCG
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                                                                                                                                                                                                                                                                                                                           GGGGAATTTAAACCGATCGCTTCAAATGACACCGAAGAAGAAGAAGAAGAAAAAACAGACGC 509
                                                                                                                                                                                                                                                                                                                                                                 GlyGluGluArgProIleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArgArg 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTCGAAATTCTCAATTTAAATCAAATTGGCATTTAAGCGTGATGCGGGCTGTCAATTTC 389
                                       WILLIAMS, PAUL
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; ORGANISM: Bacillus licheniformis US-09-974-300-1889
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US-09-974-300-1889
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                                                                               PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILLING DATE: 2000-10-06
PRIOR PPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1889
                                                                                                                                                                                                                                                          GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-674-779B-2 (1-172) x US-09-998-279-25 (1-1143)
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Best Local Similarity:
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LENGTH: 1143
                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/974,300 CURRENT FILING DATE: 2001-10-05
                                      TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  916 AAGACCAAC---AACGCACCGATCAAGGTAGGTAGGTTACGCTGACGAAAAAAACCGGTACT 972
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Sequence 11, Application US/10010160; publication No. US20030103999A1; GENERAL INFORMATION:
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                                                                                                                ; NAME/KEY: CDS
; LOCATION: (1)...(714)
US-10-010-160-11
                                                                           Alignment Scores:
                                                         Pred. No.:
Best Local Similarity:
                    Percent Similarity:
                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 717
                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NOVEL THERAPEUTIC COMPOSITIONS FOR TITLE OF INVENTION: TREATING INFECTION BY LAWSONIA SPETILE REPERENCE: DAVILIO.001AUS
CURRENT APPLICATION NUMBER: US/10/010,160
CURRENT FILING DATE: 2001-11-09
PRIOR APPLICATION NUMBER: AU PR1381
PRIOR FILING DATE: 2000-11-10
                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/249,596 PRIOR FILING DATE: 2000-11-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
                                                                                                                                                                                           ORGANISM: Lawsonia intracellularis
                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                         FEATURE:
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King, Kendall W.
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 80,
                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: NON-A, NON-B. NON-C, NON-D, NON-E HEPATITIS TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE NUMBER OF SEQUENCES: 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES
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                     ATTORNEY/AGENT INFORMATION:
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NAME:
                                      CLASSIFICATION: 435435
                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     139 GlnAlaSerValGluIleIleSerPheGlyGluGluArgProIleAlaPheGlyThrAsn 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 AlaAsnLysSerThrSerGlnValMetValAlaProAsnAlaProThrGlyTyrThrGly
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                                                                                                                                                                                                                          60064-3500
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US20020119447A1
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POREMBSKI, PRISCILLA E.
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GEORGE G. SCHLAUDER
SURESH M. DESAI
THOMAS P. LEARY
ANTHONY SCOTT MUERHOFF
                                                                                                                                                                                                                                                                                                           100 ABBOTT PARK ROAD
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SHERI L. BUIJK
ISA K. MUSHAHWAR
                                                                                                                                                                                                                                               USA
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TAMI J. PILOT-MATIAS
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                          Sequence 11, Application US/08424550B Patent No. US20020119447A1 GENERAL INFORMATION:
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INFORMATION FOR SEQ_ID_NO: 80:
                                         CORRESPONDENCE ADDRESS:
                                                                           TITLE OF INVENTION:
                                                                                                               APPLICANT:
APPLICANT:
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                                                          NUMBER OF SEQUENCES:
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MOLECULE TYPE:
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REFERENCE/DOCKET NUMBER: 55;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
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ADDRESSEE: ABBOTT LABORATORIES D377/AP6D STREET: 100 ABBOTT PARK ROAD
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STRANDEDNESS: sing
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                                                                                                    SURESH M. DESAI
THOMAS P. LEARY
ANTHONY SCOTT MUERHOFF
JAMES C. ERKER
SHERI L. BUIJK
ISA K. MUSHAHWAR
LNOW-D. NOW-D. NOW-D.
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GEORGE G. SCHLAUI
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10.16%
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; Sequence 390, Application US/08424550B
; Patent No. US20020119447A1
; GENERAL INFORMATION:
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APPLICANT:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550B
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NAME: POREMBSKI, PRISCILLA E.
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                                                                                                                    5226 CATGCAGCTACAATCCTTGCTATCATAGAGTATTGCTGTGGC 5267
                                                                                                                                                                                          5169 ---ACTAGTCCTTTCACATTGGAAACCGCCCTTGAAAAACTTAACACCTTTCTTGGGCCT 522
                                                                                                                                                                                                                                                                       5130 GTTGCTGCAATT---GACAAGCTGAAGAGTACAATCACCACA-----
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                                                                                                                                                      123 ArgArgAla-----ValAlaValArgAsnTyrLeuLeuGly 134
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JOHN N. SIMONS
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INFORMATION FOR SEQ ID NO: 390:
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CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 9143 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 708-937-6365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435435
ATTORNEY/AGENT INFORMATION:
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TOPOLOGY: li
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REGISTRATION NUMBER: 33,207
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                                                                                                                                                                                                                                         5201 TGTGTGCGGCGTTGCTGGTCTATTACATCAGTC------CCTACCGGTGCTACT 5248
5318 GTTGCTGCAATC---GATAAGCTGAAGAGTACAATAACCACA----
                                                                               5291 GCATCATTCATTCCC-----
                                   83 AlaAlaAlaIleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgVal 102
                                                                                                                 63 AlaSerLysLeuProSerLeuValTyrPheAspPheAspSerAspGluIleLysProGln 82
                                                                                                                                                                                               43 GlyVallleTyrThrGlyValAlaProLeuValAspAsnAspGluThrValLysAlaLeu 62
                                                                                                                                                                                                                                                                               23 CysAlaAsnLysSerThrSerGlnValMetValAlaProAsnAlaProThrGlyTyrThr 42
                                                                                                                                                                                                                                                                                                                                                            3 LeuHisIleGlnIleAlaAlaAlaAlaAlaAlaLeuSerValLeuThrPheMetThrGly 22
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THOMAS P. LEARY
ANTHONY SCOTT MUERHOFF
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SHERI L. BUIJK
ISA K. MUSHAHWAR
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GEORGE G. SCHLAUDER
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Indels:
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                                                                                                         ; LOCATION:
US-08-424-550B-393
Best Local Similarity:
                                   Score:
                                                                       Alignment Scores
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                  Percent Similarity:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: THOMAS P. LERRY
APPLICANT: ANTHONY SCOTT MUERHOFF
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUJUK
APPLICANT: ISA K. MUSHAHWAR
APPLICANT: ISA K. MUSHAHWAR
APPLICANT: ISA K. MUSHAHWAR
TITLE OF INVENTION: NON-A, NON-B. NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
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No.:
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ATTORNEY/AGENT INFORMATION:
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NAME/KEY:
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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T: 100 ABBOTT PARK ROAD
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TAMI J. PILOT-MATIAS
GEORGE J. DAWSON
GEORGE G. SCHLAUDER
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446..9037
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                      Conservative:
       Mismatches:
                                       Matches:
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10.16%

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US-09-674-779B-2 (1-172) x US-09-742-659-1 (1-9399)
                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                         ; LENGTH: 9399
; TYPE: DNA
; ORGANISM: GB virus-B
US-09-742-659-1
                                                                                                                                                               Query Match:
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US-09-742-659-1
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Chimeric HCV/GBV-B v
FILE REFERENCE: ID01116
CURRENT APPLICATION NUMBER: US/09/742,659
CURRENT FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: US 60/171,469
PRIOR FILING DATE: 1999-12-22
                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
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  5141 CTCGCTGTTGGCGTTGGAGTGGCTATGGCCTTATCTAGCCATTGACACTTTTGGCCGCCACT 5200
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                                       3 LeuHisIleGlnIleAlaAlaAlaAlaAlaAlaLeuSerValLeuThrPheMetThrGly 22
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41.04%
28.36%
10.16%
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; SEQUENCE DESCRIPTION: SEQ ID NO: 121: US-09-070-927A-121
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                                                                                                                 INFORMATION FOR SEQ ID NO: 121: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/066,009 FILING DATE: 1997-11-14 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides NUMBER OF SEQUENCES: 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Charles A. Kunsch
Patrick J. Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5414 CATGCAGCTACAATCCTTGCTATCATAGAGTATTGCTGTGGT 5455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5357 ---ACTAGTCCTTTCACATTGGAAACCGCCCTTGAAAAACTTAACACCTTTCTTGGGCCT '5413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5318 GTTGCTGCAATT---GACAAGCTGAAGAGTACAATCACCACA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 ArgArgAla-----ValAlaValArgAsnTyrLeuLeuGly 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 LeuValAlaGlyHisThrAspGluArgGlySerArgGluTyrAsnMetSerLeuGlyGlu 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83 AlaAlaAlaIleLeuAspGluGinAlaGlnPheLeuThrThrAsnGlnThrAlaArgVal 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 AlaSerLysLeuProSerLeuValTyrPheAspPheAspSerAspGluIleLysProGln 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43 GlyValIleTyrThrGlyValAlaProLeuValAspAsnAspGluThrValLysAlaLeu 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 CysAlaAsnLysSerThrSerGlnValMetValAlaProAsnAlaProThrGlyTyrThr 42
                                                                          TYPE: nucleic acid
                                       TOPOLOGY: linear
                                                        STRANDEDNESS: double
                                                                                                                                                               TELEFAX:
                                                                                                                                                                                                                   NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB
                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/070,927A FILING DATE: 04-May-2000 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2 SOFTWARE: ASCII Text
                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Human Genome Sciences, Inc
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20850
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US-09-886-468-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/09886468 Patent No. US20020037293A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Aventis Pasteur Limited TITLE OF INVENTION: Chlamydia antigens and corresponding DNA fragments and uses ther FILE REFERENCE: 77813-5
                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/113,284
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113,285
PRIOR FILING DATE: 1998-12-23
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113,282
PRIOR FILING DATE: 1998-12-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/113,280 PRIOR FILING DATE: 1998-12-23
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CURRENT FILING DATE: 1999-12-23
                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/113,283 PRIOR FILING DATE: 1998-12-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/113,281 PRIOR FILING DATE: 1998-12-23
                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/113,385 PRIOR FILING DATE: 1998-12-23
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APPLICATION NUMBER: 60/114,058
FILING DATE: 1998-12-28
APPLICATION NUMBER: 60/114,059
FILING DATE: 1998-12-28
APPLICATION NUMBER: 60/114,061
                                                                                                                                                                                                       APPLICATION NUMBER: 60/114,050 FILING DATE: 1998-12-28
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                                                                                                               APPLICATION NUMBER: 60/114,057 FILING DATE: 1998-12-28
                                                                                                                                                          APPLICATION NUMBER: 60/114,056 FILING DATE: 1998-12-28
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US-09-886-468-8
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Best Local Similarity:
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                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                Sequence 486, Application US/09841132 Patent No. US20020061848A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1998-12-28
NUMBER OF SEQ ID NOS: 26
                                                 APPLICANT: Bhatia, Ajay
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C8
CURRENT APPLICATION NUMBER: US/09/841,132
CURRENT FILING DATE: 2001-04-23
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           NUMBER OF SEQ ID NOS: 599 SOFTWARE: FastSEQ for Windows Version 3.0/4.0
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SEQ ID NO 486

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; LENGTH: 2895
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-841-132-171
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                                                                           SEQ ID NO 171
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                                                                                                                                                                                                                                                                                                           Sequence 171, Application US/09841132 Patent No. US20020061848A1
                                                                                                                                                               APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C8
                                                                                                            CURRENT APPLICATION NUMBER: US/09/841,132
CURRENT FILING DATE: 2001-04-23
NUMBER OF SEQ ID NOS: 599
                                                                                          SOFTWARE: FastSEQ for Windows Version 3.0/4.0
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TYPE: DNA
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Best Local Similarity:
                                                                                                                                          ; LENGTH: 2934
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-841-132-183
    Query Match:
                                            Percent Similarity:
                                                               Score:
                                                                                                   Alignment Scores:
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; Sequence 183, Application US/09841132

; Patent No. US20020061848A1
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APPLICANT: Bhatia, Ajay
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C8
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                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 3.0/4.0 SEQ ID NO 183
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                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/841,132
CURRENT FILING DATE: 2001-04-23
                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 599
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No.:
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                                                                                      US-09-674-779B-2 (1-172) x US-10-007-693-58 (1-1086)
                                                                                                                                              Query Match:
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                                                                                                                                                                                                          Score
                                                                                                                                                                                                                               Pred. No.:
                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
SEQ ID NO 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 58, Application US/10007693 Patent No. US20020146776A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/007,693
CURRENT FILING DATE: 2001-12-05
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bhatia, Ajay
APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT
TITLE OF INVENTION: AND DIAGNOSIS OF CHLAMYDIAL INFECT:
FILE REFERENCE: 210121.515C2
                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Chlamydia
                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1042 AAGGGGGCGCTATCTATATAGACGGAACCAGTAAC-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28 ThrSerGlnValMetValAlaProAsnAlaProThrGlyTyrThrGlyValIleTyrThr 47
        472 AGTGCTCTTCACAATGTGCTCTTTCCTCTTGGGGAAATGAATAAGACTGAAGTTCGTGCG 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 AlaAlaAlaAlaAlaLeuSerValLeuThrPheMetThrGlyCysAlaAsnLysSer 27
                                             12 AlaAlaLeuSerValLeuThrPheMetThrGlyCysAlaAsnLysSerThrSerGlnVal 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCTGTAGTTACCCTAGTGGATAATGGCCCTACCTACTTTATAAACAATATCGCCAATAAT 1041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ValAlaValArgAsn------TyrLeuLeuGlyLysGlyIleAsnGln----- 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlyHisThrAspGluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAla 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTTTTTATGATCCTATTGAAGTTAGCAATGCAGGG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAla 105
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; LOCATION: (1).
US-10-156-761-1993
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Query Match:
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SEQ ID NO 1993
LENGTH: 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-07
NUMBER OF COLOR
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APPLICANT:
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APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               793 ATTTATATTGTGAGG----GGGGAAGACCATCCC 822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 MetValAlaProAsnAla---ProThrGly-----TyrThrGlyValIleTyr 46
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                                     514 GAGATCGCGGCCAAGGGCGTCGGGCTCACCATCGACACCCTCGGTCTGGTGCCGAACAGC 573
26 LysSerThrSerGlnValMetValAlaProAsnAlaProThrGlyTyrThrGlyValIle 45
                                                                          6 GlnIleAlaAlaAlaAlaAlaAlaLeuSerValLeuThrPheMetThrGlyCysAlaAsn
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HORIKAWA, HIROSHI
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                                                                                                                                                                               41.30%
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Query Match:
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Best Local Similarity:
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US-10-156-761-1
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PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NIMBER OF SEC 100-08-02
                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 15109
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APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
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APPLICANT: ISHIKAWA, JUN
APPLICANT: HORKKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
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                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                    TYPE: DNA
                                                                                                                                                                                                                                                                                                                   ENGTH: 9025608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        913 CGTGAGATCGTCCGCGGTGAGGCCGCGGGCACGGGCCGTACGGACGTCGTGTCGACGGGT 972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 -----TyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGluIleIleSerPheGly 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          862 CAGGTGAACCCGGACTACGGGGTGTTGCTG-----CGGGCGGTGACCGTGCACCAAC 912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 ArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArgAsn 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             574 AAGCTGAGCAAGCAACCTCAGCTGCATCGCCGAGGCG------ACCGGCGGGCACG 621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 GlnAla-----AlaAlaTleLeuAspGluGlnAlaGlnPhe-----------------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46 TyrThrGlyValAlaProLeuValAspAsnAspGluThrValLysAlaLeu----- 62
2.66e+05
80.00
41.30%
23.37%
9.29%
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                                     Mismatches:
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                                                       Conservative:
                                                                             Matches:
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Query Match:
                       Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6221, Application US/09974300
Patent No. US20020146721A1
                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 09/680,598
                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/974,300 CURRENT FILING DATE: 2001-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Berka, Randy M. APPLICANT: Clausen, Ib Gr
                                                                                                                                                                       TYPE: DNA
ORGANISM: Bacillus clausii
                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-10-06
                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 10085.500-US
                                                                                                                                                                                                                       CENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2445790 CCGACGCTGAAGTCCGGGCTCTTCACGGACCGTGCGGAGTTCGCCCAGCACCCGCTGGTAC 2445849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2445730 GCCGCCGACAAGGTGGTGACGCCGGTCGCCGTGGACGGCCGCCGACTGCGCGAAGGCG 2445789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2445670 TACACCTCGGTGGAGCACAAGGAGGACCTCACCGACAAGGTCAACCAGCTGGTGGACCGC 2445729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2445622 AAGCTGAGCAAGCAGCTCAGCTGCATCGCCGAGGCG-----ACCGGCGGCGCACG 2445669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2445562 GAGATCGCGGCCAAGGGCGTCGGGCTCACCATCGACACCCTCGGTCTGGTGCCGAACAGC 2445621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 ArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArgAsn 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        169 GluLeuSerTyr 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                149 GluGluArgProIleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArgArgAla 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131 -----TyrLeuLeuGlYLysGlyIleAsnGlnAlaSerValGluIleIleSerPheGly 148
                                                                                                                                                                                                                       315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94 ------LeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAspGlu 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 ---AlaSerLysLeuProSerLeuValTyrPheAspPheAspSerAspGluIleLysPro 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 GlnAla-----AlaAlaIleLeuAspGluGlnAlaGlnPhe-------93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46 TyrThrGlyValAlaProLeuValAspAsnAspGluThrValLysAlaLeu-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 GlnIleAlaAlaAlaAlaAlaAlaLeuSerValLeuThrPheMetThrGlyCysAlaAsn 25
44.448
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9.128
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US-10-007-693-43/c
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Best Local Similarity:
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patent No. US20020146776A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT TITLE OF INVENTION: AND DIAGNOSIS OF CHLAMYDIAL INFECTION FILE REFERENCE: 210121.515C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/007,693
CURRENT FILING DATE: 2001-12-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143 AGCGCCCGCGCTTACAATGTCATGAAACTGTTTTTCGAATACGATCATTTTGAGCCGGCT 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 GluArgArgAlaValAlaVal---ArgAsnTyrLeuLeuGlyLysGlyIleAsnGlnAla 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 GlyHisThrAspGlu-----ArgGlySerArgGluTyr-----AsnMetSerLeuGly 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 SerValGluIleIleSerPheGlyGluGluArgProIleAlaPheGlyThrAsnGluGlu 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         263 GGAAGGCAAGCCAACCGACGCGTTGAAGTC 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                203 CAACTGTCATTTGCAGGCTACGGTGAGTATCATCCGATCGCTTCAAACGAGACTGCAGAA 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161 AlaTrpSerGlnAsnArgArgAlaGluLeu 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 CTAATCGAGCAACTATCGGCTATGCTTGCTTGACCCACCGCGCTATATTCAAATTTCT 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86 IleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAla 105
                                                                                                                                                                                                                                                           333 ---GGTAGGATCTTTTTAGTGACAATATCACAAAAAATTATGGCGGAGCTATTTACGCT 277
                                                                                                                                                                                                                                                                                                                                                390 GCTTCTGATGGAGGAGCAATTAAAGTAACTACTCGCCTAGATGTTACAGGCAATCGT--- 334
                                                                                    216 AAGGGGGGCCCTATCTATATAGACGGAACCAGTAAC------TCCAAAATT 172
                                                                                                                                                                      276 CCTGTAGTTACCCTAGTGGATAATGGCCCTACCTTATAAACAATATCGCCAATAAT 217
171 TCTGCCGACCGCCATGCTATTATTTTAATGAAAATATTGTGACTAATGTAACTAATGCA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1634
                                                                                                                                                                                                                  48 GlyValAlaProLeuValAspAsnAspGluThr-----ValLysAlaLeuAlaSerLys 65
                                                                                                                                                                                                                                                                                                    28 ThrSerGlnValMetValAlaProAsnAlaProThrGlyTyrThrGlyValIleTyrThr 47
                                         86 IleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAla 105
                                                                                                                             66 LeuProSerLeuValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAla 85
                                                                                                                                                                                                                                                                                                                                                                                         8 AlaAlaAlaAlaAlaLeuSerValLeuThrPheMetThrGlyCysAlaAsnLysSer 27
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US-10-062-254-323/c
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PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/146511
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: 60/156006
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 60/156899
PRIOR APPLICATION NUMBER: 60/157287
PRIOR APPLICATION NUMBER: 60/157287
PRIOR APPLICATION NUMBER: 60/157287
                                                               US-09-674-779B-2 (1-172) x US-10-062-254-323 (1-1762)
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                                                                                                                     Query Match:
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Best Local Similarity:
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Patent No. US20020138882A1
                                                                                                                                                                                                                                                                                                        SEQ ID NO 323
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CURRENT FILING DATE: 2002-02-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 1999-12-09
                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 1999-12-29
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                                                                                                                                                                                                                                                                 ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                    TYPE: DNA
                                                                                                                                                                                                                                                                                                     ENGTH: 1762
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4 HisIleGlnIleAlaAlaAlaAlaAla------AlaLeuSerValLeuThrPheMet 20
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Falco, Saverio Carl
Fang, Yiwen
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                                                                                                            Gaps:
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-----AspPheAspSerAsp 77

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...
US-10-156-761-6208
                                  US-09-674-779B-2 (1-172) x US-10-156-761-6208 (1-2631)
                                                                                                         Query Match:
                                                                                                                       Best Local Similarity:
                                                                                                                                           Percent Similarity:
                                                                                                                                                                                  Pred. No.:
                                                                                                                                                                                                  Alignment Scores:
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US-10-156-761-6208
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LENGTH: 2631
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PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 249-262

CURRENT APPLICATION NUMBER: US/10/156,761

CURRENT FILING DATE: 2002-05-29

PRIOR APPLICATION NUMBER: JP 2001-204089

PRIOR FILING DATE: 2001-05-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKRKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: OMURA, SATOSHI APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 153 eAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArgArgAlaGluLeuSerTyr 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 TGGGGGTTTGGATGGAAGGGAATCGATCGAT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133 uGlyfysGlyIleAsnGlnAlaSerValGluIleIleSerPheGlyGluGluArgProI1 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 CGATTCCGGAACGTCGCGCTCTCGCACCGAACCTCGACCGCCGCCACTGTCGTATTTTGT 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 GCCGTCACACAGCGATATCTCGATGTCCTCCGCGTGGCTCACCGACATCTTCGCCGCCGC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      299 ---GATAGCCTTCCGCCGCAGCGAGCCGATCTTACGCCGCCGCCGCCGTCGTCCTCCGAGTT 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 SerAspGluIleLysProGlnAlaAlaAlaIleLeuAspGluGln-----AlaGlnPhe 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     463 TGGTAGTCGTCGTGCTTGTCGGG-GAGGAGGCGGTGCGCGGGGAGGCGGTCCCGGAAGGA 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 ---GluThrValLysAlaLeuAlaSerLysLeuProSerLeuValTyrPheAspPheAsp 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 TyrThrGlyVallleTyrThrGlyValAlaProLeuValAspAsnAsp------ 56
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FILE REFERENCE: ELITRA, 011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
CURRENT FILING DATE: 2001-03-21
                                                                  PRIOR PRIOR
                                                                                           PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
                                              PRIOR
                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
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APPLICATION NUMBER: 60/257,931
                    APPLICATION NUMBER: 60/253,625 FILING DATE: 2000-11-27
                                                            APPLICATION NUMBER: 60/242,578 FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1342 GAGGTCGGCGCGGACCGGGCCGCGGAGGTGGTCGCGCGTGCTGAGCGAGGAGCCGCCGCGG 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    862 GCGACGTCCGTGGCCGAGTCCTCGCTGACGGTGCCGGGTGTGCGGGTCGTCGTGGACTGC 921
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                                                                                                                                                                                                                                                                                                                                                                                                  Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                         Carr, Grant J.
                                                                                                                                                                                                                                                                                                                                                              Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                Wall, Daniel
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; LOCATION: (1)...(1317)
US-09-815-242-9978
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9978
LENGTH: 1317
                                                                                                                                                          RESULT 33
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                           GENERAL INFORMATION:
APPLICANT: Kaser, Matthew R.
                                                                                              Sequence 60, Application US/09919039 Publication No. US20030108871A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Salmonella typhi FEATURE:
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CURRENT APPLICATION NUMBER: US/09/919,039
                TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES FILE REFERENCE: PA-0035 US
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                                                                                                                                                                                                                                                                                                                 143 GluIleIleSerPheGlyGluGluArgProIleAlaPheGlyThrAsnGluGluAlaTrp 162
                                                                                                                                                                                                                                                                                                                                                          595 AAACTGCGCGTCTACGAGAAGGCGAAAGTGTGCGTAGTGAATGCCGATGACGCGTTGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 -----AlaLeuSerValLeuThrPheMetThrGlyCysAlaAsnLys 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 ProSerLeuValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIle 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47 ThrGlyValAlaProLeuValAspAsnAspGluThrValLysAlaLeuAlaSerLysLeu 66
                                                                                                                                                                                                   715 CACCTTAATCGTCAG 729
                                                                                                                                                                                                                                      163 SerGlnAsnArgArg 167
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                                                                                                                                                                                                                                                                              ATGCCGGTACGCGGGCCCGATGAGCGTGCGTCAGCTTTGGCCTCAATATGGGTGATTAT 714
                                                                                                                                                                                                                                                                                                                                                                                                                                      HisThrAspGluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaVal 126
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US-09-919-039-60
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Best Local Similarity:
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                                  US-09-674-779B-2 (1-172) x US-09-960-253-145 (1-10300)
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                                                                                       Query Match:
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PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence 145, Application US/09960253
patent No. US20020123619A1
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                                                                                                                                                                                                                                                                                             SEQ ID NO 145
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Mohamath, Raodoh
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Incyte ID No. US20030108871A1 348072.5
                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 210121.556
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                                                                                                                                                                                                                                                             TYPE: DNA
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                                                                                                                                                                 No.:
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59 ValLysAlaLeuAlaSerLysLeuProSerLeuValTyrPheAspPheAspSerAspGlu 78
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SULT 35 -10-156-761-5966 Sequence 5966, Application US/1015676 Publication No. US20030119018A1 SEMERAL INFORMATION: APPLICANT: OMURA, SATOSHI APPLICANT: ISHIBA, TADAYOSHI APPLICANT: SHIBA, TADAYOSHI APPLICANT: HATTORI, MASAHIRA TITLE OF INVENTION: NOVEL POLYNUCLEC FILE REFERENCE: 249-262 CURRENT APPLICATION NUMBER: US/10/15 CURRENT FILING DATE: 2002-05-29 PRIOR APPLICATION NUMBER: JP 2001-27 PRIOR FILING DATE: 2001-08-02 CURRENT FILING DATE: 2001-08-02 PRIOR APPLICATION NUMBER: JP 2001-27 PRIOR FILING DATE: 2001-08-02 VNUMBER OF SEQ ID NOS: 15109 SEQ ID NO 5966 LENGTH: 465 TYPE: DNA ORGANISM: Streptomyces avermitilis FEATURE: NAME/KEY: CDS LOCATION: (1)(465) -10-156-761-5966 ignment Scores: 0.219 ore: 75.50 ignment Scores: 0.219 ore: 75.50 ignment Similarity: 38.65% st Local Similarity: 38.65% st Local Similarity: 23.31% str Local Similarity: 38.65% st Local Similarity	Db 37 GTGGAAGGTGTCGCGTACCGAGCTGACGTGACTGAATTGGGAGGGGGCAG 96  Qy 79 IleLysProGlnAlaAlaAlaIleLeuAspGluGlnAlaGlnPheLeu
Qy 161 AlaTrpSer 163  Db 388 GGAACTTCG 396  RESULT 36  US-09-815-242-4642  Sequence 4642, Application US/09815242  Sequence 4642, Application US/09815242  Sequence 4642, Application US/09815242  APPLICANT: US20020061569A1  GENERAL INFORMATION:  APPLICANT: Tawakck, John D.  APPLICANT: Application of Essential Genes in Title Reference: ELITA, 011A 65/91,078  FILLE REFERENCE: ELITA, 011A 65/91,07	Qy 47 ThrGlyValAlaProLeuValAspAsnAspGluThrValLysAlaLeuAlaSerLysLeu 66

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SOFTWARE: Fas
SEQ ID NO 8570
                                                                                     PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
                                                                                                                            PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                                                           PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: ELITRA.011A CURRENT APPLICATION NUMBER: US/09/815, CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
                                           NUMBER OF SEQ ID NOS: 14110
                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Identification of Essential Genes TITLE OF INVENTION: Prokaryotes
                                                                PRIOR FILING DATE: 2001-02-16
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                    FastSEQ for Windows Version 4.0
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Zyskind, Judith W.
Wall, Daniel
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; NAME/KEY: CDS
; LOCATION: (1)...
US-09-815-242-8570
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US-10-156-761-1454/c
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                                                                                                                                               APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIKA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-562
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
CURRENT FILING DATE: 2002-05-29
COURSENT FILING DATE: 2002-05-29
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                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1454, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
SEQ ID NO 1454
LENGTH: 1335
                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                              PRIOR APPLICATION NUMBER: JP 2001-204089 PRIOR FILING DATE: 2001-05-30 PRIOR APPLICATION NUMBER: JP 2001-272697 PRIOR FILING DATE: 2001-08-02
                                         NUMBER OF SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: OMURA, SATOSHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44 VallleTyrThrGlyValAlaProLeuValAsp-----AsnAspGluThrValLys 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27 SerThrSerGlnValMetValAlaProAsn-----AlaProThrGlyTyr------
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US-10-156-761-1454
                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                Sequence 4085, Application US/09815242 Patent No. US20020061569A1
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                                                                                                       APPLICANT:
                                                                                                                                            APPLICANT:
                            APPLICANT: Yamamoto, Robert T. APPLICANT: Xu, H. Howard TITLE OF INVENTION: Identification TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Streptomyces avermitilis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            735 CGCCTGCTCGGGGTCGGAGTCGAGCAGCGCGAGACCGACGCCCGGCCTGAACGTTGATCAC 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 TyrLeuLeuGlyLysGlyIleAsnGlnAlaSerVal------ 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 ArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArgAsn 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          987 GACGTTCGTCAGTGCCTCCTGGACGATCCGGAAGGCGGCGAGATCGGTGCCGGGCGCGAG 928
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                                                                                                               Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
                                                                                                                                                                                                               Haselbeck, Robert
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PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/257,931 PRIOR FILING DATE: 2000-12-22
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TYPE: DNA
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698 GCGTCATCGGCAAGGGCTCCCAACTGGTGGATGCCAAGGGCGACGTGGTCGGTGACGGCA 757
                                    132 --LeuLeuGlyLysGly-----IleAsnGlnAlaSerValGluIleIleSerPheGlyG 149
                                                                       638 AACAGAAGGCCGTGGCCTACGAGAGCCTGGGCGACCTCCACGACGGCGTGATGAGCGCCA 697
                                                                                                               122 luArgArgAlaValAlaValArgAsnTyr-----
                                                                                                                                              578 GTGGCTTGATCAGCGCCGAGCGTGGCGAGGAAGTGGATCATCAACCTCGCTACCGGCG 637
                                                                                                                                                                       108 -----ThrAspGluArgGlySerArgGluTyr-----AsnMetSerLeuGlyG 122
                                                                                                                                                                                                                     518 AGCAGCTCACCGAGGCGCTCTACGACACCACCTGGTCAACGGCAGCGTCGCCGAACACG 577
                                                                                                                                                                                                                                                                                          458 CCAACGAATTCATCATCTACGAGATCGATGGCAAGCGCGGCATCCTCGATGCCAAGGGCA 517
                                                                                                                                                                                                                                                                                                                                                                   398 TCGACGGCCAGGGCAAGGAAGTCCAGGCGCCGCGTTTCGACGACATCTACCCCAACAGTG
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LENGTH: 11575
TYPE: DNA
ORGANISM: Plasmid
US-09-938-956-5
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APPLICANT: Wang, Sigun
APPLICANT: Dicosimo, Deana J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/09938956 Patent No. US20020142408A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Microsoft Office 97
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Koffas, Mattheos
APPLICANT: Odom, J. Martin
TITLE OF INVENTION: Production of Monoterpene
FILE REFERENCE: CL1809 US NA
CURRENT APPLICATION NUMBER: US/09/938,956
CURRENT FILING DATE: 2001-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/229,858
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 7
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9819 ATTCTGCATTCACTCGCCCAGGCAATGATCACCGGCCCTGTAGCCGGCCCGG------ 9769
                                                                135 LysGlyIleAsnGlnAlaSerValGluIleIleSerPheGlyGluGluArgProIleAla 154
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Db 9678 TTC 9676
search completed: July 6, 2003, 15:04:07
Job time : 3796 secs
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Command line parameters:

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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AE002265 AP002547 CJ11168X1 SME591783 AP002994

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951 17355 3235 13498 951 951 981 11494 1059

LOCUS

KEYWORDS SOURCE

ORGANISM

Bacteria; Moraxella Moraxella

proteobacteria; catarrhalis catarrhalis.

Moraxella

(bases 1 to 519)

VERSION

AX011034.1 GI:9997679

REFERENCE

AUTHORS

Ruelle, J.L. Basb019 pro

TITLE

JOURNAL

source

Location/Qualifiers

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519 bp
Sequence 1 from Patent W09957277.
AX011034
        antibodies, and uses
Patent: WO 9957277-A 1 11-NOV-1999;
RUELLE JEAN LOUIS (BE); SMITHKLINE BEECHAM
                                        proteins and genes from moraxella
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AF117975
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Sequence 36 from Patent W00078968.
AX067461
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                                                                       Lagace, R.E., Patterson, C. and Berg, K.L. Nucleotide sequences of moraxella catherhalis patent: WO 0078968-A 36 28-DEC-2000;
                                                                                                                                               Moraxella
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                                                                                                                          Moraxella.
                                                                                                                                    Bacteria; Proteobacteria;
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                                                       Incyte Genomics, Inc. (US)
Location/Qualifiers
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/organism="moraxella_gatarrhalis"
/ob_xref="taxon=480"
a 17581 c 20150 g 27888 t
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Conservative:
Mismatches:
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Alignment Scores: Pred. No.:
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                                                                                                                                                          TITLE
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                                                                                                                                                                     AUTHORS
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                                                                                             antibodies, and uses
Patent: WO 9957277-A 3 11-NOV-1999;
RUELLE JEAN LOUIS (BE); SMITHKLINE |
Location/Qualifiers
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AX011036
                                                                                                                                                                                                   Bacteria; Proteobacteria;
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                                                      139
                                                                                                                                             proteins and genes from moraxella catarrhalis, antigens.
                                                                /db_xref="taxon:480"
                                                                        /organism="Moraxella catarrhalis"
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Length:
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Best Local Similarity:
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Best Local Similarity:
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Patent: WO 9957277-A 5 11-NOV-1999;
                                                                                                                                                                                                                                                  Basb019 proteins and genes from moraxella
                                                                                                                                                                                                        RUELLE JEAN LOUIS (BE);
                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
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                                                                                                                     /organism="Moraxella catarrhalis"
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Mismatches:
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Sequence 7 from Patent W09957277
AX011040
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Patent: WO 9957277-A 7 11-NOV-1999;
RUELLE JEAN LOUIS (BE); SMITHKLINE
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                                                                                                                                                                                                                                                                                                      Moraxella catarrhalis.
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                                                                                                                                                                                                                                                   (bases 1 to 519)
                                                                                                                       137
                                                                                                                                  /organism="Moraxella catarrhalis"
/db_xref="taxon:480"
                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                            catarrhalis
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Characterization of an OprL null mutant of Pseudomonas
J. Bacteriol. 178 (19), 5836-5840 (1996)
                                                                                                                                                                                                                                                Rodriguez-Herva, J.J., Ramos-Gonzalez, M.I. and Ramos, J.L. The Pseudomonas putida peptidoglycan-associated outer membrane lipoprotein is involved in maintenance of the integrity of the
                                                                                                                                                                                                                                                                                                              oprI gene; tolA gene; tolB gene; tolR gene.
Pseudomonas putida.
Pseudomonas putida
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                    X74218.2 GI:5514773
                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas putida ruvB
                                                                                                                                                                                                                                                                                                                                                                                                                         PPPALL
                                                    Direct Submission
Submitted (21-JUL-1993) I. Ramos-Gonzalez,
del Zaidin, 18008 Granada, SPAIN
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                                                                                                                                                                                                                                                                                                      Pseudomonas
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Submitted (09-JUN-1995) I.
             Direct Submission
                          Ramos-Gonzalez,I.
                                                                                           Ramos-Gonzalez,
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                                                                                                        (bases 1 to 498)
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     Ramos-Gonzalez, C.S.I.C. Estacion Exper
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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5 (bases 1 to 7577
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GVDPDAYMEGVQRAMKVAISREEKLEQSLPFLATVGSTSPYIGLFGTVWGIMNSFRG
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1807. .2259
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/codon_start=1
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1097: .1792
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                                                                                                                                                                                                                                                                                                                                                                                                 /transl_table-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="VQRLEFYNDKDLSTIVSRSANILGLAIEDQGAYEIARRARGTPR
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4730. .5230
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3374. .4675
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4751 AAATTTGCTGCGCTGGCCTCTGGCCATGGCCGTA-----GCTGTAGGTTGCTCCTCG 4801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5015 GTTGTTCTGGAAGGTAACACCGACGAGCGCGCGCGCCGCGAGTACAACATGGCTCTGGGT 5074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4958 GAAGCCATGCGCGCTCTGGACGTTCACGCCAAGGACCTGAAAGCCAACGGCAAC---CGT 5014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4901 ---GCCCTGCGCCAATCACCACCTTCTACTTCGAATACGACAGCTCGGACCTGAAGCCA 4957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5075 GAGCGTCGTGCGAAAGCCGTTCAGCGCTACCTGGTTCTGCAGGGCGTTTCCCCTGCTCAG 5134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5135 CTGGAACTGGTTTCCTACGGCGAAGAGCGTCCAGTTGCTACCGGCAACGACGAGCAGTCC 5194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102 ValLeuValAlaGlyHisThrAspGluArgGlySorArgGluTyrAsnMetSerLeuGly 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 GluArgArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSer 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                 162 TrpSerGlnAsnArgArgAlaGluLeu 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 LeuAlaSerLysLeuProSerLeuValTyrPheAspPheAspSerAspGluIleLysPro 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42 ThrGlyValIleTyrThrGlyValAlaProLeuValAspAsnAspGluThrValLysAla 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 LysSerThrSerGln------ValMetValAlaProAsnAlaProThrGlyTyr 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 GlnIleAlaAlaAlaAlaAlaLeuSerValLeuThrPheMetThrGlyCysAlaAsn
                                                                                                                                                                                                                                                       Pseudomonas aeruginosa.
Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                    P.aeruginosa oprL gene
                                                                                                                                                                                                                                                                                                                                                    PAOPRLGN
                                                                                                          Pseudomonas aeruginosa
Microbiology 143 (Pt 5), 1709-1716 (1997)
                                                                                                                                       outer-membrane peptidoglycan-associated lipoprotein (PAL)
                                                                                                                                                                                      Lim, A. Jr., De Vos, D., Brauns, M., Mossialos, D., Gaballa, A., Qing, D.
                                                                                                                                                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                       oprL gene; outer membrane protein
Submitted (12-MAR-1997) Lim A., Vrije Universiteit Brussel, Paardenstraat 65, St. Genesius Rode, Belgium
                                Direct Submission
                                                                                                                                                           Molecular and immunological characterization of OprL,
                                                                                                                                                                     and Cornelis, P.
                                                                                                                                                                                                                          Pseudomonas
                                                                                                                                                                                                                                                                                                      Z50191.1 GI:2251191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlnAlaAlaAlaIleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArg 101
                                                 Lim, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ValGluIleIleSerPheGlyGluGluArgProIleAlaPheGlyThrAsnGluGluAla 161
                                                                                                                                                                                                                                                                                                                                                                                                                  TGGGCTCAGAACCGTCGCGTAGAACTG 5221
                                                              (bases 1 to 1048)
                                                                                                                                                                                                      (bases 1 to 1045)
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3 (bases 1 to 1048)
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                                                                                                                                                                                                                                                                                                        195 a
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<1. .159
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212. .718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="unknown"
/protein_id="CAA90571.1"
/db_xref="GI:929775"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="orf3"
                                                                                                                                                                                                                                                                                                                                                                 /db_xref="SPTREMBL:Q51490"
                                                                                                                                                                                                                                                                                                                                                                                                                              /transl_table=11
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Submitted (01-AUG-1995) Lim A., Vrije Universiteit Brussel, Paardenstraat 65, St. Genesius Rode, Belgium On Jul 9, 1997 this sequence version replaced gi:929774.

Location/Qualifiers
                                                                   233 AAATTTGCTGCGCTGGCTCTGGCCATGGCTGTG------GCTGTGGGTTGCTCCTCC
         26 Lys-----SerThrSerGlnValMetValAlaProAsnAlaProThr
                                                                                                                           6 GlnIleAlaAlaAlaAlaAlaAlaLeuSerValLeuThrPheMetThrGlyCysAlaAsn 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="homology with TolB of E.coli and Haemophilus
influenzae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Pseudomonas aeruginosa"
/db_xref="taxon:287"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="memlkfgkfaalalamayaygcsskggdasgeganggydpnagy
Ganscaydgslsdeaalraittfyfeydssdlkpeamraldyhakdlkgsgoryyleg
HTDERGTREYNMALGERRAKAYQRYLYLQGYSPATLELYSYGKERPYATGHDEQSWAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="outer membrane protein"
/protein_id="CAA90573.1"
/db_xref="01:2251192"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="SPSVAPNGTMLIRHPPAGPGVLMLVSSTDAYGYLSPTAQGDVRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="mpkhlrvltflalslplaaraevpvydgvaannggnvppsgygt
agaggaftgggvttptsvQgelfmQLQ0mQdelarlrgtlerevarmasvmQrpagsr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="periplasmic protein"
/protein_id="CAA90572.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               617 GCCACGCTGGAACTGGTTTCCTATGGTAAAGAGCGTCCGGTCGCCTACCGGCCCACGACGAG
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                                                                                                                                                                                                                                                         Submitted (16-MAY-2000) Department of Medicine and Genetics, University of Washington Genome Center, University Of Washington, Box 352145, Seattle, WA 98195, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 LeuGlyGluArgArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGlyIleAsnGln 139
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2 (bases 1 to 13263)

Stover, C.K., Pham, X.-Q.T., Erwin, A.L., Mizoguchi, S.D., Warrener, P., Hickey, M.J., Brinkman, F.S.L., Hufnagle, W.O., Kowalik, D.J., Lagrou, M., Garber, R.L., Gutry, L., Tolentino, E., Coutry, L., Coutry, L., Tolentino, E., Coutry, L., Coutry, L., Tolentino, E., Coutry, L., Coutry, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stover,C.K., Pham,X.Ó, Erwin,A.L., Mizoguchi,S.D., Warrener,P., Hickey,M.J., Brinkman,F.S., Hufnagle,W.O., Kowalik,D.J., Lagrou,M., Garber,R.L., Goltry,L., Tolentino,E., Westbrock-Wadman,S., Yuan,Y., Brody,L.L., Coulter,S.N., Folger,K.R., Kas,A., Larbig,K., Lim,R., Smith,K., Spencer,D., Wong,G.K., Wu,Z. and Paulsen,I.T. Complete genome sequence of Pseudomonas aeruginosa PAO1, an
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                                                                                                                                                                                                                                                                                                                                                                                                                 Westbrook-Wadman,S., Yuan,Y., Brody,L.L., Coulter,S.N., Folger,K.R., Kas,A., Larbig,K., Lin,R.M., Smith,K.A., Spewong,G.K.-S., Wu,Z., Paulsen,I.T., Reizer,J., Saier,M.H., Hancock,R.E.W., Lory,S. and Olson,M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 LysProGlnAlaAlaAlaIleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGlnThr 99
                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                opportunistic pathogen
Nature 406 (6799), 959-964 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 LysAlaLeuAlaSerLysLeuProSerLeuValTyrPheAspPheAspBerAspGluIle 79 :::|||| :::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40 GlyTyrThrGlyValIleTyrThrGlyValAlaProLeuValAspAsnAspGluThrVal 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AE004530 AE004091
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas aeruginosa PA01, section
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290. .919
                                                                                                 /strain="PAO1"
/db_xref="taxon:287"
                                                                                                                                                           /organism="Pseudomonas aeruginosa"
                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GI:9946865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13263 bp
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on 91 of 529 of the complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spencer, D.H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="asps"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="PA0959"
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DIVFFGADKAKIVCDALGALRIKVGHDLKLLTREMAPMWVVDFPMFEENDDGSLSALH
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FNTLHLMFBGOYTELAVAVDDIAERIRALGFPAPGTYAAYARLSSIKEEBGVPEAEEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(2007. .2477)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation="MELDARMDDLECRQAFQDDTLQALNDVVVEQQRSIERLQLQVAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LVPRREDVTELFQLDVDDRQALWREATLLAEVLKDTFRADKMNVANLGNVVSQLHMHV
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CDS
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ORGANISM
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                                                                                                                                            VERSION
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US-09-674-779B-2 (1-172) x AE004530 (1-13263)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11879 AAATTTGCTGCGCTGGCTCTGGCCATGGCTGTG------GCTGTGGGTTGCTCCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12086 AAGCCGGAAGCCATGCGCGCTCTGGACGTACACGCGAAAGACCTG---AAAGGCAGCGGT 12142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12041 CGTGCGATCACCACC------TTCTACTTCGAGTACGACAGCTCCGACCTG 12085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11984 GGCTAT---GGCGCCAACAGCGGTGCCGTTGACGGCAGCCTGAGCGACGAAGCCGCTCTG 12040
                                                                                                                                                                                                                                                                                                 12323 CAGTCCTGGGCTCAGAACCGTCGCGTCGAGCTG 12355
                                                                                                                                                                                                                                                                                                                                                                                     12263 GCCCAGCTGGAACTGGTTTCCTATGGTAAAGAGCGTCCGGTCGCTACCGGCCACGACGAG 12322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12203 CTGGGCGAGCGTCGTGCCAAGGCCGTTCAGCGCTACCTGGTGCTGCAGGGTGTTTCGCCG 12262
                                                                                                                                                                                                                                                                                                                                                                                                                         140 AlaSerValGluIleIleSerPheGlyGluGluArgProIleAlaPheGlyThrAsnGlu 159
                                                                                                                                                                                                                                                                                                                                     160 GluAlaTrpSerGlnAsnArgArgAlaGluLeu 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40 GlyTyrThrGlyValIleTyrThrGlyValAlaProLeuValAspAsnAspGluThrVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 Lys-----SerThrSerGlnValMetValAlaProAsnAlaProThr 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80 LysproGlnAlaAlaAlaIleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGlnThr 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 LysAlaLeuAlaSerLysLeuProSerLeuValTyrPheAspPheAspSerAspGluIle 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 GlnIleAlaAlaAlaAlaAlaLeuSerValLeuThrPheMetThrGlyCysAlaAsn
                                                           Salmonella typhimurium LT2.
Salmonella typhimurium LT2
                                                                                                                                                                                        Salmonella typhimurium LT2, section
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                  Salmonella
                                        Bacteria; Proteobacteria;
                                                                                                                                                   AE008730 AE006468
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(bases 1 to 20941)
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namraakkaldafeerfwsgidlsklyrqagsnpdpdsgveqifragfkefsrlkqop
gydpdaymegvaramkvaisreeekleaslpflatvgstspyvglfgtvwgimnsfrg
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/transl_table=11
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63.16%
40.94%
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Matches:
                                        gamma subdivision; Enterobacteriaceae;
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CDS

RBS

gene

	CDS	RBS	-10_signal	-35_signal	gene	source	FEATURES					COMMENT	REFERENCE AUTHORS TITLE JOURNAL	JOURNAL MEDLINE	TITLE	AUTHORS
/gc.re sunc /EC_number="1.3.99.1" /EC_number="1.3.5.1" /note="similar to E. coli succinate dehydrogenase, cytochrome b556 (AAC73815.1); Blastp hit to AAC73815.1 (129 aa), 92% identity in aa 1 - 129" /codon_start=1 /transl_table=11 /product="succinate dehydrogenase, cytochrome b556" /protein_id="AAL19676.1" /db_xref="GI:16419242" /translation="MIRNVKKQRPVNLDLQTIRFPITAIASILHRVSGVITFIAVGIL	/gene="sgnc" /note="putative RBS for sdhC; RegulonDB:STMS1H001042" 179. 158	/gene="sdhc" /note="putative -10_signal for sdhc; RegulonDB:STMLTH004697" 166171	L1 H1 × ×		/Organism="Salmonella typhimurium LT2" /Strain="LT2; SSGC 1412; ATCC 700720" /db_xref="ATCC:700720" /db_xref="taxon:99287" /note="LT2" 90568	120941	This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistries or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one mil subclone.	<pre>nttp://kinich.cifn.unam.mx:8850/db/regulondb_intro.frameset</pre>	The analyses of ribosome binding sites and promoter binding sites were kindly provided by Heladia Salgado, Julio Collado-Vides and ReguonDB;	EC numbers were kindly provided by Junko Yabuzaki and the Kyoto Encyclopedia of Genes and Genomes; http://www.genome.ad.jp/kegg/, and Pedro Romero and Peter Karp at EcoCyc; http://ecocyc.PangeaSystems.com/ecocyc/	Coding sequences below are predicted from manually evaluated computer analysis, using similarity information and the programs; GLIMMER; http://www.tigr.org/softlab/glimmer/glimmer.html and GeneMark; http://opal.biology.gatech.edu/GeneMark/	Genetics, Washington University School of Medicine, 4444 Forest Park Boulevard, St. Louis, MO 63108, USA COMMENT Supported by NIH grant 5U 01 AI43283		Nature 413 (6858), 852-856 (2001) 21534948	Latreille, P., Courtney, L., Porwollik, S., Ali, J., Dante, M., Du, F., Hou, S., Layman, D., Leonard, S., Nguyen, C., Scott, K., Holmes, A., Grewal, N., Mulvaney, E., Ryan, E., Sun, H., Florea, L., Miller, W., Stoneking, T., Nhan, M., Waterston, R. and Wilson, R.K.  Complete genome sequence of Salmonella enterica serovar Typhimurium	Modiciliana is constituted in the second

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/product="succinate dehydrogenase, Fe-S protein"
/protein_id="AAL19679.1"
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/gene="sdhp"
/EC_number="1.3.99.1"
~~ ~~mher="1.3.5.1"
DLVVDMGQFYAQYEKIKPYLLNNGQNPPAREHLQMPEQREKLDGLYECILCACCSTSC
                                                                                                                                                                                                                   /note-"similar to E. coli succinate dehydrogenase, iron sulfur protein (AAC73818.1); Blastp hit to AAC73818.1 (238 aa), 96% identity in aa 1 - 238"
                                                                                                                                                                                                                                                                                                                            /gene="sdhB"
/EC_number="1.3.99.1"
/EC_number="1.3.5.1"
                                                                                                                                                                                                                                                                                                                                                                                                                2678. .2683
/gene="sdhB"
/notc="putative RBS for sdhB; RegulonDB:STMS1H001045"
2689. .3408
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SVHGANRLGGNSLLDLVVFGRAAGLHLQESIAEQGVLEDASESDVEGSLERLNRWNNN
RNGEDPVAIRKALDESOMOHNFSVFREGDAMAKGLEQLKVIRERLKNARLDDTSSSFNT
ORVECLELDNLMETAYATAVSANFRTESRGAHSRFDFPERDDANWLCHTLYQPQTESM
TRRSYNMEPKLRPAFPPKIRTY"
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/protein_id="AAL19678.1"
/db_xref="GI:16419244"
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FSEWYALDLVKNODGAVYGCTALCIETGEVYVFKARRYTVLANGGAGRIYQSTTNAHIN
TGDGVGMALRAGVPVQDMEMWQFHPTGIAGAGVLVTEGCTGEGGYLLWKHGERFMERV
APNAKDLAGRDVVARSIMIEIREGRGCDGPWGPHAKLKLDHLKGETLESRLDGILELS
                                                                                                                                                                                             /transl_table=11
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/note="STM0735"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to E. coli succinate dehydrogenase, flavoprotein subunit (AAC73817.1); Blastp hit to AAC73817.1 (588 aa), 97% identity in aa 1 - 588"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="sdhA"
/EC_number="1.3.99.1"
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892. .897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /EC_number="1.3.5.1"
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/note="putative RBS for sdhA; RegulonDB:STMS1H001044"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="succinate dehydrogenase, hydrophobic subunit"
/protein_id="AAL19677.1"
/db_xref="GI:16419243"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VYVIYGEVVVWGV"
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549. .554
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FEAGQRSAKISFVITVVLSLLAGVLVW"
549. .909
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                                                                                                                                                                                                 19574 AGCGAAGGCGGTATGCTGAACGGCGCCGCCACTGGTATGGACGCTAACGGCAACGGCAAC 19633
                                                                                                                                                                                                                                                                                               19634 ATGTCATCTGAAGAGCAAGCGCGTCTGCAGATGCAGCAGCAGCAGCAGAACAACATCGTT 19693
                                                                                                                                                                                                                                                  41
                                            71 TyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAspGluGln 90
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MetMetLeuHisIleGlnIleAlaAlaAlaAlaAlaAlaLeuSerValLeuThrPheMet 20
                                                                                                                                                                                                                                                TyrThrGlyValIleTyrThrGlyValAlaProLeuValAsp-----
                                                                                                                                                                                                                                                                                                                                              ThrGlyCysAlaAsnLysSerThrSerGlnValMetValAlaProAsnAlaProThrGly 40
                                                                                                                                             ---AsnAspGluThrValLysAlaLeuAlaSerLysLeuPro-----SerLeuVal 70
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DLFDERAGKHKEHLGTGDVKYIMGFSSDIETBGGLVHLALAFWESHLEIVSFVVMGSV
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RHAVIHNOTNGSTYTPLOHHIBGQGGDKVWDSVLSEEAVLAFEYGXATAEPRTITIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="similar to E. coli 2-oxoglutarate dehydrogenase (decarboxylase component) (AAC73820.1); Blastp hit to AAC73820.1 (933 aa), 94% identity in aa 1 - 933"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="putative -10_signal for sucA; RegulonDB:STMLTH004698"
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KGLNPTRAIGHIKSMLLQRSA"
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KQTYCGPIGAEYMHITSTEEKRWIQQRIESGRAAFSADEKKRFLNELTAAEGLERYLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="2-oxoglutarate dehydrogenase decarboxylase
component"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="sucA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="sucA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="putative RBS for sucA; RegulonDB:STMS1H001046"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="sucA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAEQNMQVCVPSTPAQVYHMLRRQALRGMRRPLVVMSPKSLLRHPLAVSTLDELANGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FQPAIGEIDELDPKAVKRVVMCSGKVYYDLLEQRRKNDQKDVAIVRIEQLYPFPHKAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EAQFGDFANGAQVVIDQFISSGEQKWGRMCGLVMLLPHGYEGQGPEHSSARLERYLQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /EC_number="1.2.4.2"
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289.00
54.95%
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                                                                                                                                                                                                                                                                                                                                                                   FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19754 GCTAACTTCCTGCGTAGCAACCCGTCTTACAAAGTCACCGTAGAAGGTCACGCGGACGAA 19813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19934 AAACCTGCCGTACTGGGCCACGACGAAGCGGCTTACGCTAAGAACCGTCGCGCTGTACTG 19993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19874 TACCTGCAGGGTAAAGGCGTTTCCGCTGACCAGATCTCCATCGTTTCTTACGGTAAAGAA 19933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19994 GTTTAC 19999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 TyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGluIleIleSerPheGlyGluGlu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 ArgProIleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArgArgAlaGluLeu 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 ArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArgAsn 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    171 SerTyr 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            parkhill, J., Dougan, G., James, K.D., Thomson, N.R., Pickard, D., Wain, J., Churcher, C., Mungall, K.L., Bentley, S.D., Holden, M.T. G., Sebahhia, M., Baker, S., Basham, D., Brooks, K., Chillingworth, T., Connerton, P., Cronin, A., Davis, P., Davies, R.M., Dowd, L., White, N., Farrar, J., Feitwell, T., Hamilin, N., Haque, A., Hien, T.T., Holroyd, S., Jagels, K., Krogh, A., Larsen, T.S., Leather, S., Moule, S., O'Gaora, P., Parry, C., Quail, M., Rutherford, K., Simmonds, M., Skelton, J., Parry, C., Quail, M., Rutherford, F., Simmonds, M., Skelton, J., Stevens, K., Whitehead, S. and Barrell, B.G. Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complete chromosome; segment 4/20.
AL627268 AL513382
AL627268.1 GI:16501953
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Salmonella enterica subsp. enterica serovar Typhi
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (25-OCT-2001) Submitted on behalf of the Salmonalla sequencing team, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO 1SA, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 294050)
Parkhill, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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21534947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                          (URL, http://www.sanger.ac.uk/Projects/S_typhi/)
                                                                                                                                                                                                                                                                                                                                                                                                                       on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Details of S. typhi sequencing at the Sanger Centre are available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E-mail: parkhill@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 294050)
               /EC_number="5.4.99.9"
/note="Similar to Klebiella pneumoniae probable
/note="Similar to Klebiella pneumoniae probable
udp-galactopyranose mutase rfbD SW:GLF1_KLEPN (048485)
udp-galactopyranose mutase SW:GLF_ECOLI
Escherichia coli udp-galactopyranose mutase SW:GLF_ECOLI
                                                                                                                                                                                                                                                                                               Typhi"
                                                                                                                                                                                                                                           /db_xref="taxon:90370"
                                                                                                                                                                                                                                                                                                                    /organism="Salmonella enterica subsp. enterica serovar
                                                                                                                                             /gene="STY0759"
                                                                                                                                                                                              /gene="STY0759"
                                                                                                                                                                                                                                                                  strain="CT18"
                                                                                                                                                                                                                                                                                                                                                                        location/Qualifiers
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misc_feature
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                                                                                   Glycosyl transferases 8.9e-42"
                                                                                                                                                                                                                                                                                                            /db_xref="STTREMBL:Q8XFZ1"
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ISRLVGIDYHKTIVIEGAGINPDIYKFSIEKKHEIPIVLFASRMLWSKGLGDLIEAKK
ISRLVGIDYHKTIVIEGAGINPDIYKFSIEKKHEIPIVLFASRMLWSKGLGDLIEAKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     galactosyltransferase wbbo or rfbF TR:Q48487 (EMBL:L31762) (377 aa) fasta scores: E(): 0, 69.1% id in 375 aa, and to Serratia marcescens galactosyltransferase wbbo or rfbF TR:Q54481 (EMBL:L34167) (380 aa) fasta scores: E(): 0, 55.2% id in 375 aa"
                                                                                                                                                                                                                               YLLKNPQIRLEMGANGRKRVKELFSSILVINKTLQIYKDTIGC"
                                                                                                /note="Pfam match to entry PF00534 Glycos_transf_1, Glycosyl transferases group 1, score 152.20, E-value
                                                                                                                                                                                                                                                      ILRQKNIHFVLNVAGILAEDDKDAIPLELIHHWHNEGLINWLGRSSNVYELIQKSNIV
ALPSIYPEGVPRLLLEASSVGRACIAYDTGGCDSLIIHNYNGLIVKSNSAQELAVELE
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/db_xref="GI:16501956"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="putative glycosyl transferase"
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2332. .3465
                                                                                                                                                                                    /gene="STY0761"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Similar to Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycosyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"Similar to Klebsiella pneumoniae RfbE rfbE TR:Q464482 (EMBL:L41518) (297 aa) fasta scores: E(): 0, 57.9% id in 297 aa, and to Shigella flexneri dtdp-rhamnosyl transferase RfbF rfbF SW:RFBF_SHIFL (P37782) (296 aa) fasta scores: E(): 5.6e-08, 24.4% id in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MSANRVTKINGRKKILIVGAGLSGAVIAROLABOGHVUNIIDQR SHIGSNAYDARDEHTGIMVYVGGPHIEHTDNETVMNYVKYAEMMPYINKVKATVNGQ VFSLPINLHTINQFFGVACSPDDARKLILQKCOSTILEPQNEBOQALRFIGKELYEAF FKGYTIKQWGLHPSALPASULKRIPVERNYDDNYFNHKFGGIPKFGYTOMVKSIVEHE WIAVELCRSFTGEMRINYDHVFFSGALDAFYSCQYGRLEYRTLDFKKIIQSDYQGCA VMNYCSIDTPYTRITEHKYFSPWERHHDASICYQEYSRBCEAGDIPYYPVRRADKMDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="STY0761"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3/posyl transferases, score 12.60, E-value 0.013"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YLYFIWQGILHGLKGISGKYH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VQTVSFVGMIIDRKVLNNHLNDIYDELFLYYDDFFFGYKLVLSGQKIRYSPEIKFIHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="STY0760"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  () (367 aa) fasta scores: E(): 0, 38.3% id in 339 aa Paralogue of E. coli yeff (GLF_ECOLI); Fasta hit to GLF_ECOLI (367 aa), 39% identity in 340 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1426.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIHGRCICPEWKYYYLCRNLLLLRKLLPVPRIFSVLSIVLRLSKYLAILPWQRKKFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="STY0760"
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                                                                                                                                                            id in 467 aa, and to Mycobacterium tuberculosis hypothetical 33.9 kDa protein cyl3dl2.16 rv3782 or mtcyl3dl2.16 TR:772048 (EMBL:Z80343) (304 aa) fasta scores: E(): 0.16, 25.6% id in 215 aa, and to Klebsiella pneumoniae RfbE rfbE TR:048482 (EMBL:L41518) (297 aa) fasta scores: E(): 0.3, 23.6% id in 233 aa. This CDS contains at least one stop codon and frameshift. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /pseudo 5172. .6
/product="conserved hypothetical protein (pseudogene)" 7138. .7971
                                                  /codon_start=1
/transl_table=11
                                                                                                                                     sequence has been checked and is believed to be correct
                                                                                                                                                                                                                                                                                                                                                                              /note="Similar to Mycobacterium tuberculosis hypothetical 71.5 kDa protein rv3808c or mtv026.13C TR:053585 (EMBL:AL022076) (637 aa) fasta scores: E(): 0.00015, 26.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Pfam match to entry PF00005 ABC_tran, ABC transporter, score 110.90, E-value 2.5e-29" 4560. .4583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="PS00017 ATP/GTP-binding site motif A (P-loop)" 5172...6945
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/product="putative polysaccharide export ABC transporter
ATP-binding protein"
/protein_id="CAD05185.1"
/db_xref="GI:16501957"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="STY0765"
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MGWOGELTGLENIKLRGLFLGLSKNEIKNITEDVIEFSELGDFIKIPVRTYSSGMVLR
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/trans1ation="MKISCKNVGVILPIFNSSHRSEKKTELQAASGGRIGSSNTGIIE
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/gene="STY0762"
/note="Pfam match to entry PF01061 ABC2_membrane, ABC-2
+vne transporter, score 21.40, E-value 5.2e-07"
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/product="putative polysaccharide export ABC transporter
permease_protein (pseudogene)"
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/gene="STY0764"
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/gene="STY0762"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 ArgProlleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArgArgAlaGluLeu 170
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                                                                                                            cydB gene; cytochrome d terminal oxidase; pal gene; peptidoglycan-associated lipoprotein; tolA gene; TolA protein; tolB gene; TolB protein; tolQ gene; TolQ protein; tolR gene; TolR gene; TogC protein; ybgC gene; YbgC protein; ybgE gene; YbgE protein; YbgF;
                                                                                                                                                                                                                                                      ECH297885 6967 bp DNA linear BCT 12-OCT-2001 Erwinia chrysanthemi cydB gene (partial), ybgT gene, ybgE gene, ybgC gene, tolQ gene, tolR gene, tolA gene, tolB gene, pal gene and
                               Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                         Erwinia chrysanthemi
                                                                                                                                                                                               AJ297885.1 GI:16116629
                                                                          Erwinia chrysanthemi.
                                                                                             ybgF gene; ybgT gene; ybgT protein
                   Pectobacterium
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(bases 1 to 6967)
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/gene="STY0767"
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Lazzaroni,J.
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/trans1_table=11
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/protein_id="CAC82702.1"
/db_xref="GI:16116630"
                                                                                                                             /gene="tolQ"
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/gene="tolQ"
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/protein_id="CAC82703.1"
/db_xref="GI:16116631"
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925. .1329
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SLAVWQGMALIWAVCTGVVHGVGFRPQRMRWRAFFSPLPAFVILAAGLYYYFL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation="FNNHPVLWAVPLLGVVLPLMTAVMARAEKGAMAFLFSSLSIACV/
                                                                                                                                                                                                                                   /translation="MSNKVFRWDVRVYYEDTDAGGVVYHARYVAFYERARTEMLRAHD
CHQRVLMSEHVAFAVRKMAVEYLAPARLDDLLEVQSEIVVVRGASLTFVQRILDSHGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="ybgE"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                function="unknown"
                                                                                                                                                                                                                                                                                                                                /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /function="unknown"
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                                                                                                                                                                                                                LLSHAEVLVACIDSFQMKPIALPKSIVAEFKQ"
                                                                                                                                                                                                                                                                                                                                                                                           function="unknown, cytoplasmic protein"
                                                                                                              /function="outer membrane integrity"
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                                                                                                                                                                                               .2012
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mat_peptide
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TONYGTAWGGSGCACHT
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TONYGTAWGGAC
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                                                                                                  /gene="pal"
5234. .5740
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QGLOSVLQLVSTDGRFKARLPATDGQVRFPAMSPYM"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KGRTCTLRIRLAPDGLLVDVKSEGGDPALCQAAIAAAKQARIPKPPSSDVYEAFKQRT
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2025. .2450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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                                                                                                                                                                                       .5740
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CDS gene CDS

gene

CDS gene

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US-09-674-779B-2 (1-172) x ECH297885 (1-6967)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mat_peptide
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5516 TCCTACAAAGTGACTGTTGAAGGTCACGCGGACGAACGCGGTACGCCGGAATACAACATC 5575
                                                                                            5456 ATTCGCCCTGACTTCGCTCAGATGCTGGATGCGCACGCTGCTTTCCTGCGCAGCAACCCG 5515
                                                                                                                                                                                     5396 CTGCAGATGCAGGAACTGCAGCGCAACAATATCGTTTACTTCGATCTGGACAAATACGAC 5455
                                                                                                                                                                                                                                                                                                                                                                           5306 ------AACAAACACGCTAATAACGACCAGTCTTCCCTGAACGGCGGCGCTGGC 5353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5261 CTGATGTTGGCTCTGCCGGTGCTGGCTGTTGCCGCATGTAGCTCC------ 5305
                                                                                                                                                                                                                                                                                                5354 ATGGAAAAT--
                           79 IleLysProGlnAlaAlaAlaIleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGln 98
                                                                                                                                                                                                                                  61 AlaLeuAlaSerLysLeuPro-----SerLeuValTyrPheAspPheAspSerAspGlu 78
                                                                                                                                                                                                                                                                                                                                               41
                                                                                                                                                                                                                                                                                                                                                                                                                       21 ThrGlyCysAlaAsnLysSerThrSerGlnValMetValAlaProAsnAlaProThrGly 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MetMetLeuHisIleGlnIleAlaAlaAlaAlaAlaAlaLeuSerValLeuThrPheMet 20
                                                                                                                                                                                                                                                                                                                              TyrThrGlyValIleTyrThrGlyValAlaProLeuValAspAsnAspGluThrValLys 60
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1740 c 1992 g 15
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ASLVLEKKQYDQAIVAFQNFVKKYDDSTYQPWANYWLGQLFYNKGKKDDAAYYFANVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="peptidoglycan-associated lipoprotein" 5750. .6574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MQFNKVLKGLMLALPVLAVAACSSNKHANNDQSSLNGGAGMENGGNMSSAEQARLQMQELQRNNIVYFDLDKYDIRPDFAQMLDAHAAFLRSNPSYKVTVEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="pal"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /transl_table=11
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287.50
255.17%
37.36%
33.39%
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Matches:
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RESULT 12
AE005987/c
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5576 GCGCTGGGCGAACGTCGTGCCAACGCTGTGCAGATGTACCTGCAGGGCAAAGGCGTGTCT 5635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5696 GAAGCTGCATGGTCCAAAAACCGTCGTGCCGTTCTGGTATAC 5737
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nierman, W.C., Feldblyum, T.V., Laub, M.T., Paulsen, I.T., Nelson, K.E., Eisen, J., Heidelberg, J.F., Alley, M.R., Ohta, N., Maddock, J.R., Potocka, I., Nelson, W.C., Newton, A., Stephens, C., Phadke, N.D., Ely, B., DeBoy, R.T., Dodson, R.J., Durkin, A.S., Gwinn, M.L., Haft, D.H., Kolonay, J.F., Smit, J., Craven, M.B., Khouri, H., Shetty, J., Berry, K., Utterback, T., Tran, K., Wolf, A., Vamathevan, J., Ermolaeva, M., White, O., Salzberg, S.L., Venter, J.C., Shapiro, L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 10029)

Nierman,W.C., Feldblyum,T.V., Paulsen,I.T., Nelson,K.E., Eisen,J., Heidelberg,J.F., Alley,M.R.K., Ohta,N., Maddock,J.R., Potocka,I., Nelson,W.C., Newton,A., Stephens,C., Phadke,N.D., Ely,B., Nelson,W.C., DeBoy,R.T., Dodson,R.J., Durkin,A.S., Gwinn,M.L., Haft,D.H., Kolonay,J.F., Smit,J., Craven,M., Kbouri,H., Shetty,J., Berry,K., Utterback,T., Tran,K., Wolf,A., Vamathevan,J., Ermolaeva,M., White,O., Salzberg,S.L., Shapiro,L., Venter,J.C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caulobacter crescentus CB15. Caulobacter crescentus CB15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (31-JAN-2001) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete genome sequence of Caulobacter crescentus
Proc. Natl. Acad. Sci. U.S.A. 98 (7), 4136-4141 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11259647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SerLeuGlyGluArgArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGlyIleAsn 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(79. .1305)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(79. .1305)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Caulobacter crescentus CB15"
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                                                                                                                                           GVFEIDPAGAIRLPRDVVPAHLAAALLCASGAERPPRGDRLARLVERLRSGARFTATL
                                                                                                                                                                             VLRPLLTLTRAEIRDALTREGETWLDDPANLDLRYARARARAAGALTPLLPVRESPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="identified by Glimmer2; putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=J
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YAAFQAKDLLLAGDYANAEQAFAAYVNNYPESARTPEARYWLGETQFVREAYTDAAGN
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/gene="CC3228"
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complement(2228. .2794)
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NGQVTVGADGGLRVDFRLENDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLEQDLIGNLERSGLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(2991. .4289)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="identified by match to protein family HMM"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transl_table=11
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ARPAMGAATGLSAAALGRLQGEVQDRWNPNCEVEGGSNVNVRVVTIGPGGRVVGQPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FREGPSGNPRLWTVDITGRILRPAAYSGSASDPAWSPLLD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RSRATTRITTDPAIDTSDSESPDGTKIVFNSDRGGQAQIYVMNTDGSGVRRISYGGGR
YTTPVWSPRGDFIAFTKQTGGEFHIGVNRADGGDERLLTTSYLDEGPTWAPNGRVLMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALRPTGSSIYLLNLETSRQETVGKFPGMVFAPRFSPDGSKVAFSVERNGNSDIYVMDL
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                                                                                                                                                                                                                                                                                                                                                                                     SPGTSSPDPVVKAASDRAIRALFAASPFAYLPSDLYGQKIALNFNAKQACSR*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="CC3231"
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                                                                                                                                                                                                                                      /gene="CC3232"
                                                                                                                                                                                                                                                                           complement (5139.
                                                                                                                                                                                                                                                                                                                 /gene="CC3232"
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                                                                                                                                                                          GPVGVETIAYAIAEARDAVEDVIEPYLMQQGFIQRTPRGRMACGKAYLHLGLTPPAAP
                                                                                                                                                                                                    RVAGRLLRRVRDFATADGADRIDRKAAAMALARLEVDESGLDSLDRRYLRAMIENYGG
                                                                                                                                                                                                                             AAKGRGEALDHVLLFGPPGLGKTTLAQIVARELGVNFRATSGPVLNKPGDLAAILTNL
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                                                                                                                                                                        PGQAQGALFDEG'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MKASSMRLIRLLTAGLAAVGLAVSLAAISAAGAPRNALIVQALAAGLAYGLALLVGWFWRRARWRLWVLMAACGLALVLTLMNGVSLEGAKRWVALGPVQLHTASIVLPFAAFAFARGFGDRRVAPIAALIALLLLLYQHDAASSLAWALALAAAALVERPRQAIPWACVAIAGLLAYGAWVEPDTLPAVPYVEGLLDQTFAANPVLGVLAGVLMISLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="identified by match to TIGR protein family HMM
TIGR00635"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APFILVARARPERRAEALALAALWTGWIAGNLFGNYPAPVLGYGAAPILAWGLSLGLV
LGDSVDQDPPAP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="hypothetical protein"
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complement(6915. .7781)
/gene="CC3235"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="CC3236"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MIEPTAGVFEGREHQLPVRIYYEDTDFTGIVYHANYLRYLERGR
SDFFRAVGISHTELAKQDTGFAVIRMELDFKRAARIDDALLVRTLFERAEGVRLHVRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="conserved hypothetical protein"
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/db_xref="GI:13424918"
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           7.38e-20
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58.24%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="MotA/TolQ/ExbB proton channel family protein"
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/db_xref="GI:13424917"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="identified by match to protein family HMM"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
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Conservative:
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ORGANISM
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                                                                                                                                                                        TITLE
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                                                                                                                                                   JOURNAL
                                                                                                                                                                                           AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2533 TACGTCATTCGCGCCGACGCCCAACCGGTGCTGGCCGGTCAGGCCCAGTGGCTGAACCGC 2474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2593 GGTTCGGTGCAGGACTTTGTCGTCAATATCGGCGACCGGGTCTATTTCGACACCGACGAA 2534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2638 TACACGCCGCCGCCCCCCCCGCCGGTGACCAGCGGTATCCTGCCC--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157 ThrAsnGluGluAlaTrpSerGlnAsnArg 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                137 IleAsnGlnAlaSerValGluIleIleSerPheGlyGluGluArgProIleAlaPheGly 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 AsnMetSerLeuGlyGluArgArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGly 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2698 CCGAAGCCCCAGCCCGTCACGCCGCCGCCCGCTCAGCCGCAGCCGACCCAACCGACGCCT
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Submitted (05-DEG-2001) Genoscope and CNRS UMR-8030, 2 rue Gaston Cremieux, CP5706, 91057 Evry Cedex, France, Laboratoire de Biologie Moleculaire des Interactions Plantes-Microorganismes INRA-CNRS, BP27, 31326 Castanet-Tolosan Cedex, France, Fondation Jean Dausset-CEPH, 27 rue Juliette Dodu, 75010 Paris, France, LMGM CNRS 118 Route de Narbonne, F 31062 Toulouse Cedex 4, Genoscope and INRA URGV, 2 rue Gaston Cremieux, CP5706, 91057 Evry Cedex, France,
                                                                                                                                                                                                                                                                            Salanoubat,M., Genin,S., Artiguenave,F., Gouzy,J., Mangenot,S., Arlat,M., Billault,A., Brottier,P., Camus,J.C., Cattolico,L., Chandler,M., Choisne,N., Claudel-Renard,C., Cunnac,S., Demange,N., Gaspin,C., Lavie,M., Moisan,A., Robert,C., Saurin,W., Schiex,T., Siguier,P., Thebault,P., Mangel,M., Wincker,P., Levy,M.,
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                                                                                                                                                                    Direct Submission
                                                                                                                                                                                           Boucher, C.A
                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                         Weissenbach, J. and Boucher, C.A. Genome sequence of the plant pathogen Raistonia solanacearum
                                                                                                                                                                                                                                                                                                                                                                                                                                Ralstonia solanacearum
Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 GluThrValLysAlaLeuAlaSerLysLeuProSerLeuValTyrPheAspPheAspSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 TyrThr------GlyValIleTyrThrGlyValAlaProLeuValAspAsnAsp 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27 SerThrSerGlnValMetValAlaProAsnAla-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ralstonia solanacearum GMI1000 chromosome, complete sequence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AL646060 AL646052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ralstonia solanacearum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    segment 4/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL646060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 IleAlaAlaAlaAlaAlaAlaLeuSerValLeuThrPheMetThrGlyCysAlaAsnLys 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AACCTGGCTCTGGGCGCCGCCGCCCAACGCCGTGCGCGACTTCCTGATCGCCCAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AspGluIleLysProGlnAlaAlaAlaIleLeuAspGluGlnAlaGlnPheLeuThrThr 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AsnGlnThrAlaArgValLeuValAlaGlyHisThrAspGluArgGlySerArgGluTyr 116
                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 212050)
                                                                                                                                                                                                             bases
                                                                                                                                                                                                           1 to 212050)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GI:17427566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38.24%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------GCCTGCGCTTCGCGT 2699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50
21
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
                                                                                                                                                                                                                                                                                                                                                                                                              gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://sequence.toulouse.inra.fr/R.solanacearum.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INRA, BP27, r31326 Castanet-Tolosan Cedex
Christian.Boucher@toulouse.inra.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratoire de Biometrie et Intelligence Artificielle INRA, BP27, F31326 Castanet Tolosan Cedex. Laboratoire de Genetique Cellulaire
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="RS04909"
59. .757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Ralstonia solanacearum"
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/db_xref="GI:17427567"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       predicted by Homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             predicted by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene name confidence : hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /function="miscellaneous; hypothetical/global homology"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLVALMVRLPLIVTLAAALLGYLAGDMLVTDPVDAGWFMQAIPYADVAIGCLGALIVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HDGLWPAIRTILIADLVMSLDNVVAVAAAAEKGPPGTDVALLVLGLGLSIPLIIFGST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              predicted by FrameD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="RSc0556"
                                                                                                                                                                                                                                                                                                                  1739. .2245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              predicted by Homology predicted by FrameD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         structures"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="pilAl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IVGWWMGRRSLRQA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=
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structures"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               predicted by Codon_usage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="pilA1"
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/function="miscellaneous; hypothetical/global homology" /note="product confidence: hypothetical gene name confidence: hypothetical predicted by Codon_usage predicted by FrameD"
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/gene="RSc0559"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KYAPAECR"
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/note-"RS00560; RS04905"
complement(4289. .4765)
/gene-"moaC"
/function-"small molecule metabolism; biosynthesis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(4289. .4765)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="HYPOTHETICAL TRANSMEMBRANE PROTEIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="RSc0559"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cofactors, carriers; molybdopterin"
/note="Product confidence : probabl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                predicted by Codon_usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene name confidence : probable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALAFQGKTDEALTQVRRLHNQYWIDYAGDSKLLTLVCTKKLEGLATFCARLKAENLVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="moac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="PROBABLE MOLYBDENUM COFACTOR BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                       Gene name confidence : hypothetical
                                                                                                                                                                                                                                                                                                                                         /note="Product confidence :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              by Homology
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                                                                                                                                                                                                                                                                                                                                                    hypothetical
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US-09-674-779B-2 (1-172) x AL646060 (1-212050)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
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182482 GCACAGAACCGCCGCTCCGATATCGTCTAC 182511
                                                                                                                                                                                       182362 AAGCGTGCCGAGGCCGTGCGCCGCGCGCTGTCCTCGCTGGGCGTGCCCGACAGCCAGATG 182421
                                                                                                                                                                                                                                                                                        182302 CTGATCCAGGGCAACACCGACGAGCGCGCGCACCAGCGAGTACAACCTGGCGCTGGGCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182122 GCCGACACCCGCAACGTGACGCCCGTCGACGTGAGCCGCGATGAACTGACCGATCCGAAC 182181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182077 CTGGATGACACCTCGAAG-------AACGCCACGGGTGGTGCCGCCGCCGGGT 182121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182017 ATCAAGCTGGCGGCGATTGCCGCGCTGCTGGCGCTTGGGGCGCTTGCAGCTCGGGTGTGAAG 182076
                                               163 SerGlnAsnArgArgAlaGluLeuSerTyr 172
                                                                                                                                     143 GluIleIleSerPheGlyGluGluArgProIleAlaPheGlyThrAsnGluGluAlaTrp 162
                                                                                                                                                                                                                                                                                                                                                                  103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 AlaSerLysLeuProSerLeuValTyrPheAspPheAspSerAspGluIleLysProGln 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44 ValileTyrThrGlyValAlaProLeu---ValAspAsnAspGluThrValLysAlaLeu 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 IleGlnIleAlaAlaAlaAlaAlaAlaLeuSerValLeuThrPheMetThrGlyCysAla 24
                                                                                         GAATCCGTGAGCCTGGGCAAGGAAAAGCCGCAGGCCTCGGGCCACGACGAGGAGTCGTGG 182481
                                                                                                                                                                                                                                       ArgArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSerVal 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                      AlaAlaAlaIleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgVal 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AsnLysSerThrSerGlnValMetValAlaProAsnAlaProThrGly---TyrThrGly 43
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LGMLFWGDRTFDIOPIRSDEAERRFGFVRHPAALA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(7139. .8254)
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QALLEARRLYCNIPGLTSGSPSLDVTAIELARARNRVPEBALTMARAALAAYPLSRAVG
ITYAQTLLAAGBAGDAIPYLQDKAREDTAQPIWWDMLARAYADQGKRVEQHRALAEKY
ARDGAWGAAVEQLKLARDAGDADFYTLSEVDARLHQMERQYRBEKQEEKALPK"
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/gene="RSc0562"
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                                                                                                             136 ATGCAACTGAACAAAGTGCTGAAAGGGCTGATGATTGCTCTGCCTGTTATGGCCAATTGCG 195
41 TyrThrGlyVallleTyrThrGlyValAlaProLeuValAspAsnAspGluThrValLys 60
                                                                        21 ThrGlyCysAlaAsnLysSerThrSerGlnValMetValAlaProAsnAlaProThrGly 40
                                                                                                                                                1 MetMetLeuHisIleGlnIleAlaAlaAlaAlaAlaAlaLeuSerValLeuThrPheMet 20
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terminator"
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/translation="MOLNKVLKCLMIALPVMAIAACSSNKNASNDGSEGMLGAGTGMD
/TGGNGLMSSEEQARLQMQLQQNNIVYFDLDKTDIRSDFAQMLDAHANFLRSNPSYK
VTVEGHADERGTPEYNISLGERRANAVKMYLQGKGVSADQISIVSYGKEKPAVLGHDE
AAYSKNRRAVLVY"
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/protein_id="CAA28771.1"
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Lazzaroni, J.C. and Portalier, R.
Lazzaroni, J.C. and Portalier, R.
The excC gene of Escherichia coli K-12 required for cell envelope integrity encodes the peptidoglycan-associated lipoprotein (PAL) Mol. Microbiol. 6 (6), 735-742 (1992)
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Submitted (04-JUN-1992) J. Lazzaroni, Lab de Microbiologie et Submitted (04-JUN-1992) J. Lazzaroni, Lab de Microbiologie et Genetique Moleculaire, UMR 106, CNRS, Bat 405, University Claude Bernard Lyon I, F-69622 Villeurbanne Cedex, FRANCE
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Lazzaroni, J.
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3 (bases 1 to 1531)
Lazzaroni, J.C.
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                   /translation="GQVKFPAWSPYL"
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/prottain_id="CAA46672.1"
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/db_xref="SWISS-PROT:P19935"
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                                                                                                                                                                                                                                                                                                                      431 TCCCTGGGTGAACGTCGTGCGAACGCCGTTAAGATGTACCTGCAGGGTAAAGGCGTTTCT
                                                                                                                                                                                                                                                                                                                                                                                           371 TCTTACAAAGTCACCGTAGAAGGTCACGCGGACGAACGTGGTACTCCGGAATACAACATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   311 ATCCGTTCTGACTTCGCTCAAATGCTGGATGCACATGCAAACTTCCTGCGTAGCAACCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251 CTGCAAATGCAACAGCTGCAGCAGAACAACATCGTTTACTTCGATCTGGACAAGTACGAT 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 ATGCAACTGAACAAAGTGCTGAAAGGGCTGATGATTGCTCTGCCTGTTATGGCAATTGCG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 TyrThrGlyValIleTyrThrGlyValAlaProLeuValAspAsnAspGluThrValLys 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 ThrGlyCysAlaAsnLysSerThrSerGlnValMetValAlaProAsnAlaProThrGly 40
                                                                                                                                                                               551
                                                                                                                                                                                                                                                                                                                                                                                                                             99 ThralaargValLeuValAlaGlyHisThraspGluArgGlySerArgGluTyrAsnMet 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79 IleLysProGlnAlaAlaAlaIleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGln 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 AlaLeuAlaSerLysLeuPro-----SerLeuValTyrPheAspPheAspSerAspGlu 78
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                                  genome.
AE000177 U00096
AE000177.1 GI:1786955
                                                                                     Escherichia coli K12 MG1655 section
                                                                                                        AE000177
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                                                                                                                                                                             GluGluAlaTrpSerGlnAsnArgArgAlaGluLeuSerTyr 172
                                                                                                                                                                                                                                                 GCAGACCAGATCTCCATCGTTTCTTACGGTAAAGAAAAACCTGCAGTACTGGGTCATGAC
                                                                                                                                                                                                                                                                                                                                           SerLeuGlyGluArgArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGlyIleAsn 138
                                                                                                                                                                                                                                                                                    GlnAlaSerValGluIleIleSerPheGlyGluGluArgProIleAlaPheGlyThrAsn 158
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AL Submitted (13-0CT-1998) Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.

This sequence was determined by the E. coli Genome Project at the University of Wisconsin-Madison (Frederick R. Blattner, director). From the Misconsin-Madison (Frederick R. Blattner, director). The entire sequence was independently roject and NCHGR). The entire sequence was independently frames were determined using GeneMark software, kindly supplied by Mark Borodovsky, Georgia Institute of Technology, Atlanta, GA, 3032 [e-mail: mark@amber.gatech.edu]. Open reading frames that have been correlated with genetic loci are being annotated with CG Site Nos., unique ID nos. for the genes in the E. coli Genetic Stock Center (GGSC) database at Yale University, kindly supplied by Correlating it with other data. Comments to the genome is an ongoing task whose goal is to make the genome sequence more useful by correlating it with other data. Comments to the authors are Genome Project's World Wide Web site (http://www.genetics.wisc.edu). *** The E. coli K12 sequence and its annotations are periodically undated: this is version MSA No.
                                                                                                                                                                                                                                                                                                                                                                                                                       its annotations are periodically updated; this is version M54. No sequence changes. Annotation updates: updated gene identifications and products; all new functional assignments courtesy of Monica Riley; added promoters, protein binding sites, and repeated sequences described in reference 1. The unique numeric identifiers beginning with a lowercase 'b' assigned to each gene (protein or RNA-encoding) are now designated as gene synonyms instead of
                                                                                                                                                                                                                                                                                                                                                                                                   names
                                                                                                                                                                                                                                                                                                                                                                                                      labels. This should allow them to be searched for in Entrez as gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 (bases 1 to 10693)
Plunkett, G. III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (02-SEP-1997) Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (16-JAN-1997) Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                   /function="orf; Unknown"
                                                                                                                                                                                                                                 /db_xref="taxon:83333"
                                                                                                                                                                                                                                                             /sub_strain="MG1655"
                                                                                                                                                                                                                                                                                                          /organism="Escherichia coli K12"
                                                  /gene="ybgE"
                                                                                                    note="b0735"
                                                                                                                             /gene="ybgE"
                                                                                                                                                                       /note="factor Sigma70; predicted +1 start at 773447"
                                                                                                                                                                                                                                                                                         /strain="Kl
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                           /note="b0739"
2127. .3392
/gene="tolA"
                                                                              /gene="tolA"
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/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="tolR"
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/function="orf;
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                                                                                                                   /product="putative inner membrane protein, involved in the tonB-independent uptake of group A colicins" /protein_ide"AAC/73832.1" /db_xref="GI:1786959"
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/db_xref="G1:178958"
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/note="0142; 100 pct identical to TOLK_ECOLI SW: p05829"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QATLQMVAPGIAEALIATAIGLFAAIPAVMAYNRLNQRVNKLELNYDNFMEEFTAILH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="inner membrane protein, membrane-spanning,
maintains integrity of cell envelope; tolerance to group A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /function="membrane; Colicin-related functions" /note="0230; 100 pct identical to TOLO_ECOLI SW: P05828; alternate gene name fil"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FSQQALMAERVAFVVRKMTVEYYAPARLDDMLEIQTEITSMRGTSLVFTQRIVNÄENT
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/protein_id="AAC73830.1"
/db_xref="GI:1786957"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELEIWHGLLLMWAVCAGVIHGVGFRPQKVLWQGIFCPLLADIVLIVGLIFFFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="factor Sigma70; predicted +1 start at 774366"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation="MNTTLFRWPVRVYYEDTDAGGVVYHASYVAFYERARTEMLRHHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  factor Sigma70; predicted +1 start at 773933"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pct identical to YBGC_ECOLI SW: P08999; GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P37343; 42
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                              US-09-674-779B-2 (1-172) x AE000177 (1-10693)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        promoter
                                                                   4972 ---ACTGGTATGGATGCGAACGGCGAACGGCAACATGTCTTCCGAAGAGCAGGCTCGT 5028
                                                                                                                                                                        4912 GCATGTTCTTCCAACAAGAACGCCAGCAATGACGGCAGCGAAGGCATGCTGGGTGCCGGC 4971
                                                                                                                                                                                                                                                                         4852 ATGCAACTGAACAAAGTGCTGAAAGGGCTGATGATTGCTCTGCCTGTTATGGCAATTGCG 4911
                                                                                                                 41 TyrThrGlyValIleTyrThrGlyValAlaProLeuValAspAsnAspGluThrValLys 60
                                                                                                                                                                                                                      {\tt 21~ThrGlyCysAlaAsnLysSerThrSerGlnValMetValAlaProAsnAlaProThrGly~40}
                     61
                                                                                                                                                                                                                                                                                                                                μ
                                                                                                                                                                                                                                                                                                                          MetMetLeuHisIleGlnIleAlaAlaAlaAlaAlaLeuSerValLeuThrPheMet 20
             AlaLeuAlaSerLysLeuPro-----SerLeuValTyrPheAspPheAspSerAspGlu 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="mskateqndklkraiiisavlhvilfaaliwssfdenieasagg
gggssidavmvdsgavveqykrmqsqessakrsdeqrkmkeqqaaeelrekqaaeqer
lkqlekerlaaqeqkkqaeeaakqaelkqkqaeeaakkaaadakakababakaaeeaa
kkaaadakkkaeaeaakaaaeaqkkaebaaaalkkkaeaaeaaaaaaarkkaateaaek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               membrane integrity"
/protein_id="AAC73833.1"
/db_xref="GI:1786960"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alternate gene names cim, excC, lky"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MKQALRVAFGFLILWASVLHAEVRIVIDSGVDSGRPIGVVPFQW
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GAFRIRIAYVVQTNGGQFPYELRVSDVDGYNQFVVHRSPQPLMSPAWSPDGSKLAYVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AKAEAEKKAAAEKAAADKKAAAEKAAADKKAAEKAAAEKAAAEKAAADKKAAAEKAAADKKAA
AAKAAAEKAAAAKAAAEADDIFGELSSGKNAEKTGGGAKGNNASPAGSGNTKNNGASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transl_table=11/
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/note="0421; 100 pct identical to TOLA_ECOLI SW: P19934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGQIRQVTDGRSNNTEPTWFPDSQNLAFTSDQAGRPQVYKVNINGGAPQRITWEGSQN
QDADVSSDGKFMVMVSSNGGQQHIAKQDLATGGVQVLSSTFLDETPSLAFNGTMVIYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="periplasmic protein involved in the tonb independent uptake of group A colicins" /protein_id="AAC73834.1" /db_xref="GI:1786961"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAKLAKIPKPPSQAVYEVFKNAPLDFKP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          \mathtt{ADINNYAGQIKSAIESKFYDASSYAGKTCTLRIKLAPDGMLLDIKPEGGDPALCQAAL}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="membrane spanning protein, required for outer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSQGMGSVLNLVSTDGRFKARLPATDGQVKFPAWSPYL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FESGRSALVIQTLANGAVRQVASFPRHNGAPAFSPDGSKLAFALSKTGSLNLYVMDLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /function="factor; Colicin-related functions" /note="0430; 99.8 pct identical to TOLB_ECOLI SW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="tolB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3525. .4817
/gene="tolB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="b0740"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4789. .4816
/gene="tolB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="tolB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="factor Sigma70; predicted +1 start at 778261"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="factor Sigma70; predicted +1 start
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="b0741"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="pal"
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285.50
56.90%
38.51%
33.16%
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Matches:
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at 778139"
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
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                                                                                                                                                                                        gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5029 CTGCAAATGCAACAGCTGCAGCAGAACAACATCGTTTACTTCGATCTGGACAAGTACGAT 5088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5269 GCAGACCAGATCTCCATCGTTTCTTACGGTAAAGAAAAACCTGCAGTACTGGGTCATGAC 5328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5149 TCTTACAAAGTCACCGTAGAAGGTCACGCGGACGACGTGGTACTCCCGGAATACAACATC 5208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5329 GAAGCGGCATACTCCAAAAACCGTCGTGCGGTACTGGTTTAC 5370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      159 GluGluAlaTrpSerGlnAsnArgArgAlaGluLeuSerTyr 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 SerLeuGlyGluArgArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGlyIleAsn 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79 IleLysProGlnAlaAlaAlaIleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Rose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Posfai, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L., Grotbeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Welch, R.A. and Blattner, F.R.

Welch, R.A. and Blattner, F.R.

Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7

Nature 409 (6819), 529-533 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli 0157:H7 EDL933.
Escherichia coli 0157:H7 EDL933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (22-OCT-2000) Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlnAlaSerValGluIleIleSerPheGlyGluGluArgProIleAlaPheGlyThrAsn 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCCCTGGGTGAACGTCGTGCGAACGCCGTTAAGATGTACCTGCAGGGTAAAGGCGTTTCT 5268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ThralaargValLeuValAlaGlyHisThrAspGluArgGlySerArgGluTyrAsnMet 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 11670)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 11670)
                                                                                                                                                                                        /note="0-island #35; Region of the EDL933 chromosome not homologous to E. coli K-12 MG1655" complement(93. .260)
                                                                                                                                    complement (93. .260)
                                                                                                                                                                                                                                                                                            /note="enterohemorrhagic"
                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:155864"
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                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Escherichia coli 0157:H7 EDL933"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
          /transl_table=11
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/note="No significant matches"
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                                                                                                               /gene="20896"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GI:12513661
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H7 EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA linear BCT 21-MAR-2001 genome, contig 1 of 3, section 76
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CDS

gene

οy

Score Pred. No.:

gene

CDS

Qy

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PROTEIN Id="AAG55069.1"

/ Ab_xref="GI:12513666"

/ Ab_xref="GI:12513666"

/ translation="mmldivelsrlofaltamyhelevoltigmafilaimetvyvls

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MAFFLESTFYGLFFFGWRLGKVOHMCYTWLVALGSULSALWILVANGWONPIASDF

METMRUSMYSFSELVLMPVAOVKFVHTVASGYVTGAMFILGISAWYMLKGRDEAFAK

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GSTDQAVRDQPNSMKKDLGYGLLLKRYTPNVADATEAQLQQATKDSIFPVAPLYEAFR

GSTDQAVRDQPNSMKKDLGYGLLLKRYTPNVADATEAQLQQATKDSIFPVAPLYEAFR

GSTDQAVRDQPNSMKKDLGYGLLLKRYTPNVADATEAQLQQATKDSIFPVAPLYEAFR

GMAIGEVLPTAVANGSLTAGDLIFSMVLICGLYTLFLVAELFLMFKFARLGPSSLKTG
/gene="cydB"
/note="Z0901" .
                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Residues 1 to 523 of 523 are 100.00 pct identical to residues 1 to 523 of 523 from Escherichia coli K-12 Strain MG1655: B0733"
                                                                                                                                                                                                                                                                                                                                                                      /product="cytochrome d terminal oxidase, polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transl_table=11
/protein_id="AAG55068.1"
/db_xref="GI:12513665"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MSPDNIGSAVNRFSGWPSNDSLKTDKESMTSPVTVQVIKMIAAI LDPHRIVVGIDTLYTTQRETFTSESQOLIESALOTLKYMLNNLETNRDEESHYLAFE YNVDTSDRITYSAYNEKKPGCYGQCLVIQDDETDLFNLIKIKIFEARHNYVAQLMSDP EFMFKFSYSAQQNRLEPHLLVPAYFPLKTNEPVTQEDVLLLYRFFKMNDDFNKLTSDE YMSILTPLMKCERSVHDNNRYVTGKDTLLLDYPPSGNQIHFHVFPDESATLVLYFSNN
                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /function="enzyme; Energy metabolism, carbon: Electron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="cydA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="cydA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="Z0899"
/function="orf; Unknown function"
/note="No significant matches"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DIECFVFERDIPSQYRFFKMFTNLALVIDQLTEANKIL
COMPLEMENT (2077. . 2118)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MSTDRKPVMLLFH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="Z0899"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="20900"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /transl_table=11
/protein_id="AAG55067.1"
/db_xref="GI:12513664"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(958. .1902)
/gene="Z0898"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(958. .1902)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VIFSILSSLIDSAISKFQHQIPVNGSVNRELLYEDYTD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="AAG55066.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               function="orf; Unknown function"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="Z0898"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSRCLASIHPTLAKNIYETENLSDQKLLHIDCRSTNEIKINIFFGQQREGLIEINSDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(454. .876)
/gene="Z0897"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="No significant matches"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="Z0897"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MNCSEIRLKSYEMHLLMAKTTSQKCKLEVDHNYLNTLNQVNFKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AAG55065.1"
/db_xref="GI:12513662"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             function="orf; Unknown function"
                                                .5431
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                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
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                                                                                                                                                                                                                                                                                                                                6403. .7095
/gene="tolQ"
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                                                                                                                                                                                                                                                                                                                                                                                                       /gene="tolQ"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="ybgC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="Z0904"
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/note="Z0903"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="ybgE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transl_table=11
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/translation="MTDMNILDLFLKASLLVKLIMLILIGESIASWAIIIQRTRILNA
AAREAEAFEDKEWSGIELSRLYQESQGKRDNLTGSEQIFYSGEKEFVRLHRANSHAPE
AVVEGASRAMRISMNRELENLETHIPFLGTVGSISPYIGLFGTVWGIMHAFIALGAVK
QATLQMVAPGIAEALIATAIGLFAAIPAVMAYNRLNQRVNKLELNYDNFMEEFTAILH
                                                                                                                                                                                                                                                                                                                                                                 /_uuction="membrane; Colicin-related functions" /note="Residues 1 to 230 of 230 are 100.00 pct identical to residues 1 to 230 of 230 from Escherichia coli K-12 Strain MG155; B0737"
                                                                                                                                                                                                            maintains integrity of colicins"
                                                                                                                                              /protein_id="AAG55073.1"
/db_xref="GI:12513670"
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/function="orf; Unknown function"
/function="Residues 1 to 134 of 134 are 100.00 pct identical
to residues 1 to 134 of 134 from Escherichia coli K-12
Strain MG1655; B0736"
                                                                                                                                                                                                                                                             /product="inner membrane protein, membrane-spanning,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FSQQALMAERVAFVVRKMTVEYYAPARLDDMLEIQTBITSMRGTSLVFTQRIVNAENT
LLNEAEVLVVCVDPLKMKPRALPKSIVAEFKQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  translation="MNTTLFRWPVRVYYEDTDAGGVVYHASYVAFYERARTEMLRHHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="orf, hypothetical protein"
/protein_id="AAG55072.1"
/db_xref="GI:12513669"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELEIWHGLLLMWAVCAGVIHGVGFRPQKVLWQGIFCPLLADIVLIVGLIFFFF"
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ERRIMINSIAFHDGNOVMLITAGGALFAAWPMVYAAAFSGFYVAMILVLASLFFRPV
GEDYRSKIEETRWRNMDWGIFIGSFVUPLVIGVAFGRLLQGVPFNVDEYLRLYYTGN
FFQLLNFFGLLAGVVSVGMITTGGATVLQMRTVGELHLRTRATAQVAALVTLVCFALA
GVWVMGIDGYVVKSTMDHYAASNPLMKEVVREAGAWLVNFNNTPILMAIPALGVVLD
LTILTARMDKAAWAFVFSSLTLACIILTAGIAMFPVMPSSTMMNASLTMMDATSSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MSKITATLYAVMDKRPLRALSFVMALLLAGCMFWDPSRFAAKTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="orf, hypothetical protein"
/protein_id="AAG55071.1"
/db_xref="GI:12513668"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /function="orf; Unknown function"
/note="Residues 1 to 97 of 97 are 100.00 pct identical to residues 1 to 97 of 97 from Escherichia coli K-12 Strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LTLNVMTWVAVVLVPIILLYTAWCYWKMFGRITKEDIERNTHSLY"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="AAG55070.1"
/db_xref="GI:12513667"
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/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /function="enzyme; Energy metabolism, carbon: Electron
transport"
                                                                                                                                                                                                                                               cell
                                                                                                                                                                                                                              envelope; tolerance to group A
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match:
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                                                                                                                                                                                                                                  REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COCUE
                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10236 ATGCAACTGAACAAGTGCTGAAAGGGCTGATGATTGCTCTGCCTGTTATGGCAATTGCG 10295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10296 GCATGTTCTTCCAACAAGAACGCCAGCAATGACGGCAGCGAAGGCATGCTGGGTGCCGGC 10355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10473 ATCCGTTCTGACTTCGCTCAAATGCTGGATGCACATGCAAACTTCCTGCGTAGCAACCCC 10532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10413 CTGCAAATGCAACAGCTGCAGCAGAACAACATCGTTTACTTCGATCTGGACAAGTACGAT 10472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10356 ---ACTGGTATGGATGCGAACGGCGAACGGCAACATGTCTTCCGAAGAGCAGCTCGT 10412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10533 TCTTACAAAGTCACCGTAGAAGGTCACGCGGACGAACGTGGTACTCCGGAATACAACATC 10592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10713 GAAGCGGCATACTCCAAAAACCGTCGTGCGGTACTGGTTTAC 10754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10653 GCAGACCAGATCTCCATCGTTTCTTACGGTAAAGAAAACCTGCAGTACTGGGTCATGAC 10712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10593 TCCCTGGGTGAACGTCGTGCGAACGCCGTTAAGATGTACCTGCAGGGTAAAGGCCTTTCT 10652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   159 GluGluAlaTrpSerGlnAsnArgArgAlaGluLeuSerTyr 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139 GlnAlaSerValGluIleIleSerPheGlyGluGluArgProIleAlaPheGlyThrAsn 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 TyrThrGlyValIleTyrThrGlyValAlaProLeuValAspAsnAspGluThrValLys 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99 ThrAlaArgValLeuValAlaGlyHisThrAspGluArgGlySerArgGluTyrAsnMet 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79 IleLysProGlnAlaAlaAlaIleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGln 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 AlaLeuAlaSerLysLeuPro-----SerLeuValTyrPheAspPheAspSerAspGlu 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 ThrGlyCysAlaAsnLysSerThrSerGlnValMetValAlaProAsnAlaProThrGly 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MetMetLeuHisIleGlnIleAlaAlaAlaAlaAlaAlaLeuSerValLeuThrPheMet 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli genomic DNA.
D90713 AB001340
D90713.1 GI:1651326
                 Oshima, T., Alba, H., Baba, T., Fujita, K., Hayashi, K., Honjo, A., Ikemoto, K., Inada, T., Itoh, T., Kajihara, M., Kanai, K., Kashimoto, K., Kimura, S., Kitagawa, M., Makino, K., Masuda, S., Miki, T., Mizobuchi, K., Mori, H., Motomura, K., Nakamura, Y., Nashimoto, H., Mizobuchi, K., Mori, H., Motomura, K., Nakamura, Y., Nashimoto, H., Nishio, Y., Saito, N., Sampei, G., Seki, Y., Tagami, H., Takemoto, K., Wada, C., Yanamoto, Y., Yano, M. and Horiuchi, T., Wada, C., Yanamoto, Y., Yano, M. and Horiuchi, T., Wada, C., Yanamoto, Y., Yano, M. and Horiuchi, T., Wada, C., Yanamoto, Y., Yano, M. and Horiuchi, T., Wada, C., Yanamoto, Y., Yano, M. and Horiuchi, T., Wada, C., Yanamoto, Y., Yano, M. and Horiuchi, T., Wada, C., Yanamoto, Y., Yano, M. and Horiuchi, T., Waland, C., Yanamoto, Y., Yano, M. and Horiuchi, T., Waland, Y., Waland, Y., Waland, Y., Yano, M. and Horiuchi, T., Waland, Y., Waland, Y., Yano, M. and Horiuchi, T., Waland, Y., Waland, Y., Yano, M., Waland, Y., Yano, M., Waland, Y., Waland, Y., Yano, M., Waland, Y., Waland, Y., Yano, W., Yano, W.,
                                                                                                                                                                                                                                                                                                                                                                                                 Complete and shotgun sequencing; hrsa; ybgB; cydA; cydl; cyd2; ybgE; ybgC; tolQ; fii; tolR; tolA; cim; excC; lky; ybgF; nadA; nicA; pnuC.
                                                                                                                                                                                                                                                                                                                                Escherichia coli(strain:K12) DNA, clone:Kohara clone #178.
Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D90713
                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Wada,C., Yamamoto,Y., Yano,M. and Horrichia.
A 718-kb DNA sequence of the Escherichia coli K-12 genome
                                                                                                                                                                                                                                                                          Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerLeuGlyGluArgArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGlyIleAsn 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="tolR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ROAFTVSESNKG"
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56.90%
38.51%
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ic DNA. (16.5 - 16.9 min).
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene
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Alba,H., Baba,T., Fujita,K., Hayashi,K., Honjo,A., Horiuchi,T., Ikemoto,K., Inada,T., Isono,K., Isono,S., Itoh,T., Kanai,K., Kasai,H., Kashimoto,K., Kim,S., Kimura,S., Kitagawa,M., Kitakawa,M., Makino,K., Masuda,S., Miki,T., Mizobuchi,K., Mori,H., Motomura,K., Nakamura,Y., Nashimoto,H., Nishio,Y., Oshima,T., Saito,N., Sampei,G., Seki,Y., Tagami,H., Takemoto,K., Wada,C., Yamamoto,Y. and Yano,M.

The systematic sequencing of the Escherichia coli genome in Japan Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (18-MAY-1996) Hirotada Mori, NARA Institute of Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and Technology, Res. & Edu. Center 1
Takayama, Ikoma, Nara 630-01, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Collaboration Information:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (E-mail:hmori@gtc.aist-nara.ac.jp, Tel:81-7437-2-5660,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kimura, S., Kitagawa, M., Kitakawa, M., Makino, K., Masuda, S., Miki, T., Mizobuchi, K., Mori, H., Motomura, K., Nakamura, Y., Nashimoto, H., Nishio, Y., Oshima, T., Saito, N., Sampei, G., Seki, Y., Tagami, H., Takemoto, K., Wada, C., Yanamoto, Y. and Yano, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The Japan E. coli genome DNA sequencing group
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Information operator:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Address: National Institute of Basic Biology, Okazaki, 444, Japan E-mail: kishori@nibb.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Address: NARA Institute of Science and Technology,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name: Takashi Horiuchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http:bsw3.aist-nara.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E-mail: hmori@gtc.aist-nara.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name: Hirotada Mori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Japan E. coli genome database
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                     ADKPALAPGFAAGLAANMIGSGFLGAVVGGLIAGYLMRWVKNHLRLSSKENGFLTFYL
YPVLGTLGAGSLMLFVVGEPVAMINNSLTAWLNGLSGSNALLLGAILGFMCSFDLGGP
                                                                                                                                                                                                                                                                                        similar to PIR Accession Number JC4598"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"Nucleotide position 767359-783777 from the initiation site of ThrA (0 min.). This clone is from Kohara lambda miniset library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="K12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Escherichia coli"
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VNKAAYAFCIGAMANGVYGPYAIFASVKMVSAFTVTASTMLAPRLFKEFEIETGKSTW
                                                                                                           /product="Heat-responsive regulatory protein"
/protein_id="BAA35397.1"
/db_xref="GI:4062318"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /map="16.5-16.9 min"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:562"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
                                                                                   IVAGGTYLAVAYLLSQIFGLQDLFNEENSWLWMYRKLGGGLLGILWYPYLAAYTAYSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="Kohara clone #178"
                                                                                                                                                                                                                                /transl_table=11
                                                                                                                                                                                                                                                                  /codon_start='
                                                                                                                                                                                                                                                                                                                    /note="ORF_ID:0177#5
                                                                                                                                                                                                                                                                                                                                                     /gene="hrsA"
                                                                                                                                                                                                                                                                                                                                                                                                          /gene="hrsA"
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gene CDS

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/translation="MIDYEVLRFIWMLLVGVLLLIGFAVTDGFDMGVGMLTRFLGRNDT
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FFQLLNPFGLLAGVVSVGMIITQGATYLQMRTVGELHLRTRAIAQVAALVTLVCFALA
                                                                          GVWYWYGIDGYVVKSTMDHYAASNPLNKEVVREAGAWLVNFNNTFILWAIPALGYVLP
LLTILTARWDKAAWAFVFSSLTLACIILTAGIAMFPFVWPSSTMMNASLTMWDATSSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /LIANSLATION "MLDLVELSRLQFALTAMYHFLFVPLTIGMAFILAIMETVYLSG KQIYKMTKFWGKLFGINFALGVATGLTMEFQFGTNWSYYSHYVGDIFGAPLAIEGLM AFFLESTFYGLFFFGWDRLGKVQHMCVTWLVALGSNLSALWILVANGWMQNPIASDFN FETRMKMEMYSFSELVLNPVAQVKFVHTVASGYVTGANFILGIGAWYMLKGRDFAFAKR SFAIAASFGMAVLSVIYLGDESGYEMGDVQFKLAAIFAEWETQPAPAAFTLFGIPD QEEETNKFAIQIPYALGIIATRSVDTPVIGLKELMVQHEERINGMXAYSLLEQLFSG STDQAVEDQFNSMKKDLGYGLLKRYTPNVADATEAQIQATKDSIPRVAPLYFAFRI MVACGFLLLAIIALSFWSVIRNRIGEKKWLLRAALYGIPLFWIAVEAGWFVAEYGRQ MVACGFLLLAIIALSFWSVIRNRIGEKKWLLRAALYGIPLFWIAVEAGWFVAEYGRQ MVACGFLLLAIIALSFWSVIRNRIGEKKWLLRAALYGIPLFWIAVEAGWFVAEYGRQ
                                  LTLNVMTWVAVVLVPIILLYTAWCYWKMFGRITKEDIERNTHSLY"
7499. .7792
                                                                                                                                                                                                                                                                                                                         /product="Cytochrome d ubiquinol oxidase subunit II (EC
                                                                                                                                                                                                                                                                                                                                                                                                                  similar to SwissProt Accession Number P11027"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="cydB"
6232. .7371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  \mathtt{WAIGEVLPTAVANSSLTAGDLIFSMVLICGLYTLFLVAELFLMFKFARLGPSSLKTGR}
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/notce="ORF_ID:0178#2
similar to SwissProt Accession Number P11026"
                                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=]
                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="ORF_ID:o178#3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YHFEQSSTTTQPAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DKDSGVRYDRVLQIEESSDDGDEYDYSPAKEEWVITAANAKPQCDIIHEAWQSRAVIR
YDMAVPLNLSERSARQSTGRVGVVLVVTLSHNSRRIDVDINLDNQADDHRLRVLVPTP
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SEGLREFEVIGEEKKTFAITLLRGVGLLGKEDLLLRPGRPSGIKMPVPDSQLRGLLSC
                                                                                                                                                                                                                                                                                                                   ..10.3.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="cyd2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="cyd2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="BAA35399.1"
/db_xref="GI:1651327"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RLSLLSYTGTPTAAGVAQQARAWLTPVQCYNKIPWDVKKLNKAGENVPESYSLLKMPP
VGCLISALKKAEDRQEVILRLENPAESATCDATVAFSREVISCSETMMDEHITTEENQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEFDIQINQIVPSMGYRTLYIEANQPGNVIAAKSDAEGILENAFWQIALNEDGSLQLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MPWPREEVINTTVRLRASQFNLRDDRGQPVPYFIRHAREIDPGLIDRQIVHYGNYDPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NGHDOMPLOONIFEVMDKLREIYPORKFVMSRFEEEVFEKIEAORDNLATLKGEFIDGK
YMRVHRTIGSTRMDIKIAHARIENKIVNLLEPLATLAWTLGFEYHHGLLEKMWKEILK
NHAHDSIGCCCSDKVHREIVARRELAEDMADNLIRFYMRKIADNMPOSDADKLVLFNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="cyd1"
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RNLMYGMRDCLAFGEPMKIGYLPDSFGMSGQLPHIYNGFGITRTMFWRGCSERHGTDK
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/protein_id="BAA35398.1"
/db_xref="GI:4062319"
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DNGAGGVMAAIGWFGAALVGAAISTAILLMWRRHAVKHGNYLTDGVMP"
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12614 TCCCTGGGTGAACGTCGTACGAACGCCGTTAAGATGTACCTGCAGGGTAAAGGCGTTTCT 12673
                                                                                                          12554 TCTTACAAAGTCACCGTAGAAGGTCACGCGGACGAACGTGGTACTCCGGAATACAACATC 12613
                                                                                                                                                                                                                  12494 ATCCGTTCTGACTTCGCTCAAATGCTGGATGCACATGCAAACTTCCTGCGTAGCAACCCG 12553
                                                                                                                                                                                                                                                                                                                            12434 CTGCAAATGCAACAGCTGCAGCAGAACAACATCGTTTACTTCGATCTGGACAAGTACGAT 12493
                                                                                                                                                                                                                                                                                                                                                                                                                                         12377 ---ACTGGTATGGATGCGAACGGCGCAACGGCAACATGTCTTCCGAAGAGCAGGCTCGT 12433
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                                                                                                                                                                                  99
                                                                                                                                                                                                                                                          79 IleLysProGlnAlaAlaAlaIleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGln 98
                                                                                                                                                                                                                                                                                                                                                                                61 AlaLeuAlaSerLysLeuPro-----SerLeuValTyrPheAspPheAspSerAspGlu 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 TyrThrGlyVallleTyrThrGlyValAlaProLeuValAspAsnAspGluThrValLys 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 ThrGlyCysAlaAsnLysSerThrSerGlnValMetValAlaProAsnAlaProThrGly 40 ::::||||||::: |||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MetMetLeuHisIleGlnIleAlaAlaAlaAlaAlaAlaLeuSerValLeuThrPheMet 20
                                                   SerLeuGlyGluArgArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGlyIleAsn 138
                                                                                                                                       ThrAlaArgValLeuValAlaGlyHisThrAspGluArgGlySerArgGluTyrAsnMet 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="tolQ"
8343. .9035
/gene="fii"
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similar to PIR Accession Number B25980"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="mnttlfrwpvrvyyeDtDAGGVVYHASYYAFYERARTEMLRHHHFSQQALMAERVAFVVRRMTVEYYAPARLDDMLEIQTEITSMRGTSLVFTQRIVNAENTLLNEAEVLVVCVDPLKMKPRALPKSIVAEFKQ"
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/protein_id="BAA35402.1"
/db_xref="GI:4062321"
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/note="ORF_ID:o178#5
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/db_xref="GI:4062320"
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Escherichia coli 0157:H7 DNA, co
Ap002553 BA000007
AP002553.1 GI:13360211
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                                                                                                                                                                                                                                                                                                                                                                                                         Hayashi,T., Makino,K., Ohnishi,M., Kurokawa,K., Ishii,K., Yokoyama,K., Han,C.-G., Ohtsubo,E., Nakayama,K., Murata,T., Tanaka,M., Tobe,T., Iida,T., Takami,H., Honda,T., Sasakawa,C., Ogasawara,N., Yasunaga,T., Kuhara,S., Shiba,T., Hattori,M. and Shinagawa,H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete nucleotide sequence of the prophage VT2-Sakai carrying the verotoxin 2 genes of the enterohemorrhagic Escherichia coli 0157:H7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete nucleotide sequence of the prophage VT1-Sakai carrying the Shiga toxin 1 genes of the enterohemorrhagic Escherichia coli 0157:H7 strain derived from the Sakai outbreak Gene 258 (1-2), 127-139 (2000)
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                                                                                                                                                                                                                                                                                                                                       0157:H7 and genomic comparison with a laboratory strain K-12 DNA Res. 8 (1), 11-22 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hayashi,T
                                                                                                               Information Research Center; 3-1, Yamadaoka, Suita, Osaka 565-0871, Japan (E-mail:ken@gen-info.osaka-u.ac.jp, URL.http://www.gen-info.osaka-u.ac.jp/, Tel:81-6-6879-8365,
                                                                                                                                                                                                                                                           5 (bases 1 to 297816)
Ohnishi, M., Kurokawa, K., Makino, K., Yasunaga, T., Shinagawa, H. and
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                                                                                                                                                                                           Submitted (26-JUN-2000) Ken Kurokawa, Osaka University, Genome
                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20564182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (sites)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (sites)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (sites)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Appl. Microbiol. 23 (3), 315-324 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ed from the Sakai outbreak
Genet. Syst. 74 (5), 227-239 (1999)
                                                                                                .-6-6879-2047)
                                                                    project
organism="Escherichia coli 0157:H7"/
                                             Location/Qualifiers
                         .297816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complete genome, section 4/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA
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                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                 gene
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'product="succiny1-Coa synthetase beta subunit"

/product="succiny1-Coa synthetase beta subunit"

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/db_xref="Gr:13360212"

/db_xref="Gr:13360212"

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VKCOVHAGGEKAGGVKYVNSKEDIRAFAENWLGKRLVTYQDELICIDGKCGA

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RELAFKLGLEGKLVQQFTKIFMGLATIFLERDLALIEINPLVITKQGELICIDGKCGA

DGNALFRQDELAEMTOQSQEDPREAQAAQWELMYVALDGNIGGMVNGAGLAMGTMDIV

KLHGGEPANFLDVGGGATKERVTEAFKIILSDDKVKAVLVNITGGIVRCDLLADGIIG

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KJHGGEPANFLDVGGGATKERVTEAFKIILSDDKVKAVLVNITGGIVRCDLLADGIIG

KJHGGEPANFLDVGGGATKERVTEAFKIILSDDKVKAVLVNITGGIVRCDLLADGIIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="ECs0754"
1245. .2114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:83334"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sub_strain="RIMD 0509952"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="0157:H7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"probable transcriptional regulator, similar to transcriptional regulators e.g. glycine cleavage system transcription activator (gcv operon activator) - Escherichia coli gi|417043|sp|P32064|GCVA_ECOLI percent identity 31 in 300 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="mSILIDKNTKVICOGFTGSOGTFHSEQAIAYGTKMVGGVTPGKG
GTTHLGLPVENTYREAVAATGATASVIYVPAPFCKDSILEAIDAGIKLIITITEGIPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="similar to SUCD_ECOLI gi|1786949 percent identity
100 in 289 aa (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="ECs0753"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="ECs0753"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="ECs0755"
2781. .3686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAYIKEHVTKPVVGYIAGVTAPKGKRMGHAGAIIAGGKGTADEKFAALEAAGVKTVRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LDMLTYKVKLDEAGYRMIGPNCPGYITPGECKIGIQPGHIHKPGKVGIVSRSGTLTYE
AVKQTTDYGFGQSTCVGIGGDPIPGSNFIDILEMFEKDPQTEAIVMIGEIGGSAEEEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="succinyl-CoA synthetase alpha subunit"
/protein_id="BAB34177.1"
/db_xref="GI:13360213"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="ECs0754"
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                                                                                                                                                                                                                                                                                                                                                                                                                      \label{locallpreal} \textbf{NGPREDLLSMLIAAVRSNLGVALLPREALQHDLDSGDMVIPCDVPIRTGNREIMTWOEEKSDSPHLOQFREWLLAKSVVPQEM"}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EEFLRTPLESHSKKRIFLNDTGKYYLGIVKETLNKLERDINIIMTWQPTVQVIELAVN
PTFSTHWLIPNLHEFTKLHPDIIVNIHSLANNGDFLNREYDAVIMRENFCAPWAEVEY
LFEEEILPVCSGSLLANSDQKLSVAELLTELPLLHQSTRITGWEEWFALSGVSSPLVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transl_table=1
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                                                                                                                                                                       /note="probable cob(I)alamin adenosyltransferase, similar to cob(I)alamin adenosyltransferases (corrinoid adenosyltransferases) e.g. [Escherichia coli]
                                                                                                                                                                                                                                                                                complement(3720. .4322)
/gene="ECs0756"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="putative transcription regulator"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="ECs0755"
                                                                                                                                      gi|115148|sp|P13040|BTUR_ECOL; percent identity
                                                                                                                                                                                                                                                                                                                                                                                            complement(3720. .4322)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="BAB34178.1"
/db_xref="GI:13360214"
/translation="MRGKIPKTELLVTFEVVARHESYTRAAEELALTQSAVFRQVSAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /transl_table=11
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/transl_table=11
                                                                                                                                                                                                                                                                                                                                                   /gene="ECs0756"
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                                     /evidence=not_experimental
                                                                   /codon_start=1
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Query Match:
DB:
                                Percent Similarity:
Best Local Similarity:
                                                                                                        Alignment Scores: Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                  gene
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                                                                                                                                                                                                                                                                                               complement(7533. .7850)
/gene="ECs0759"
                                                                                                                                                                                                                                                                                                                                                           complement(7533. .7850)
                                                                                                                                                                                                                                                                                                                                                                                            GTLEKLEQFGVSPKIASFVLPIGYSFNLVGSNAYCSFATVFIAQACNIHLSIGBQITM
LLILMLTSKGNAGVPRASMVVIAATLNQFNIPEAGLILLMGVDPFLDMGRSATNVMSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MKKISLITMILLALVLGMIIGVVLNNTASPETAKLYAQEISIFT
TIFLRLIKMIIAPLVVSTLVVGIAKMEDAKALGRIFSKTLFLFICASLLSIALGLITV
NFFMPGTGINFVAHGAETTGVVAAEPFTLKVFISHAFPTSIVDAMAHNEILQIVFSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="putative transport protein"
/protein_id="BAB34181.1"
/db_xref="GI:13360217"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             glutamate/aspartate transport proteins (proton glutamate symport proteins) e.g. [Bacillus stearothermophilus] gi|121467|sp|224943|GLTT_BACST percent identity 38 in 416 aa,also similar to C4-dicarboxylate transpor"
                                                                                                                                                             /product="hypothetical protein"
/protein_id="BAB34182.1"
                                                                                                                                                                                                                         /evidence=not_experimental
                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                           /gene="ECs0759"
                                                                                                                                                                                                                                                                                                                                                                           AMGAAMVSRWEGEHFGEGCRGKALKPNESNVALP"
                                                                                                                                                                                                                                                                                                                                                                                                                                   FLGCSLTAIGEKGSAIVHALDSLAHAMLKLTGYVMLFAPLTVFAAISALIAERGLAVM
VSAGIFMGEFYFTMLLLMVLLIGLAIVYVGPCIRRLTRALSEPALLAFTTSSSEAAFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="ECs0758"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALTILLARQAFYEASFELRSAHLQQVASILINDQASSNDKYVALQLIANAEVSAKGVLP
MCQDTGTATIVASKGQOIWTGGNDABALSKGIYSTPOENNLRFSQNAPLDMYTEVNTQ
TNLPAQIDISAVAGDEYHFLCVKKGGGSANKAALYQETKSLLOPEKLTAFLIEKMKSL
GTAACPPYHLAFVVGGLSADQTLKLAKLASTRYDNLPTSGNEOGOAFRDIELEKVLL
EKLEHNPGQYIPASLREENHAQHVQLDINRPLRDVKQDLAKLPVGTRVSLSGPIVVAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="ECs0758"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DIAHAKIKARLDSGEPMPEYLKHHIVYYAGPAKTPENMACGSLGPTTGGRMDGYIDTF
QAAGGSLVMLSKGNRSQQVTDACHKHGGFNLGSIGGAAALLAQEYVKSLRCLEYPELG
                                                                                                                                                                                                            transl_table=11/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEAVWMMEVENLPAFILVDDKGNNFFSQFEQQHRCASCPAGH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="probable transport protein, similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91|120598|sp|P00923|FUMA_ECOLI percent identity 68 in 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="probable fumarate hydratase, similar to fumarate hydratases e.g. fumarate hydratase class I, aerobic (fumarase) - Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="putative fumarate hydratase"
/protein_id="BAB34180.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(4332. .5984)
/gene="ECs0757"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(4332. .5984)
/gene="ECs0757"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KSTAAFGTVTRAVGHGKTVGVAQYIRGGWDNGEYNLLQPLGVEFHIMGTGFTWETQNR
QADIDAAKEVWSESKRWLADKRYDLVVLDELTYMLAYHYLDTEEVIASLQNRPAQQSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="MSKPFIWQEPFLQNKDGTEYTLISDQHITVTELDGEEVIKIAPE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="GI:13360216"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IVTGRGCHSQILKMADTVSEIRPVKHAFDNGIQAQPGIDW"
           285.50
56.90%
38.51%
33.16%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="GI:13360215"
/translation="MEARISTERHYQROOKLKEQVDTRVAAAIEKKGILIVFTGNGKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transl_table=11/
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/protein_id="BAB34179.1"
                                                                                                 7.29e-18
    Indels:
                           Mismatches:
                                                Conservative:
                    297816
67
32
72
                                                            FEATURES
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                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                   TITLE
                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                    PUBMED
                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24570 GAAGCGGCATACTCCAAAAACCGTCGTGCGGTACTGGTTTAC 24611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24510 GCAGACCAGATCTCCATCGTTTCTTACGGTAAAGAAAACCTGCAGTACTGGGTCATGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24450 TCCCTGGGTGAACGTCGTGCGAACGCCGTTAAGATGTACCTGCAGGGTAAAGGCGTTTCT 24509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24390 TCTTACAAAGTCACCGTAGAAGGTCACGCGGACGAACGTGGTACTCCGGAATACAACATC 24449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24330 ATCCGTTCTGACTTCGCTCAAATGCTGGATGCACATGCAAACTTCCTGCGTAGCAACCCG 24389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24270 CTGCAAATGCAACAGCTGCAGCAGAACAACATCGTTTACTTCGATCTGGACAAGTACGAT 24329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24213 ---ACTGGTATGGATGCGAACGGCGAACGGCAACATGTCTTCCGAAGAGCAGGCTCGT 24269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24153 GCATGTTCTTCCAACAAGAACGCCAGCAATGACGGCAGCGAAGGCATGCTGGGTGCCGGC 24212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24093 ATGCAACTGAACAAAGTGCTGAAAGGGCTGATGATTGCTCTGCCTGTTATGGCAATTGCG 24152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               159 GluGluAlaTrpSerGlnAsnArgArgAlaGluLeuSerTyr 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139 GlnAlaSerValGluIleIleSerPheGlyGluGluArgProIleAlaPheGlyThrAsn 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 SerLeuGlyGluArgArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGlyIleAsn 138
                                                                                                                                                                                                                            Deng, W., Burland, V., Plunkett, G. III, Boutin, A., Mayhew, G.F., Liss, P., Perna, N. T., Rose, D. J., Mau, B., Zhou, S., Schwartz, D.C., Fetherston, J.D., Lindler, L.E., Brubaker, R.R., Plana, G.V., Straley, S.C., McDonough, K.A., Nilles, M.L., Matson, J.S., Blattner, F.R. and Perry, R.D.
                                                                                                                             Submitted (21-FEB-2002) Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                    Deng, W., Burland, V., Plunkett, G. III, Boutin, A., Mayhew, G.F., Liss, P., Perna, N.T., Rose, D.J., Mau, B., Zhou, S., Schwartz, D.C. Fetherston, J.D., Lindler, L.E., Brubaker, R.R., Plana, G.V., Straley, S.C., McDonough, K.A., Nilles, M.L., Matson, J.S., Blattner, F.R. and Perry, R.D. Genome Sequence of Yersinia pestis KIM J. Bacteriol. 184 (16), 4601-4611 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99 ThrAlaArgValLeuValAlaGlyHisThrAspGluArgGlySerArgGluTyrAsnMet 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79 IleLysProGlnAlaAlaAlaIleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGln 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AlaLeuAlaSerLysLeuPro-----SerLeuValTyrPheAspPheAspSerAspGlu 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 TyrThrGlyVallleTyrThrGlyValAlaProLeuValAspAsnAspGluThrValLys 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yersinia pestis KIM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 ThrGlyCysAlaAsnLysSerThrSerGlnValMetValAlaProAsnAlaProThrGly 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yersinia pestis KIM section 306 of 415 of the complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AE013906.1
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                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 11138)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 11138)
                                                    /organism="Yersinia pestis KIM"
/db_xref="taxon:187410"
                                 /strain="KIM"
                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GI:21959961
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gene
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                          gene
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177. .512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AE008713) induced by phosphate starvation [Salmonella typhimurium LT2]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function="enzyme; energy metabolism, carbon: Glycolysis"
/note="residues 29 to 278 of 278 are 87.99 pct identical
to residues 1 to 250 of 250 from E. coli K12: B0755;
residues 29 to 278 of 278 are 89.99 pct identical to
residues 1 to 250 of 250 from GenPept: >emblCAD05220.1|
(AL627268) phosphoglycerate mutase 1 [Salmonella enterica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="psif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="putative starvation-inducible protein"
/protein_id="AAM86597.1"
/db_xref="G1:21959962"
/translation="MRLFPLWLLSAGULLSANVMAADPPKTPSPAQAAQQQQMTDCNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QASTQSLKGDERKNFMSQCLKAQTAPDGKALTPQQQKMKSCNAEAAQKMLKGDERKTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                              /function="enzyme; amino acid biosynthesis: Phenylalanine" /note="DAHP synthetase, phenylalanine repressible; residues 1 to 349 of 350 are 86.24 pct identical to residues 1 to 349 of 350 from E. coli K12: B0754; residues 1 to 349 of 350 from E roll to 12: B0754; residues 1 to 349 of 350 from GenPept: >emb|CAD05217.1| (AL627268) phospho-2-dehydro-3-deoxyhaptonate aldolase (AL627268) phospho-2-dehydro-3-deoxyhaptonate aldolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NNENNETGWYDVDLSEKGRSEAKAAGKLLKDEGFTFDFAYTSVLKRAIHTLWNILDEL
DOAWLPTEKTWKLNERHYGALOGLNKSETAEKYGDEQVKQWRRGFAITPPALEKSDER
FPGHDPRYAKLTDAELPTTESLALTIERVIPYWNDVIKPRIASGERVIIAAHGNSLRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="phosphoglyceromutase 1"
/protein_id="AAN86598.1"
/db_xref="GI:21959963"
/translation="MIRLIERSORTCSLKYDGHIPNLIGVNVMAVTKLVLVRHGESQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        subsp. enterica serovar Typhi]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="gpmA"
/note="y3048"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
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AIGARTTESQVURRELASGLSCPWGFKNOTDGTIKVAIDAINAASAPHCFLSVTKWGHS
AIVNTAGNGDCHIILRGGKEPNYSSKHVNAVEEGLIKAGLEPOIMIDESHANSCKOFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(1793. .2845)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(1793. .2845)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="gpmA"
                                                                                                                                                                                                                                                                                                                                                                                 (DAHP synthetase) phenylalanine repressible [Salmonella enterica subsp. enterica serovar Typhi]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LVKYLDDLGEDEILELNIPTGVPLVYEFDENFKPIKHYYLGNADEIAAKAAAVANQGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="aroG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="y3049"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="aroG
                                                  EALLRQLAGAVRARRO"
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/db_xref="GI:21959964"
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                                                                                                                                                                                                                                                                                                                                   /transl_table=11
                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
/gene="y3050"
                                                                             KQMEVGTDVCQQIAQGEKSIIGVMIESHLVEGSQNLESGEPLTYGQSITDACIGWKDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "psif"
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                        trna
                                                                                                                           tRNA
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                     complement(6725. .6797)
                                             /function="RNA; tRNA"
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/product="putative transport system permease protein"
/protein_id="AAM86600.1"
/protein_id="AAM86600.1"
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/translation="MAVSTIFSQDSNSKRLLIAFAITTLAAFVNAAALLIIVILIVW
DAGHMLTDSAALFIALMAVHFSQRKPDPRHTFGYLRLTTLAAFVNAAALLIIVILIVE
EAVHREFSPHEVMGTPMLIIAIAGLLANIFCFWILHKGEEKKINVRAAALHVLSDLL
EAVHREFSPHEVMGTPMLIIAIAGLLANIFCFWILHKGEEKEKLUKGEAQOEIDIN
GSVGAMIAAIVILTTGWTPIDPILSVLVSVLIILRSAWRLLKESFHELLEGAQOEIDIN
GSVGAMIAAIVILTTGWTPIDPILSVLVSVLIILRSAWRLLKESFHELLEGAQOEIDIN
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/function "putative transport"
/function "putative 1310 of 312 are 66.12 pct identical to
/note "residues 4 to 310 of 312 from E. coli K12: B0752;
residues 9 to 309 of 312 are 67.44 pct identical to
residues 9 to 309 of 312 are 67.44 pct identical to
residues 14 to 312 of 312 from GenPept : >gb|AAL19697.1|
(AE008731) putative CDF family transport protein
[Salmonella typhimurium LT2]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLRKDLCTNIYEVRNIHHVHLMQVGEQRLMTHAQVIPPLDHDALLQRIQDYLLHHYR ISHATVQMEYQHGGTPDCGINQAAPADGHHRHHHHE" complement (4347. .5072)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene-"pnuC"
/function="transport; transport of small molecules;
/function="transport; transport of small molecules;
Nucleosides, purines, pyrimidines"
Nucleosides, purines, pyrimidines"
/note="residues 1 to 238 of 239 from E. coli K12: B0751;
residues 1 to 240 from E. coli K12: B0751;
residues 1 to 241 of 241 are 100.00 pct identical to
residues 1 to 241 of 241 from GenPept: >emb|CAC89971.1|
(AJ414146) intergral membrane NMN transport protein PnuC
(Yersinia pestis]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="y3050"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="residues 1 to 346 of 353 are 82.08 pct identical to residues 1 to 346 of 347 from E. coli K12: B0750; residues 1 to 346 of 353 are 82.94 pct identical to residues 1 to 346 of 347 from GenPept: >gb|AAL19695.1| (AE008731) quinolinate synthetase, A protein [Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(5194. .6255)
/gene="nadA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="nucleoside/purine/pyrimidine transporter"
/protein_id="AAM86601.1"
/db_xref="G1:21959966"
/translation="MDFLSTGNILVHIPLGAGGYDLSWIEAIGTLFGLLCIWFASKEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="y3052"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="nadA'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(5194. .6255)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FWDSTMMVLSIAAMILMTRKYVENWLIWVVIDVISVAIFAYQGVYAMALEYAFLTLIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IINYLEGLINVTLEAVIEFQIOLYASLLLQLEFEGANIYGWYAWSKQTPDNQAELKIR
WLSLPKALAWAAVCIAGIYLMTLHIDTVEAWLTRVAVTVWQSLGANVQMPELQPDAFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
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                                                                                                                                                                                                                                                VAHYYTDDEIQALAEETGGCVADSLEMARFGNNHPASTLLVAGVREMGETAKÎLNPEK
KVLMPTLNAECSLDLGCPVDEFTAFCDSHPDRTVVVYANTSAAVKAKADWVVTSSIAV
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/protein_id="AAN86602.1"
/db_xref-"GI:21959967"
/translation="MSEIFDVNAAIYDFPARPVPLDTNEKAFYREKIKTLLKQRDAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pyridine nucleotide"
       /product="tRNA-OTHER"
/note="setima"
                                                                                                                                                                        ELIEHLDSLGEKIIWAPDRHLGSYVQKKSGADVLCWQGACIVHDEFKTQALARWKALY
PDAAVLVHPESPQAVVDMADAVGSTSQLIQAAKTLPQKTLIVATDRGIFYKMQQACPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         typhimurium LT2]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /function="enzyme; biosynthesis of cofactors, carriers:
                                                                                                         LNRMLDFANQLKLQVKGNA"
                                                                                                                                       KELFEAPTAGEGATCRSCAHCPWMAMNGLRAIAEGLEQGGVMHEIHVDEELRQQALIP
/note="anticodon:
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RESULT 21
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                                                                                      7954 GAAGCAGCCTTTGCTAAAAACCGTCGTGCAGTTCTGGTTTAC 7913
                                                                                                                                                            8014 GCTGACCAGATCTCTATCGTTTCTTACGGTAAAGAGAAACCAGCAGTACTGGGCCATGAC
                                                                                                                                                                                                                              8074 GCTTTGGGTGAGCGTCGTGCTAGCGCAGTGAAAATGTACCTGCAAGGTAAAGGCGTTTCT 8015
                                                                                                                                                                                                                                                                                                   8134 TCTGACAAAGTTGTTGTAGGCCCACGCGGATGAACGCGGTACGCCAGAATACAACATC 8075
                                                                                                                                                                                                                                                                                                                                                                       8194 ATCGGTTCTGACTTCGCTCAAATGCTGGATGCACATGCTGCATTCCTGCGTAGCAACCCA 8135
                                                                                                                                                                                                                                                                                                                                                                                                                                            8254 CTTCAGATGCAAGAACTGCAAAAGAACAACATCGTTTACTTCGGTTTCGATAAATACGAT 8195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8296 ------ACAGAGAACGGCAGCAACCTGTCTTCTGAAGAGCAACCATGT 8255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8356 GCTTGTAGTTCCAACAAAAGCGCAAATAATGACCAATCTGGCATGGGCGCGCTGGCACTGGT 8297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8416 ATGCAACTGAACAAAGTGCTAAAAGGGCTAATGTTGGCTTTGCCTGTTCTGGCTGTGGCG 8357
                                                                                                                        159 GluGluAlaTrpSerGlnAsnArgArgAlaGluLeuSerTyr 172
                                                                                                                                                                                            139 GlnAlaSerValGluIleIleSerPheGlyGluGluArgProIleAlaPheGlyThrAsn 158
                                                                                                                                                                                                                                                    119 SerLeuGlyGluArgArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGlyIleAsn 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 AlaLeuAlaSerLysLeuPro-----SerLeuValTyrPheAspPheAspSerAspGlu 78
Yersinia pestis strain CO92 complete genome; segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 TyrThrGlyValIleTyrThrGlyValAlaProLeuValAspAsnAspGluThrValLys 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 ThrGlyCysAlaAsnLysSerThrSerGlnValMetValAlaProAsnAlaProThrGly 40
                          AJ414146
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                                                                                                                                                                                                                                                                                                                        ThralaargValLeuValAlaGlyHisThraspGluArgGlySerArgGluTyrAsnMet 118
                                                                                                                                                                                                                                                                                                                                                                                                         IleLysProGlnAlaAlaAlaIleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGln 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="hypothetical protein"
/protein_id="AAM86603.1"
/db_xref="GI:21959968"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="residues 1 to 269 of 269 are 69.62 pct identical to residues 1 to 263 of 263 from E. coli K12: B0742; residues 1 to 269 of 269 are 76.64 pct identical to residues 1 to 269 of 269 are 76.64 pct identical to residues 1 to 274 of 274 from GenPept: >emb|CAC82711.1|(AJ297885) YbgF protein [Pectobacterium chrysanthemi]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(7091. .7900)
/gene="y3053"
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/transl_table=11
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/gene="y3053"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation="MNSNFRRHLVGLSLLVGVAVPWAATAQAPISNVGSGSVEDRVTQ"
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AJ414146.1 GI:15979072
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Addition Adjusted Adj
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HLILNGYSESIANVLSGVAGSTVDIIGGADTALTANNSGFLGQYALAGNSKLTVASTN
NLGASSSVALAGAGDTLSLSGFNGTFGUSVTGSGVLQVTDDAEVTLTSSNGVGRTVKV
DIADATLNLNDIALEDHYLTGNGTLNVAKNLATTAFDGGSTVGGAFSGLYNLTNTTGTF
LSADNAAALARATLKLSDDSVTTVGTTPRILHGLDLNGGTLIFDGSPPQSQANGVVTV
TDLALMSGTISTGAGNWENEHPVTPPNVSLLEQDRGDILLQLLDADNVTGNANDLEL AIHNYGLTSSNGNGGSGLYVNYTLSALELLANGANALLLATESGLTANRYLNAELFGV GGLVVDAQNGALTLANGNNRYEGTTTVTAGELILGANGAFQCTSLLNIASGASANING YRQTVGAVTNSGAVTLGNGGVLTSGLLTNGGILDLTGGALNLAAGGSSTVAGGLTGAG TLNINGGDLAVSATNSGLSGQTHIADVASVTLTGTGTLGTSAVEVLGTLNLNGANAAM ANGAFGOTSLINIASGASANINGYROTYGAVTNTGTVTLGNGGELTSTDTLINTGMIN
VTDGILNLENGGASSISGGLTGNGILNIKGGDFTISTDNNGLAGOTNISDGASVTLGN
GGTIIGTGNLGSSVIDVLGDLNLVADNSLANVISDGTINTTATVTLKGNSSFSGAHQ
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DTALTANNSGFLGQYALAGNSKLTVASTNNLGASSSVALAGTGDTLSLSGFNGTFGNS
VTGSGVLQVTDDAEVTLTSSNGVSNAVTIDIADATLNLDDIALFNHALTGNGLLNVAK DRTLHGLDLNGGTLIFDGSPPOSQANGVVTVTDLALNSGTISITGAGNWENEHPVTPP NVSLLEQDRGDILLELINAANVTGNANNLDLLVDGTAITSGTQGVESAIQQGGSTVAN GĀDTALTANNSGĒLGOYALAGNSKLTVĀSTNNLGASSSVĀLAGĀGDTLSLSGFNGTĒG NSVTGSGVLQVTDDAEVTLTSSNGVSNAVTIDIADATLNLDDIALFNHVLTGNGLLNV ELLADGADALLLATESGLTANRYLNAELFGYGGLYVDAQNGALTLANGSNRYEGTTTV TAGELILGANGAFGOTSLLDIASGASANINGYSQTYGAVTNVGTYTLGSGGVLTSGLL /note="similar to neighbouring CDSs vPO1007 and vPO1006. Similar to Salmonella typhimurium leucine-rich repeat protein SIrP TR:Q9XCV2 (EMBL:AF127079) (765 aa) fasta scores: E(): 0, 39.0% id in 644 aa, and to Shigella flexneri 65.4 kDa antigen IpaH 4.5 SW:IPA4\_SHIFL (P18009) (574 aa) fasta scores: E(): 0, 40.4% id in 589 aa" MINGTTISAGGGVQSTVQQGGYTVANATHNYGMTSNGGSGLYVNYTLSALELLAÞGAN ALLLATESGLTANRELNAELSGYGGLVVDAQNGALTLANGNNRVEGTTTVTAGELILG TNVLSGGGVINTNAAVTLSGNNSFSGAHQIGTDGELTVGQASNLGASSATVNLGTLTS  ${ t AKNDASTAFDFGSTVGGAFSGIVNLTNTTFALSADNAAALARATLKLSDDSVTTVGAT$ HQIGTDGELTVGQASNLGASSATVNLGTLTSHLILNGVSESIANVLSGVAGSTVDIIG ASVTLTDTGTLGTSAVEVLGTLNLNGANAAMTNVLSGDGT INTNAAVTLSGNNSFSGA  ${ t TNGGILDLTGGALNLTAGGASTVAGGLTGAGTLNINGGNLSVSAANSGLSGQTHIADV}$ ADRMGETLYTDVFTGEOKTTSLWLRNEGSHNRSRDDSGELKTQDNRYVMQLGGDVAOW SRNAQDLWRVGVMAGYANSSSSTVAQVAGYRSTGSVDGYSVGIYGSWLADNADDTGAY NIGTLAMNGGTLLFDNIVDNAGIITSDGTIAANSINTTGGGEVRVNLPSNLAPSLDGL SVMELDEGEIIVTLATGAATGTGHELTLTDENGDPISAVTYQGVHNAGSTSAAATGSF complement(12049 .13929) /gene="YPO1005" VDSWVQYSWFDNRVSGQDLATEKYDSKGFTASVEGGYAFKVGESVNQSYFIQPKAQVVWNGVKADDHTETNGTVISGDGNGNIQTRLGAKAFINPSDKAKVSGPAFKDFVEANWIH  ${\tt NYGMTTGEDYDGLYVNYGLTALELLSTGSEALVLTAILANNGTQSNDLSAQITGSGDL}$ NDASTAFDFGATVGGAFTGTVNLNNSTFDLSGNNTTVLAQATLKLSSGNLTSVGNGVQ complement(12049. .13929) LGVKYNF" NTKDFGTTLDGVTVKQAGTANIAELKLGVDGQVNSQLNLWGNIGQQVGNKGYSETSVV QLENTAREKVKILKTLNVNSVDDIEVYLAYQVKLLNSLQLSSVNKEMRFFGVSHVTAD DLLSAETRVKTAENQDFSRWLSQWSFWKSVVQRIEPERYAAAVEKQYHALENIYPDKL SVTSNOLTQLDETLPASLSFLMVLSNRLTKLPENLPGSLRCISAEYNQLSOLPDLARL PQNCEILLEGNPLSTSTLQVLQHLRINPYYQGPRINWSELDNLPPASLRNIVATWLPP EQQNRLAGDWANIETEANSAAFSVFLHRLATTQNANNIPEFKQQIAAWLLQLADSPTL LPATLPDNIQKLNASFNQLRTLPDTLPASLLSLNYYGNELERLPESLPEGLKELDVND NESLQLPNRLPPNLESLGIASCGLTELPTLPNSLKRLDADSNQLRTLPDTLPISLLNL /db\_xref="Sptrembl:Q8ZHA0"
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/translation="MNLSNITSNVSMPNIEPDREIHSARTSTAALTPADYYAIWEKWE
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/protein\_id="CAC89848.1"
/db\_xref="GI:15979074" /gene="YP01005"  ${ t REQTFLIAQEASATCEDRITLTHNDMQKAVMLHEVEKGKYDEKLPELMARGREMFRLE}$ /transl\_table=11 AAELAANGMTGDVDANRIVGKRINDELMGEIDMALTHEVLSAKGASSLLDNLWMEYLI

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                                            152592 GCTTGTAGTTCCAACAAAAGCGCAAATAATGACCAATCTGGCATGGGCGCTGGCACTGGT 152651
                                                                                                                                 152532 ATGCAACTGAACAAAGTGCTAAAAGGGCTAATGTTGGCTTTGCCTGTTCTGGCTGTGGCG 152591
41 TyrThrGlyValIleTyrThrGlyValAlaProLeuValAspAsnAspGluThrValLys 60
                                                                                        21 ThrGlyCysAlaAsnLysSerThrSerGlnValMetValAlaProAsnAlaProThrGly 40
                                                                                                                                                             1 MetMetLeuHisIleGlnIleAlaAlaAlaAlaAlaAlaLeuSerValLeuThrPheMet 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Pfam match to entry PF00560 LRR, Repeat, score 10.40, E-value 30" complement(13468. .13539)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"Similar to neighbouring CDSs vpO1005 and vpO1007. /note-"Similar to regions of Salmonella typhimurium secreted Similar to regions of Salmonella typhimurium secreted protein h2 TR:09RPH0 (EMBL:AF160727) (788 aa) fasta scores: E(): 2.5e-24, 41.9% id in 272 aa, and to regions of versinia pestis outer membrane protein YopM TR:068701 (EMBL:AF053946) (409 aa) fasta scores: E(): 7e-23, 40.5%
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Repeat, score 9.30, E-value 44"
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LPTTLPDNLQTLKASYNQLRTLPNTLPASLLSLKVHMNELERLPEPLPEGLKTLDVGC
NTSLQLPSRLPPVLESLDISNCNLTELPTLPNSLKELDAHGNQLRILPDTLPISLLRL
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/protein_id="cac89849.1"
/db_xref="GI:15979075"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Pfam match to entry PF00560 LRR, Leucine Rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(13543. .13602)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="YP01005"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="Pfam match to entry PF00560 LRR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="YP01005"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(14657. .14728)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            id in 259 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="YP01006"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="YP01006"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="YP01005"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="YP01005"
                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Pfam match to entry PF00560 LRR, Repeat, score 9.30, E-value 43"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LRLSTKPNYQGPRIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NVAYNQLTALPENLPGSLRCIYTEYNQLSQLPDLAHLRQNCNICLDGNPLSPSTLLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation="MYLSNITSNVSMPNIGPDREIHADRPAATALTPADYHAIWEKWE/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="YP01006"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="SPTREMBL:Q8ZH99"
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37.93%
32.87%
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283.00
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Matches:
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Indels:
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                                                                                                                                                                                                                                                                                                                                           Conservative:
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                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                         PUBMED
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Gasilva, A.C.R., Ferro, J.A., Reinach, F.C., Farah, C.S., Furlan, L.R.,
Quaggio, R.B., Monteiro-Vitorello, C.B., Van Sluys, M.A., Almeida
Jr., N.F., Alves, L.M.C., do Amaral, A.M., Bertolini, M.C.,
Camargo, L.E.A., Camarotte, G., Cannavan, F., Cardozo, J.,
Chambergo, F., Ciapina, L.P., Cicarelli, R.M.B., Coutinho, L.L.,
Cursino-Santos, J.R., El-Dorry, H., Faria, J.B., Ferreira, A.J.S.,
Ferreira, R.C.C., Ferro, M.IT., Formighieri, E.F., Franco, M.C.,
Greggio, C.C., Gruber, A., Katsuyama, A.M., Kishi, L.T., Leite
Jr., R.P., Lemos, E.G.M., Lemos, M.V.F., Locali, E.C., Machado, M.A.,
Madeira, A.M.B. N., Martinez-Rossi, N.M., Martins, E.C., Meidanis, J.,
Menck, C.F.M., Miyaki, C.Y., Moon, D.H., Moreira, L.M., Novo, M.T.M.,
Okura, V.K., Oliveira, M.C., Oliveira, V.R., Pereira Jr., H.A.,
Rossi, A., Sena, J.A.D., Silva, C., de Souza, R.F., Spinola, L.A.F.,
Santos, M., Truffi, D., Tsai, S.M., White, F.F., Setubal, J.C. and
Kitaima, J.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      152994 GAAGCAGCCTTTGCTAAAAACCGTCGTGCAGTTCTGGTTTAC 153035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               152934 GCTGACCAGATCTCTATCGTTTCTTACGGTAAAGAGAAACCAGCAGTACTGGGCCATGAC 152993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    152694 CTTCAGATGCAAGAACTGCAAAAGAACAACATCGTTTACTTCGGTTTCGATAAATACGAT 152753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           159 GluGluAlaTrpSerGlnAsnArgArgAlaGluLeuSerTyr 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      139 GlnAlaSerValGluIleTleSerPheGlyGluGluArgProIleAlaPheGlyThrAsn 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 SerLeuGlyGluArgArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGlyIleAsn 138
      da Śliva, A.C.R., Ferro, J.A., Reinach, F.C., Farrah, C.S., Furlan, L.R., Quaggio, R.B., Monteiro-Vitorello, C.B., Van Sluys, M.A., Almeida Jr., N.F., Alves, L.M.C., do Amaral, A.M., Bertolini, M.C., Camargo, L.E.A., Camarotte, G., Cannavan, F., Cardozo, J., Chambergo, F., Ciapina, L.P., Cicarelli, R.M.B., Coutinho, L.L., Cursino-Santos, J.R., El-Dorry, H., Faria, J.B., Ferreira, A.J.S., Ferreira, R.C.C., Ferro, M.I.T., Formighieri, E.F., Franco, M.C., Greggio, C.C., Gruber, A., Katsuyama, A.M., Kishi, L.T., Leite, Jr., R.P., Lemos, B.M., Lemos, M.V.F., Locali, E.C., Machado, M.A., Martina, E.C., Machado, M.A., Menck, C.F.M., Miyaki, C.Y., Moon, D.H., Moreira, L.M., Novo, M.T.M., Okura, V.K., Oliveira, M.C., Oliveira, V.R., Pereira Jr., H.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of 460 of the complete genome. AE012414 AE008922 AE012414.1 GI:21114210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Comparison of the genomes of two Xanthomonas pathogens with differing host specificities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 417 (6887), 459-463 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xanthomonas campestris pv. campestris str. ATCC 33913
Xanthomonas campestris pv. campestris str. ATCC 33913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AE012414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AlaLeuAlaSerLysLeuPro-----SerLeuValTyrPheAspPheAspSerAspGlu 78
                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 12393)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rossi,A., Sena,J.A.D., Silva,C., de Souza,R.F., Spinola,L.A.F., Takita,M.A., Tamura,R.E., Teixeira,E.C., Tezza,R.I.D., Trindade Santos,M., Truffi,D., Tsai,S.M., White,F.F., Setubal,J.C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                    'translation-"MLQRLERDYGLKHRSGTSYMRGGVCPACSKKELYTFEPKPWVIK
GREAKKGHELIVKDLYDDLFDDWSKRFPMTQASPTASADAYLESSRGFALAPLRGLY
TQESYYDIKVKEGTATVFRALDKGGWEERLIDRPHRFGKQKARFADGKSYAGAWWCAP
AAAELMRTATEVWIVEGIFDAIALLQHGVCAVSAMSCNAFPDESIRQLKKLRAGNULPT
LVWGLDNEPGAEDYTHKHARRADALGFNSRAALIAQPYTGKKIDWNDLHLRAQAGGDS
                        FPHDANSVKGTFTGGHISSASEFKKRLISLAAGAMFTGSGHQLDRLIEEQTEAIKTVE
AIDFVGYSKEHRAYLLGDIAVRDGEVVTANEEDYFSFKKLRLKSTQKSIRLEIQRDPE
{	t AFRMDWLPWLWQCFGTHGMVAMTFWFGSLFAEQIRAGHKSFPFLEATGEAGAGKTTLL}
                                                                                QKQWDAALTEARYQGULLMARSATEKGLLMYDHNQASDFWLEYRSRLYWFEFDTYRFE
KLLRDYEPEEDSEIDPDKLAKIRRAACSVNKIANCYPEALYFQRQEVTDESWYYFRID
                                                                                                                                                                                                                                                                                     /product="phage-related protein"
/protein_id="AAM42274.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene=":
                                                                                                                                                                                                                                                                                                                                                                                                                               /note="identified by sequence similarity; putative; ORF
located using Blastx/Glimmer/Genemark"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                    /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AHLASGGAYEVITTPRPIGKSLAALALRSTVRKGG"
                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="orf37"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="xcc3002"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="orf37"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation="MSQSNGWATAQAPRFVDAPSQASQQYVAPHKKREQADVLRLQVE/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="MAQLMLRGLLMSSRTHSMHALATDAAMELLDYGSVAREISA"/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="hypothetical protein"
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/db_xref="GI:21114211"
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/db_xref="ATCC:33913"
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ELKDFFGGGTLATRGVENGGNDTYEPPFRGTIVISQNAAVDASEAILTERIVKLHEKRP
QVTTESRIAADNLNALQVEELSHFLIKAVRCEGAILEKFAERWKEYEBARLEKEPDFRL
ERVIKNHAQMLALLDCLEMVITIPEEMIKATROALLEMAFERQKAISADHAQVNEFWE
VYEYLEATGNGKPVVNHSRDASRIAINLNQFAAKAAQFSQVVPDLKVLRGLLADSRRH
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4103. .4327
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/translation-"MNSYRATAYPEDADYTISEEEHDRLWRVQQAASLLATLNHDIAT
RAGISHDGIAAVADFMREELLDIACNARHVREPTKPPTGADLI"
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/protein_id="AAM42275.
/db_xref="GI:21114215"
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5238. .5513
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THDAVVVVAALTMGQHSSAAQRWERRRGPGKGWKLISGPRLFTSEAHRISNALAKFMD
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/protein_id="AAM42277.1"
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                                                                  /gene="XCC3008"
5606. .5755
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/protein_id="AAM42278.1"
/db_xref="GI:21114218"
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/protein_id="AAM42279.1"
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/translation="MAESIVVYGPMASGKSLNAEAICQAYGLKRVVELDERLQRKGED
                                                                                                                                                                                                                                                                                                            /gene="XCC3007"
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/note="putative; ORF
/codon_start=1
                                             /gene="XCC3008"
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                                                                                                                                                         the complete genome. AE011958 AE008923 AE011958.1 GI:21109
da Silva.A.C.R., Ferro,J.A., Reinach,F.C., Farah,C.S., Furlan,Juaggio,R.B., Monteiro-Vitorello,C.B., Van Sluys,M.A., Almeida Jr.,N.F., Alves,L.M.C., do Amaral,A.M., Bertolini,M.C., Camargo,L.E.A., Camarotte,G., Cannavan,F., Cardozo,J.,
                                                                                            xanthomonas axonopodis pv. citri str.
xanthomonas axonopodis pv. citri str.
Bacteria; proteobacteria; gamma subdiv
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/db_xref="GI:21114220"
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/protein_id="AAM42280.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RS da Silva, A.C.R., Ferro, J.A., Reinach, F.C., Farah, C.S., Furlan, L.R., Quaggio, R.B., Monteiro-Vitorello, C.B., Van Sluys, M.A., Almeida Jr., N.F., Alves, L.M.C., do Amaral, A.M., Bertolini, M.C., Camargo, L.E.A., Camarotte, G., Cannavan, F., Cardozo, J., Chambergo, F., Ciapina, L.P., Cicarelli, R.M.B., Coutinho, L.L., Cursino-Santos, J.R., El-Dorry, H., Farial, J.B., Ferreira, A.J.S., Ferreira, R.C.C., Ferro, M.I.T., Formighieri, E.F., Franco, M.C., Greggio, C.C., Gruber, A., Katsuyama, A.M., Kishi, L.T., Leite Jr., R.P., Lemos, E.G.M., Lemos, M.V.F., Locali, E.C., Machado, M.A., Madeira, A.M.B.M., Martinez-Rossi, N.M., Martins, E.C., Meddanis, J., Menok, C.F.M., Miyaki, C.Y., Moon, D.H., Moreira, L.M., Novo, M.T.M., Okura, V.K., Oliveira, M.C., Oliveira, V.R., Pereira JT., H.A., Rossi, A., Sena, J.A.D., Silva, C., de Souza, R.F., Spinola, L.A.F., Takita, M.A., Tamura, R.E., Teixeira, E.C., Tezza, R.I.D., Trindade dos Kitha, M.A., Tamura, R.E., Teixeira, E.C., Tezza, R.I.D., Trindade dos Kitha, M.A., Tamura, R.E., Teixeira, E.C., Setubal, J.C., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chambergo, F., Ciapina, L.P., Cicarelli, R.M.B., Coutinho, L.L., Cursino-Santos, J.R., El-Dorry, H., Faria, J.B., Ferreira, A.J.S., Ferreira, R.C.C., Ferro, M.I.T., Formighieri, E.F., Franco, M.C., Greggio, C.C., Gruber, A., Katsuyama, A.M., Kishi, L.T., Leite Jr.R.P., Lemos, E.G.M., Lemos, M.V.F., Locali, E.C., Machado, M. Madeira, A.M.B.N., Martinez-Rossi, N.M., Martins, E.C., Meidanis, J., Menck, C.F.M., Miyaki, C.Y., Moon, D.H., Moreira, L.M., Novo, M.T.M., Okura, V.K., Oliveira, M.C., Oliveira, V.R., Pereira, Jr., H.A., Rossi, A., Sena, J.A.D., Silva, C., de Souza, R.F., Spinola, L.A.F., Takita, M.A., Tamura, R.E., Telxeira, E.C., Tezza, R.I.D., Trindade dos Santos, M., Truffi, D., Tsai, S.M., White, F.F., Setubal, J.C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (28-NOY-2001) Departmento de Bioquimica, Universidade de
Sao Paulo, Av. Prof. Lineu Prestes 748, Sao Paulo, SP 05508-900,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Comparison of the genomes of two Xanthomonas pathogens with differing host specificities
Nature 417 (6887), 459-463 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .2024217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2896.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         {\tt QGDSCRLDPRRALALSMALHELCTNALKHGALSLPAGNVLVSWERSTRGEQELLELIW}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="identified by sequence similarity; putative;
located using Blastx/Glimmer/Genemark"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(1614.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .3570
                                                                                                                                                                                                                                                                                               .5480)
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gene

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gene

**trna** 

145

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US-09-674-779B-2 (1-172) x AE011958 (1-11713)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
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                                                                                                                                                                                                                                                                                                     5855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5975 TCCCTGCTGTCCGTTGCTGCTGGCTGGTTGCTCGAAGAAGGTGAAGGAAACTCCGCCC 5916
                                                                                                 5915 CCTGCGACCGATACCACCGCTGGTTCCTCGGTTCCCACCGGCCCGTCCACCTCTGGCCTG 5856
                                               106 GlyHisThrAspGluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAla 125
                                                                                                                                                                                                                                                                                                                                                    46
                                                                                                                                                  86
                                                                                                                                                                                                                                                   66
                                                                                                                                                                                                                                                                                                                                                                                                                                                   27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 AlaLeuSerValLeuThrPheMetThrGlyCysAlaAsnLys------
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SerThrSerGlnValMetValAlaProAsnAlaProThrGly---TyrThrGlyValIle 45
GCCAATGCTGACGAGCGCGGTTCGCGTGAGTACAACATGGGTCTGGGCGAGCGTCGCGGC 5640
                                                                                                                                                                                                                                                                                                     TAT---GGTCCGGGCGACCTG---GATGCCGATGCCTGCCTGCGT----
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                                                                                                                                                IleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAla 105
                                                                                                                                                                                                       ---CAGCGCGTTGTTTACTTCGATCTGGATCAGGACTCCCTGAAGCCGGAATTCCAGGCC
                                                                                                                                                                                                                                                 LeuProSerLeuValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAla 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NDLLNQLQQARSDLQALRSTVEQLQHDNEQLKQQSKDQYLDLDGRLNRLEGAGGATPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(5487. .6032)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(6063. .7382)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="identified by sequence similarity; putative; ORF
located using Blastx/Glimmer/Genemark"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="tolB"
/note="XAC3142"
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37.13%
31.65%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (05-DEC-2000) Takakazu Kaneko, Kazusa DNA Research Institute, The First Laboratory for Plant Gene Research; Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kanèko,T., Nakamura,Y., Sato,S., Asamizu,E., Kato,T., Sasamoto, Watanabe,A., Idesawa,K., IShikawa,A., Kawashima,K., Kimura,T., Kishida,Y., Kiyokawa,C., Kohara,M., Matsumoto,M., Matsuo,A., Mochizuki,Y., Nakayama,S., Nakazaki,N., Shimpo,S., Sugimoto,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mesorhizobium loti (strain:MAFF303099) DNA. Mesorhizobium loti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              URL:http://www.kazusa.or.jp/rhizobase/,
Tel:81-438-52-3935(ex.2338), Fax:81-438-52-3934)
On May 11, 2001 this sequence version replaced gi:11994978.
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(54
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                                                                                                                                                        VATPHLGASTAEAQENVALQVAEQMSDYLIKGAVSNAINMPSITAEEAPRLKPPVKLA
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                                                                                                                                                                                                                                    RGVGLKMHVVAFDÞFÍSDKRAEELGVEKVELDELFARADFITLHTÞLTDKTRNIIDAG
AIAKMKNGVRIINCARGGLIVEADLIAALKSGKVAGAGIDVFEVEPABQNALFGMENV
                                                                                                                                                                                                                                                                                ÓYDGLAIRSATKVTEKLINAATRLKVIGRAĞIGVDNVDIPAASRKGIIVMNTPFGNSI
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complement(5193. .6545)
/gene="ml13879"
complement(5193. .6545)
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/transl_table=11
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6913. .7779
                                                                                                                                                                                                                                    /gene="mlr3880"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MENTARKALLALLFAGLASPVFAADLPEPQVEEAPPPVYEQPVDVGGWYIRGDIDYHKSDVRGIDYMTYGIDPCNCTVIPGGKSFDYGKLKGGFSLGGGVGYVKINDRLRADYWFKSNFNGGTSDLVSTSTEVSKMSALLLLANAYVDIGTWHGITPYVGAGIGGARVKWDTYYDPNTAETNPGASNWRFAYALMAGASYCLTDKIILDAGYRFS
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YLPGNKIGIGYDDSLSVVPPATSTVASADLKNYAYSLMLNAYVDLGTYVGITPYLGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HIQGGRMFEWDASSAGPGFDRGINTHEVRGGLRYQFGGNNGCAAPVVAYQPEPEPIYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="ml13877"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
/transl_table=11
Pred. No.:
Score:
                                                             Alignment Scores:
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4.45e-16 269.50

Length: Matches:

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SLELPSLFGDKKKPDQVQFAQOSNGAGATGLEDQLRQWNGKIEELNFQILQMQBQMRK
QQEDNEFRFQQLEGGAQGGQPPAPKKSDATTNTNTDVAAAPATQAPADAGAAPGGNQS
AGGKTVEDVIVESPEGDPGKVIPGTGAPEKTFGSITVDKNGNVIDAGGNTQSTAPTQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YDWREWIVRPLLGTRRSALRDFLRREHVGWAEDPTNIDEAFERPRVRAALAGESAGHM
ENTLRLAGQAAVERGQLGASAANLIRRIASQPSTGLIRLDPALLIADDQAAIYALRIL
LATAGGAAFLPDQARSAALFVRLKAGFLCATLSRTVVDERHAGLFLRREARGLPPAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
/trans1_table=11
/protein_id="BAB50680.1"
/protein_id="BAB50680.1"
/protein_id="BAB50680.1"
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RTGSS&KLLAVTIDHGLRQGSAAEAQAVAKLCAERGIAHRTLTWTGRKPSTGLPAAAR
DARYHLLAEAARAEGIGIIVTGHTADDQAETVLMRHAEDRELADLAGRGLAGMAPATL
\mathtt{AAPATKAPAKAGKSNGTIVAALPSTNDPEELYRNSYQFILSGDYGTAEQGFRDHISRF}
                                                                                                                                                                                                                                                                                                                                                                                                                    complement(12098. .13210)
/gene="ml13886"
                                                                                                                                                                         /protein_id="BAB50681.1"
/db_xref="GI:14024077"
                                                                                                                                                                                                                                                                               /note="unknown protein"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                   complement(12098. .13210)
/gene="ml13886"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSAD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QAFENLGLPQGEPRLPVFAARPVVSPFARFLPSFDLAPARAVAELIGASPLPASPLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVDNTIWDGRRHITLNDMSGALLIAPLGAAAARRLAIDDGETPASLIRAALAAEPTLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           deaminase-related protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Similar to YaeN protein [Bradyrhizobium japonicum], contains similarity to cell cycle protein MesJ/cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(10675, .12039)
/gene="mll3884"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(10675. .12039)
/gene="ml13884"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ILKVHVRNVPLAPNVDLKVVARGTPGESGADLMNLVNESALMAARRNKRLVTMAEFED
AKDKIMMGAERRSSAMTQAEKELTAYHEAGHAILALNVPSADPLHKATIIPRGRALGM
VMQLLEGDRYSMSYKYMISRLAIMMGGRVAEBEKFGKENITSGASSDIEQATKLARAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NSLFGYLISWLPMILILGVWIFFMRQMOSGSGRAMGFGKSKAKLLTEAHGRVTFQDVA
GVDEAKEDLEEIVEFLRDPQKFQRLGGKIPRGVLLVGPPGTGKTLLARSVAGEANVPF
FTISGSDFVEMFVGVGASRVRDMFDQAKKNAPCIIFIDEIDAVGRHRGAGLGGGNDER
EQTLNQLLVEMDGFESNESIILIAATNRPDVLDPALLRPGRFDRQVVVPNPDIVGREK
                                                                                                                                     translation="MHLRSVLSGTLAALLLSGFTALASGPGASGPGQSTDSGFSFHLP/
                                                                                                                                                                                                                                              /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RRKKGPEPEGGMEPQPSS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SILTKKKKEWIALAQGLLEYETLSGDEIKQLIAGEKPARDLGDDTPPSRGSAVPKSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DVAAGRVKTVTIAGARITGTYTDNSTGFQTYSPGDPQLVSRLQDKNVTINARPEADGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="metalloprotease (cell division protein); FtsH" /protein_id="BAB50679.1" /db_xref="GI:14024075" /translation="MNPNYRNLALWAIIAVLLIALFNLFQTPQTRGASSDVPYSQFLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(8624. .10552)
/gene="mll3882"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(8624. .10552)
/gene="mll3882"
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8079. .8537
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/transl_table=11
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KTEKPAKARMKTCLQGYHGNKEAGTLNGLRWIQKGGGYYSLCNARLKAES"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAKPTTVAPKGVTFPSAISPKYASETPGKGRMHTCLDQYYALKDANALGGLKWIQKGG
GFYSLCNAKLKG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MPNLKLAVLAVTASVAWSVAPASALTMKECGETYRTAKEGGTLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="BAB50678.1"
/db_xref="GI:14024074"
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/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
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                                                                                                                                                 REFERENCE
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                                                                                                              AUTHORS
                                                                                                                                                                                                                                MEDLINE
                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                  TITLE
                                                                                                                                                                                     PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13567 GACTTCCTGGTTTCCAAAGGTGTCGCTTCCAGCCGTCTGAAGACCATTTCATACGGCAAG 13508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13792 ACGCCCGGCTCGGCGCAGGACTTCACCGTC-------ACATTTGGCGACCGC 13748
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alvarenga, R., Alves, L.M., Araya, J.E., Baia, G.S., Baptista, C.S., Barros, M.H., Bonaccorsi, E.D., Bordin, S., Bove, J.M., Briones, M.R., Bueno, M.R., Camargo, A.A., Camargo, L.E., Carraro, D.M., Carrare, H., Colauto, N.B., Colombo, C., Costa, F.F., Costa, M.C., Costa-Neto, C.M., Coutinho, L.L., Cristofani, M., Dias-Neto, E., Docena, C., El-Dorry, H., Facincani, A.P., Ferreira, A.J., Ferreira, V.C., Ferro, J.A., Franca, S.C., Franco, M.C., Frome, M., Furlan, L.R., Garnier, M., Goldman, G.H., Goldman, M.H., Gomes, S.L., Gruber, A., De P. Mobele, J. T., Pragnaja, J. B., Gomes, S.L., Gruber, A., Goldman, M.H., Gomes, S.L., Gruber, A., De P. Mobele, J. T., Pragnaja, M. F., Gomes, S.L., Gruber, A., De P. Mobele, J. T., Pragnaja, M. F., Gomes, S.L., Gruber, A., De P. Mobele, J. T., Pragnaja, M. F., Gomes, F. M., Weller, A. T. De P. Mobele, J. T., Pragnaja, M. F., Gomes, F. M., Weller, A. T. De P. Mobele, J. T., Pragnaja, M. F., Gomes, F. M., Weller, A. T. De P. M., Gomes, S.L., Gruber, A. T. De P. M., Gomes, G. M., G. M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Simpson, A.J., Reinach, F.C., Arruda, P., Abreu, F.A., Acencio, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xylella fastidios: AE004009 AE003849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xylella fastidiosa 9a5c.
Xylella fastidiosa 9a5c
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Simpson, A.J.G., Reinach, F.C., Arruda, P., Abreu, F.A., Acencio, M., Alvarenga, R., Alves, L.M.C., Araya, J.E., Bala, G.S., Baptista, C.S., Barros, M.H., Bonaccorsi, E.D., Bordin, S., Bove, J.M., Briones, M.R.S. Bueno, M.R.P., Camargo, A.A., Camargo, L.E.A., Carraro, D.M.,
                                                                                                                                                                                                                                                                                                                                  The genome sequence of the plant pathogen Xylella Xylella fastidiosa Consortium of the Organization
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ho, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AE004009
                                                                                                                                                                                                                                                            Sequencing and Analysis
Nature 406 (6792), 151-157 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xylella
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAsp 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAspGlu 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---ProLeuValAspAsnAspGluThrValLysAlaLeuAlaSerLysLeuProSerLeu 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----CCGAACAACGCCGCCGACCTCGGCCTCAACGGC------GCCGGTGCGGCA 13793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ValAlaProAsn-----AlaProThrGlyTyrThrGlyValIleTyrThrGlyValAla 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCGCTGGTGGCGATGCTCGCCATCGCCGGTTGCGCTTCGAAGAAGACG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGGCGCAGTGGCTGAACCAGTACAAGCAGTACGCCATCGTCGTCGAAGGTCACGCCGAC 13628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAACGTCCGGTCGCGGTCTGCGACGACATCTCCTGCTGGTCGCAGAATCGCCGCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGluIleIleSerPheGlyGlu 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 10833)
                                                                                                                                                 (bases 1 to 10833)
                                                                                                                                                                                                                                                                                                                                                                                                                         Marino, C.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fastidiosa 9a5c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hoheisel, J.D., Junqueira, M.L., Kemper, E.L., Kitajima, J.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proteobacteria; gamma subdivision; Xanthomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55.97%
40.25%
31.30%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GI:9106980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10833 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (1-349116)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0833 bp DNA linear BCT 15-JUN-2001 section 155 of 229 of the complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53
53
57
                                                                                                                                                                                                                                                                                                                                                  for Nucleotide
                                                                                                                                                                                                                                                                                                                                                                                      fastidiosa. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BCT 15-JUN-2001
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                               gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gomes, S.L., Gruber, A., Ho, P.L., Hoheisel, J.D., Junqueira, M.L., Kemper, E.L., Kitajima, J.P., Krieger, J.E., Kuramae, E.E., Laigre Lambais, M.R., Leite, L.C.C., Lemos, E.G.M., Lemos, M.V.F., Lopes, C.R., Machado, J.A., Machado, M.A., Madeira, A.M.B.N., Madeira, H.M.F., Marino, C.L., Marques, M.V., Martins, E.A.L., Martins, E.M.F., Matsukuma, A.Y., Menck, C.F.M., Miracca, E.C., Martins, E.M.F., Matsukuma, A.Y., Menck, C.F.M., Miracca, E.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Costa-Neto,C.M., Coutinho,L.L., Cristofani,M., Dias-Neto,E., Docena,C., El-Dorry,H., Facincani,A.P., Ferreira,A.J.S., Ferreira,V.C.A., Ferro,J.A., Fraga,J.S., Franca,S.C., Franco,Frohme,M., Furlan,L.R., Garnier,M., Goldman,G.H., Goldman,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Miyaki,C.Y., Monteiro-Vitorello,C.B., Moon,D.H., Nagai,M.A., Nascimento,A.L.T.O., Netto,L.E.S., Nhani Jr.,A., Nobrega,F.G., Nunes,L.R., Oliveira,M.A., de Oliveira,M.C., de Oliveira,R.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (02-JUN-2000) Organization for Nucleotide Sequencing and Analysis, Bioinformatics Lab - IC/Unicamp, C.P. 6176, Campinas, SP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carrer, H., Colauto, N.B., Colombo, C., Costa, F.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QAEQGYDYYTVHAGVLRDFIPLTASRLTGIVSRGĞSIMARWCQAHRSENFLYTHFEEL
CEIMRAYDVAFSLGDGLRPGCIADANDAAQFAELEILGELTHLANNHQVQVMYBGDGH
VPMHLIKANMDKOLAACGEAPFYTLGPLTTDIA HAGYDHITSAIGAAMIGWGGTPALCS
VTPKEHLGLPNILQDVHDGIIAYKIAAHAADLAKCHPAAQARDDALSKARFEERWQDQF
HLSLDPEKALALHDESLPKEAHKRAAFCSMCGPQFCSMKISQEVRDASSNELSDGNTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOLEYARRGLYTPEMEEVAIREQQRREQTVENLRGQRHAGDAWGALVGTPITPEEVRD
EIARGRAILPNNINHPESEPMIIGRNFLTKINANIGTSALSSSIAEEVEKLVWAIRWG
ADTIMDLSTGRDIHATREWILKNSPVFVGTVPIYQALEKVGGHVEALSWAVERDTLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MDRAARPPWQRRKVPRRREVPSLSGRTIVNITTALPLPTHLLSE
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ATIDLACGLPRLRAAWIDERADTVEAALYFKVPESVSVTAPPFFTAPRPRRARDNVAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment coverage: 91.4 %/subject alignment coverage
97.5 %); identified by sequence similarity; putative;
located using Glimmer/RBSfinder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="XF1888"
192. .2081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="thiamine biosynthesis
/protein_id="AAF84694.1"
/db_xref="GI:9106981"
                                                                                                                                                                                /note="similar to SP|Q44532 (percent identity: 59 %/que-
alignment coverage: 97.3 %/subject alignment coverage:
97.7 %); identified by sequence similarity; putative; O
located using Glimmer/RBSfinder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Xylella fastidiosa 9a5c"
/db_xref="taxon:160492"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .10833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to SP|P45740 (percent identity: 67 %/query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="XF1888"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="9a5c"
/product="ferredoxin-NADP reductase"
/protein_id="AAF84695.1"
/db_xref="GI:9106982"
                                                                                                     /transl_table=11
                                                                                                                                                                                                                                                                                                                          2213. .2992
/gene="XF1889"
                                                                                                                                                                                                                                                                                                                                                                   /gene="XF1889"
2213. .2992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TNDAI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ocation/Qualifiers
                                                                                                                                                  /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brazi
                                                                                                                                                                                                                                                                                                                                                                                                                                       .2992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Costa, M.C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Franco, M.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lopes, S.A.
                                                                                                                                                                                                                                                                                                59 %/query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laigret, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .н.ѕ.,
                                                                                                                                                                                                                                    ORF
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TEARPLLRAYSIASANWEEQLEFLSIKVQNGLLTSRLQHIKPGDKILVGKKPTGTLLI HDLHDGRHLYLLGTGTGLAPWLSIIKDPETYERFDKVILTHGVRYSKDLAYRDYFEKE LPQHELLGETIRKKLLYYPAVTREDFPNRGRLTHLIESGAMQNTLGLPIIDQANDRFM

translation="MSPAFGTETVIHVHHWTDAYFSFITTRDSGFRFENGQFVMIGLE/

TITLE

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gene
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                                                                                                                                                       alignment coverage: 98.8 %/subject alignment coverage: 98.4 %); identified by sequence similarity; putative; ORF located using Glimmer/RBSfinder*
                                     /product="phosphoglyceromutase"
/protein_id="AAF84699.1"
/db_xref="GI:9106986"
                                                                                                                                                                                                                                                                                                    /gene="XF1893"
6397. .7146
                                                                                                                                                                                                                                                                                                                                                                                   RIVLKDDLNLLSEPTLLAGFDVGFEDEGRTTRAAAVLMNACDLKLLETHVVRVTTSMP
YVPGILLSFRELPALLQALTQLSRIPALVFVDGHGIAHPRRLGIAAHFGLVTNLPCIGV
AKKRLVGDFVEPGTAFGEHTPILLHGTQVGWALRSKIRCKPLMISPGHKISLHSALTW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"similar to SP|P32679 (percent identity: 53 %/query alignment coverage: 83.1 %/subject alignment coverage: 94.6 %); identified by sequence similarity; putative; ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MSVDTVKNTVYLATPPTOLPKFETIFGHPKPLWMLFMAEFWER FAFYGIRWALTLY IVTOFFDONSIGEONANSTYGAYLALVYASAIFGGFIADRIIGYQ RSIIIGAV IMACGLELITVPSRTWFELGLATIV IGNGLEKPHISSLVÇOLYABGDTRR DRGFTIFYMGINAGSLFSLITSWLAGOVEGTPMQDNYKVPFIASGIGWFHISLLWFWI GKROLKGIGLPEKDGESIFRTFLIIFGALLAIPLAYLLLAKLNATTLAWILGLLFAAL ATLLIVTALRNGKIQRORVIAMLIIFVENVKFWWFEFBOAGSSEWFLAKNIVDROILSN ATLLIVTALRNGKIQRORVIAMLIIFVENVKFWWFEFBOAGSSEWFLAKNIVDROILSN
          /	ext{translation="MTRKLVLLRHGQSQWNSMNRFTGWVDIGLTEQGHQEATMAGHLM}}
                                                                                                                                                                                                       /note="similar to SP|P31217 (percent identity: 56 %/query allgnment coverage: 98.8 %/subject allgnment coverage:
                                                                                                                                                                                                                                                                                                                                                                      TQRCLNGYRLPEPTRQADRLASRRGQKTVSDLPSLL"
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/protein_id="AxF84698.1"
/db_xref="GI:9106985"
                                                                                                                          /transl_table=11
                                                                                                                                               /codon_start=
                                                                                                                                                                                                                                                                         /gene="XF1893"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation="MPVYALISDTGMMVFMKISSIDSIFAGWDGSITEARRLQSDMAE/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(5578. .6342)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (5578.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WEFPVGWFQSVNPLAIILLAPIIAVIWSLLDKYRIEPŠIPRKFSLGLMENGFGFILLM
YALSNLLNASNMIPFWSLIAVYVIQTVGELCLSPIGLSMVTKLAPVRLVGFAMGGWFL
STAIGNNLSGVFASFVSGEEGMTVSSALRGYTFGFWSLIGSGILLFLISPLINRLMHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="similar to SP|P94408 (percent identity: 35 %/query alignment coverage: 96.7 %/subject alignment coverage: 100.2 %); identified by sequence similarity; putative; ORF located using Glimmer/RBSfinder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="XF1892"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="XF1892"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="di-tripeptide ABC transporter membrane protein"
/protein_id="AAF84697.1"
/db_xref="GI:9106984"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             located using Glimmer/RBSfinder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="mhthyshafasklsllsldrfpmssiytftftrldgrpqaladw
RGQVLLLVNVASRCGGTPQYAGLEMLWQRYRDAGLIVIGFPCDQFAGQEPGDEAKIAE
FCTLNYGVDFPMAAKIKVNGADAHPLWQWLKHRRRGLFGMAAIKWNFTKFLIGRNGQP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="glutathione peroxidase-like protein"
/protein_id="AAF84696.1"
/db_xref="GI:9106983".
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                     AR089419
LOCUS
DEFINITION Sequence 178 from patent US 5994066.
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                             AR089419
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US-09-674-779B-2 (1-172) x AE004009 (1-10833)
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                                                                                                                                                                                                              8917 AACTCTGTGTTGTATTCATTACAGGCGAATGGTGCTTCGTCGGGACAGTTGAACGTTGTT 8858
                                                                                                                                                                                                                                                                                                                                                                                                                                               9037 GTTCTTGGTTGCCATGCAAAATATCTTCGCAACCGTCCCTCTGCACACATCACATTACAG 8978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9094 ----CAACGTGTCGTCTATTTCGACTTTGATAAAGATGATGTGAAAAAAGAATTTCAAACG 9038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9133 TACACA-----GCCGCTGACTTAGATACCGATGCTTGCTTGCGT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9190 CCAACTGTTTCTACGCCCGCACCCACCACTACGGCGCCAACCGATTCTTCTGGG---CTT 9134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9250 CTTGTCGCCTGTTCAAAAAAAGTTAAGGAGCAACCACATGTGCCTGTCAAAACTATGGCA 9191
                                                   166 ArgArgAlaGluLeuSerTyr 172
                                                                                                                                                                                                                                                                  126 ValAlaValArgAsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGluIleIle 145
                                                                                                                                                                                                                                                                                                                                                                106 GlyHisThrAspGluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAla 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86 IleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAla 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 ------AlaPro-----AsnAlaProThrGlyTyrThrGlyValIle 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 MetThrGlyCysAlaAsnLysSerThrSerGlnValMetVal---------
                                                                                                 AGTTACGGTGAAGAGCGTCCGGTTTGCACTGAATCAACAGAAAGTTGCTGGTCACGTAAC 8798
CGGCGCGTTGAAATCGTCTAT 8777
                                                                                                                                                 SerPheGlyGluGluArgProIleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsn 165
                                                                                                                                                                                                                                                                                                                               GGCAATACTGATGAGCGCGGTTCGCGTGAGTATAATATAGCTCTGGGTGAACGGCGCGGT 8918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuProSerLeuValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAla 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TyrThrGlyValAlaProLeuValAspAsnAspGluThrValLysAlaLeuAlaSerLys 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="mndorhunrlmnatrsqlkiseiflstqggeansvgwptvfyrlt
GCPLRCQYCDTAYAFHGGEWCSIDTIVSEVRSYGVRHVCVTGGEPLAQKRCLLLLEKL
CDAGFEVSLETSGALDIAAVDLRVSRVVDIKTFGSGEAHRNHWPNLALLTPHDQIKFV
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/protein_id="AAF84700.1"
/db_xref="GI:9105987"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEEGLEFDVAHTSLLKRAIHTLQDALKALDQDWLPIYKSWRLNERHYGALQGLDKIDT AAKHGEEQVNIWRRSYDIQPPPIDLDDPSHPMRDRRYAALDRKVLPVTESLKNTLERV LPYWNDAIAPQLNKITVLISAHGNSLRALYKYLNQESDEKILNVNIPTGIPLLFELS DTLQVVSYRYLGDPDAAQRASEMVANQGKAK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transl_table=11
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Query Match:
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                  JOURNAL
MEDLINE
                                                                                               TITLE
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PUBMED
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No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 GTATATTTTGGTTTTGATAAATACGACATCACCGGTGAATACGTTCAAATCTTAGATGCG
                                                                                                                                                                                                                                                                                                                                                                                                             451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bergeron, M.G., Picard, F.J., Ouellette, M. and Roy, P.H.
Species-specific and universal DNA probes and amplification primers
to rapidly detect and identify common bacterial pathogens and
associated antibiotic resistance genes from clinical specimens for
routine diagnosis in microbiology laboratories
Patent: US 5994066-A 178 30-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AR089419.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unknown.
                                                  Deich,R.A., Metcalf,B.J., Finn,C.W., Farley,J.E. and Green,B.A. cloning of genes encoding a 15,000-dalton peptidoglycan-associated outer membrane lipoprotein and an antigenically related 15,000-dalton protein from Haemophilus influenzae
                                                                                                                                                                                         lipoprotein; outer membrane lipoprotein.
H.influenzae (strain S2, sub-species Rb)
Haemophilus influenzae
                                                                                                                                                                                                                                                                                                           H.influenzae PC protein (15kd peptidoglycan-associated outer
                                                                                                                                                                                                                                                      M18878.1 GI:148859
                                                                                                                                                                                                                                                                                           membrane lipoprotein), complete cds.
                                                                                                                                                                                                                                                                                                                                HEAA15KLP
                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAsp 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                LeuSerTyr 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGTTATTTAGCAGGTAAAGGTGTTGATGCTGGTAAATTAGGCACAGTATCTTACGGTGAA 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGluIleIleSerPheGlyGlu 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArg 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAAAACCTGCAGTATTAGGTCACGATGAAGCTGCATATTCTAAAAACCGTCGTGCAGTG 450
                                                                                                                                                                                                                                                                                                                                                                                                             TTAGCGTAC 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GluargProIleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArgArgAlaGlu 169
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                                      Bacteriol. 170 (2), 489-498 (1988)
                                                                                                                                  (bases 1 to 737)
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85 c 103 g
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1 (bases 1 to 737)
Anilionis, A., Seld,
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QQRYNTYYFGFDKYDITGEYYQILDAHaaylnatpaakvlvegntdergtpeynialg
QRRADAYKGYLAGKGYDAGKLGTVSYGEEKPAVLGHDEAAYSKNRRAVLAY"
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/protein_id="AAA24940.1"
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Deich,R.A., Zlotnick,G. and Green,B.
VACCINES AND DIAGNOSTIC ASSAYS FOR HAEMOPHILUS INFLUENZAE
Patent: WO 8804932-A 2 14-JUL-1988;
                                                                                                                                                                                                                                                                                                                    Sequence 2 from Patent WO 108799
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                                                                                                                                                                                               Unreported.
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and Rekosh,D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
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H.influenzae (isolate 1479) DNA, clone pBUD5.
Haemophilus influenzae
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                                                                                                                                                                                                                   253
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                                                                                                                                                                                                                                                                                                       /translation="MNKFVKSLLVAGSYAALAACSSSNNDAAGNGAAQTFGGYSVADL
QQRYNTVYFGFDKYDITGEYVQILDAHAAYLNATPAAKVLVEGNTDERGTPEYNIALG
QRRADAVKGYLAGKGVDAGKLGTVSYGEEKPAVLGHDEAAYSKNRRAVLAY"
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                                                                                                                                                                                                             /product="outer membrane protein P6' 168 c 175 g 271 t
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                                                                                                                                                                                                                                                                  /note="outer membrane protein P6 signal peptide
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/protein_id="AAA24994.1"
/db_xref="GI:148961"
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                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="outer membrane protein P6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:727"
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BCT 29-MAY-1998

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                                                                                                                                                                                                                                                                                                                 70 ValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAspGlu 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 867)
Murphy, T.F. and Apicella, M.A.
Plasmid for production of membrane protein, bacterium containing
same, monoclonal antibody therefore, and method for the
identification of haemophilus influenzae
Patent: EP 0281673-A1 1,14-SEP-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1 from Patent EP 0281673. I05561
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           GGTTATTTAGCAGGTAAAGGTGTTGATGCTGGTAAATTAGGCACAGTATCTTACGGTGAA
                                                   AsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGluIleIleSerPheGlyGlu 149
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Haemophilus influenzae Rd section 37 of 163 of the complete genome.
032722 L42023
                                                                                                                                                                                                                                                                                                                                     Medical Center Dr. Rockville, MD 20850, USA
The H. influenzae sequence has been updated by R. Pleischmann. New
database matches have been assigned, product names have been
improved, and a number of frame shifts have been corrected. We
gratefully acknowledge the work of Tatusov et. al. We have
incorporated their annotation into the /notes fields of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tatusov,R.L., Mushegian,A.R., Bork,P., Brown,N.P., Borodovsky,M., Rudd,K.E. and Koonin,E.V. Metabolism and evolution of Haemophilus influenzae whole-genome comparison with Escherichia coli Curr. Biol. 6 (3), 279-291 (1996)
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                                                                                                                                             Submitted (28-MAY-1998) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA
The whole genome was shifted by 588 nucleotides for a new start on Sep 30, 1996 this sequence version replaced gi:1221050.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Whole-genome random sequencing and assembly of Haemophilus
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                                                                                                                                                                                                                                                    White,O., Clayton,R.A., Kerlavage,A.R., Fleischmann,R.D., Peterson,J., Hickey,E., Dodson,R. and Gwinn,M.
                                                                                                                                                                                                                                                                                                                   corresponding H. influenzae genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (27-SEP-1997) The Institute for Genomic Research,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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                                          complement(61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clayton, R.A., Kerlavage, A.R. and Fleischmann, R.D.
complement(61. .513)
                                                            /db_xref="taxon:
                                                                                                                           Location/Qualifiers
                                                                                   /organism="Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (5223), 496-512 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rd
Rd
                                          .513)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gamma subdivision; Pasteurellaceae;
                                                                 71421"
                                                                                     influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20850,
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Hayes, W.S., deduced from a

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/translation="MKLLKRLVSVFAIVLAVGSNAFAGDEVRIVIDEGVDGARPIAVV PFVGSAPEDISKIVADDLRNSGKFNPIAVSQWPQRPYSAAEVNFEAWSNIGIDAIVIG OVVPSGNAFSTTYQLLDTVGASGFSGTVLMQNSYTVTNKWLRYGAHTVSDEVFDKLTA IRGAFRTRIAYVVQKNGGSQPYEVRVADYDGYNQFIVNRSAQPLMSPAWSDDGQFRLY VSFENKKSQLVVQDLNSGARKVVASFGGHNGAPAFSPDGSRLAFASSBDGVLNJYVNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="peptidoglycan-associated outer membrane lipoprotein (pal)"
/protein_id="AaC22039.1"
/db_xref="rd1:1573351"
/db_xref="MNKFVKSLLVAGSVAALAACSSSNNDAAGNGAAQTEGGYSVADL OQRYNTYFGFDKYDITGEYVQILDAHAAYLNATPAAKVLVEGNTDERGTPEYNIALG ORRADAVKGYLAGKGVDAGKLGTVSYGEEKPAVLGHDEAAYSKNRRAVLAY"
                                                                                                                                                      AQISADGKTLYMINGNNNVVKQDLTTGVSEVLSTSFLGESPSLSPNGIMIIYSSTQGL
GKVLQLVSADGRFKASLPGSDGQVKFPAWSPYLTK"
/note="similar to GB:M28232 SP:P19934 PID:148019 GB:U00096
                                                                     complement(3543. .4661)
                                                                                                                          complement(3543. .4661)
                                                                                                                                                                                                            ANGGTPTQLTSGAGNNTEPAWSPDGNSILFTSDRSGSPQVYRMDASGGSATAVGGRGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to SP:P10324 PID:1573351 SP:P10324 GB:M18878 PID:1573351 percent identity: 100.00; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                  /product="colicin tolerance protein (tolB)"
/protein_id="AAC22040.1"
/db_xref="GI:1573352"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similar to PID:1685080 percent identity: 96.96;
identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(2218. .3501)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(2218. .3501)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="codon recognized: AAG" complement(1733, .2194) /gene="HI0381"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="HI0382"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="HI0382"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(1733. .2194)
/gene="HI0381"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="tRNA-Lys-3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="tRNA-Lys-3"
complemen+'''
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MLENIRIVLIETSHSGNIGSAARAMKTMGLTQLGLVSPKSVDEQ
SYALSAGAENIVKNARVVDSFDEAVDDCPLVIGTSARLRHLQNTLIEPRECAEKVVAY
KGKIAIVFGRERIGLTNEELLKCHYHLNIPANPDYSSLNLAMAVQLVSYELRMAFLVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similar to GB:U00096 PID:1788881 percent identity: 54.43; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MKLTSKGRYAVTAVLDIALNADGGPVSLADISERQHISLSYLEQ LFAKLRKDGLVKSVRGPGGGYQLGLPSEQISVGMIIAAVNENIHVTKCLGRENCKNGV ECLTHELWEDLSLRIESFLNETTLAELVNKRNVKRQSHRDFNNLLVNQ"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELNILNGMLSAVEKRIDLTKEDN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NNKKNSLSLIEKNYPTTDQLAYFFDYTERIYQSLGFIQNQGVMRKLKRLYYRAKLEKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="tRNA-Lys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAC22038
/db_xref="GI:1573350"
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/protein_id="AAC22038.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(566. .1291)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table=11
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/protein_id="AAC22037.1"
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/db_xref="GI:1573349"
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gene CDS

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Query Match:
                                                          Best Local Similarity:
                                                                              Percent Similarity:
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                                                                                                                                                                                           /gene="HI0387"
6606. .8528
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to SP:P08999 PID:1128977 GB:U00096 PID:1786957 percent identity: 53.08; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="colicin transport protein (tol0)"
/protein id="AAC22043.1"
/db_xref="GI:1573355"
/translation="MTAELNFLDLFLKASIVVOLVIVILISESIISWAIIIQRSRILT
NALKEARTFEDRFWSGEDLNKLYEGLSNRRDGLTGSEQIFCVGFKEFSRLKQVWPDAP
EAIIKGTMRANNLAMMREIESLENRVEFLATVASVSFYIGLFGTVWGIMHAFMALSGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MARRORKAIKSEINIVPFLDVLLVLVLIFMATAPIISQSVQVEL PDSVQSQEVSNEDKVPVILEVAGIGKVAISIGGERQEGLTEEMVTQLSRQEFDKDNNT LFLVGGAKEVPYEEVIKALNILHLAGIKSVGLMTNPI" complement(5168. .5854) /gene"H10385"
                                                                                                                                                                                                                                                                    MLSKATVKVACVDLGKMKPVAFPKEVKAAFHHLK"
                                                                                                                                                                                                                                                                                                                                    /product="conserved hypothetical protein"
/protein_id="AAC22044.1"
/db_xref="GI:1573356"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(5871. .6281)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KQATLQMVAPGIAEALIATAIGLFAAIPAVMAYNRLSLRVNAIEQDYGNFIDEFTTIL
HRQAFGKAPH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(5871. .6281)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"similar to SP:005828 PID:1128978 GB:000096 PID:1651329 PID:1786958 percent identity: 68.47;
                                                                                                                                                                                                                                                                                      ?TQQTLLEEQQLAFVVKTLAIDYCVAAKLDDLLMVETEVSEVKGATILFEQRLMRNTL
                                                                                                                                                                                                                                                                                                             translation="MLDNGFSFPVRVYYEDTDAGGVVYHARYLHFFERARTEYLRTLN"
                                                                                                                                                                                                                                                                                                                                                                                                                  transl_table=11/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="colicin transport protein (tolk)"
/protein_id="AAC22042.1"
/db_xref="GI:1573354"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="similar to SP:P05829 PID:1128980 GB:U00096 PID:1651330 PID:1786959 percent identity: 61.76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DICSAALSAVARTKKYPAAPSDEIYEKYKSPIIDFDIR" complement(4677...5096)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="outer membrane integrity protein (tola)"
/protein_id="AAC22041.1"
/db_xref="GI:1573353"
/translation="MONNROKKGINAFAISILLHFILFGLLILSSLYHTVEIMGGGEG
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ORQEELKRQQOEQRQOEIKKQQEQARGAKKKAAAAEAKLKAAAEAKK
PRANIFOKTERINGSTENSOK
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                                                                                                                                                                                                                                                                                                                                                                                                                                            codon_start=1/
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LGSGDGGKVGDQYAGVIKKEIQRRFLKDPNFAGKVCRIKIQLGRDGTILGYQKISGSD
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49.51%
30.66%
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             gene
                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1984 CACGCTGCATATTTAAATGCAACGCCAGCTGCTAAAGTATTAGTAGAAGGTAACACTGAT 1925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2044 GTTTATTTCGGTTTTGATAAATATGACATTACTGGTGAATACGTTCAAATCTTAGACGCG 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1744 TTAGCGTAC 1736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 ValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAspGlu 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90 GlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAsp 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Capela,D., Barloy-Hubler,F., Gouzy,J., Bothe,G., Ampe,F., Batut,J. Boistard,P., Becker,A., Boutry,M., Cadleu,E., Dreano,S., Gloux,S., Godrie,T., Goffeau,A., Kahn,D., Kiss,E., Lelaure,Y., Masuy,D.,
                                                                                                                                                                                                                                           France, Laboratoire de Genetique et Developpement UMR6061-CNRS, Faculte de Medecine, 2 avenue du Pr. Leon Bernard, F-35043 Rennes, France, GAPC GmbH, Fritz-Arnold-str. 23, D-78467 Konstanz, Germany, Universitaet Bielefeld, Biologie IV (Genetik) Universitaetstr 25, D-33615 Blelefeld, Germany, Unite de Biochimie physiologique, Universite Catholique de Louvain, Place Croix du Sud 2, Bte 20, B-1348 Louvain-la-Neuve, Belgium, Unite de Microbiologie, Faculte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sinorhizobium meliloti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL591791 AL591688
AL591791.1 GI:15075538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sinorhizobium meliloti 1021 complete chromosome; segment 10/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (26-JUL-2001) Gouzy J., Submitted on behalf of the MELILO EU Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sinorhizobium meliloti strain 1021
Proc. Natl. Acad. Sci. U.S.A. 98 (17), 9877-9882 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pohl,T., Portetelle,D., Puehler,A., Purnelle,B., Ramsperger,U., Renard,C., Thebault,P., Vandenbol,M., Weldner,S. and Gallbert,F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sinorhizobium meliloti.
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                                                                                                                                                              des Sciences Agronomiques de Gembloux, Avenue Marechal Juin 6,
B-5030 Gembloux, Belgium. E-mail:Jerome.Gouzy@toulouse.inra.fr
http://sequence.toulouse.inra.fr/meliloti.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratoire de Biologie Moleculaire des Relations plantes-Microorganismes, UMR215-CNRS-INRA, BP27, F-31326 Castanet,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MELILO EU Consortium:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Analysis of the chromosome sequence of the legume symbiont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGTTATTTAGCTGGTAAAGGTGTTGATGCTGGTAAATTAGGCACAGTATCTTACGGTGAA 1805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArg 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1481430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuSerTyr 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAAAAACCTGCAGTATTAGGTCATGATGAAGCTGCATATTCTAAAAAACCGTCGTGCAGTG 1745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GluArgProIleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArgArgAlaGlu 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGluIleIleSerPheGlyGlu 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 340900)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 340900)
                                                              /organism="Sinorhizobium meliloti"
/strain="1021"
                                         /db_xref-"taxon:382"
                                                                                                                                              Jocation/Qualifiers
                                                                                                                        .340900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Batut, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
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QDDIIIEGGELHLPVGKPVKMLLRSUDYLHDFYVPEFRAKMDWYDMNTYFWLTFTRT
QDDIIIIEGGELHLPVGKPVKMLLRSUDYLHDFYVPEFRAKMDWYDMNTYFWLTFTRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLYPEPTIDE II TRANSMEMBRANE
/protein_id="CAC47095.1"
/db_xref="GI:15075540"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TKMVFPGLKKDEEIANVIAYLKQHPK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="SPTREMBL:Q92MU4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="PUTATIVE CYTOCHROME /protein_id="CAC47094.1" /db_xref="GI:15075539"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               predicted by FrameD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(1457. .1513)
/note="Sm-5 OR SMC04646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       predicted by Homology predicted by FrameD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               electron transport"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /transl_table=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="SMc01981"
                                                                                                                                                                                                                                                                                                                                                                   /note="Product confidence : probable
Gene name confidence : probable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="coxN OR SMc01983"
1634. .3415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         predicted by Homology"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GFPSGIATEQGTGASALFKEERECFGPAATTVAASAAQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTFEILCAELCGVGHPQMRGTVVVDTEEDYQAWLAEQQTFSQLSASSETRAVPEKVCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence=not_experimental
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /function="small molecule metabolism; energy transfer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="coxM OR SMc01982"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /evidence=not_experimental
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Qysmfaiaigmvalvlswlirlolgfpgtfelidaeryyofitmhgmimviylltalf
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/protein_id="CAC47096.1"
/db_xref="GI:15075541"
                                                                                                                                                                                                                                                                                                                                                                                                                       electron transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1634..3415
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/EC_number="1.9.3.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT SM-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="PROBABLE ALTERNATIVE CYTOCHROME C OXIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Product confidence :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon_start=1/
                                                                                                                                                                                                                                                                                         predicted by
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                                                                                                                                                                                                                                                                                                                                          predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  /EC_number="1.9.3.1"
/function="small molecule metabolism; energy transfer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /evidence=not_experimental
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                                                                               /db_xref-"SPTREMBL:Q92MU2"
                                                                                                                                                                                                                                                                codon_start=1
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                                                                                                                                                                                                                                                                                                                                             by Codon_usage
                                                                                                                                                                                                                                                                                            Homology
FrameD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C TRANSMEMBRANE PROTEIN"
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gene

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AAQFGSTFFMITGFHGTHVTFGVIFLLIVARKVWRGDFETERRGFFTSRKGRYEIVEI
TGLYWHFVDLVWVFIFAFFYLW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TFLLSDTFVFGCFLLAYMSARMSTSVPWPNPSEVFALEIGGTHNPLILIAIMTFVLIS
SSGTMAMAVNYGYRRDRRKTAALMLLTALFGAAFVGMQAFEWSKLIAEGVRPWGNPWG
                                                                                                                                                                                                    predicted by Codon_usage predicted by FrameD"
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/note="Product confidence: hypothetical
Gene name confidence: hypothetical
                                                                                                                                                                                                                                                                                                                                                                                /gene="SMC01986"
4857. .5216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="PROBABLE CYTOCHROME-C OXIDASE PROTEIN"
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/db_xref="GI:15075544"
                                                                                 /product="HYPOTHETICAL
                                                                                                               /evidence=not_experimental
/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="msivafflaaiaaiiamwlagorltsrpwlevghfhdrrgatrl
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/db_xref="GI:15075542"
/db_xref="SPTREMBL:092MU1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WASGVIEFCROLLT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 {	t TGMHGLHIIGGLFALGRVTAHASQTPLGNRTRLSIELCAIYWHFMLIVWLVLFALFAG}
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                                                                                                                                                                            codon_start=]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              153 IleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArgArgAla 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          133 LeuGlyLysGlyTleAsnGlnAlaSerValGluIleTleSerPheGlyGluGluArgPro 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 SerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArgAsnTyrLeu
1 (bases 1 to 10906)

1 (bases 1 to 10906)

1 (chen,Y., Woo,L., Kitajima,J.P., Okura,V.K., Almeida Jr.,N.F., Chen,Y., Woo,L., Kitajima,J.P., Okura,V.K., Almeida Jr.,N.F., Zhou,Y., Bovee Sr.,D., Chapman,P., Clendenning,J., Deatherage,G., Gillet,W., Grant,C., Guenthner,D., Kutyavin,T., Levy,R., Li,M., McClelland,E., Palmieri,A., Raymond,C., Rouse,G., Baenphimmachak,C., Wu,Z., Gordon,D., Eisen,J.A., Paulsen,I., Karp,P., Romero,P., Zhang,S., Yoo,H., Tao,Y., Biddle,P., Jung,M., Krespan,W., Perry,M., Gordon-Kamm,B., Liao,L., Kim,S., Hendrick,C.,
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                                                                                                                                                                                                                    Agrobacterium tumefaciens str. C58 (U. Washington).
Agrobacterium tumefaciens str. C58 (U. Washington)
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
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YFGLQGYLRWSLILIFMMLKAGLIVAVFMHMAWERLALIYAIILPPLLVLVFVALMVS
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/function="small molecule metabolism"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhao, Z., Dolan, M., Tingey, S.V., Tomb, J., Gordon, M.P., Olson, M.V.
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98195-7242, USA
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/gene="mrsA"
                                                                                                                                                                AGVDEAKQDLEEIVEFLRDPQKFQRLGGKIPRGVLLVGPPGTGKTLLARSVAGEANVP
FFTISGSDFVEMFVGVGASRVRDMFEQAKKNAPCIIFIDEIDAVGRHRGAGLGGGNDE
REQTLNQLLVEMDGFEANEGIILIAATNRPDVLDPALLRPGRFDRQVVVPNPDIVGRE
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NGININLECGSTHPEALQKKLHEVRADIGIALDGDADRVIIVDERGEIVDGDQLMAVI
ADSWAADNTLRGGGIVATVMSNLGLERFLGDKGLTLARTKVGDRYVVEHJKRNHUVNVG
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/protein_id="AAL44519.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(113. .1489)
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MVMQLPEGDRYSMSYKWMVSRLVIMMGGRVAEELTFGKENITSGASSDIEQATKLARA
MVTQWGFSDALGQVAYGENQQEVFLGHSVSQSKNVSEATAQTIDTEVRRLIDEAYTEA
RRILTDNHDGFVAIAEGLLEYETLTGEEIKALLRGEKPARDLGDDSPGSRGSAVPKAG
                                                                                                 RILKVHVRNVPLAPNVDLKILARGTPGFSGADLMNLVNEAALMAARRNKRVVTMQEFE
DAKDKIMMGAERRSSAMTEAEKKLTAYHEAGHAITALKVAVADPLHKATIIPRGRALG
                                                                                                                                                                                                                                                                                                                                                                /product="metalloprotease"
/protein_id="AAL44520.1"
/db_xref="GI:17742132"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(1654. .3600)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GEQSGHIVLSDYGTTGDGLVAALQVLAKVKRSGLTVSEVCRKFEPVPQLLKNVRISGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RRGHHRHRVVIGKDTRLSGYMLENALVAGFTAAGLDVFLLGPIPTPAVAMLTRSLRAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="identified by sequence similarity; putative;
located using Blastx/Glimmer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="mrsA"
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                                                                                                                                                                                                                                                                     SSGFLSYLGTLLPMFLILGVWLFFMRQMQGGSRGAMGFGKSKAKLLTEAHGRVTFDDV
                                                                                                                                                                                                                                                                                                        DVDSGRVRDVTVTGNRVLGTYTENGTAFQTYSPVIDDSLMERLQSKNVTIVARPESDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="identified by sequence similarity; putative; ORF
located using Blastx/Glimmer"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="ftsH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISSARSAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IGVMISASHNPFSDNGIKLFGPDGYKLSDELELEIEDLLDKDIYAQLAKPAEIGRAKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Atu3709"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:180835"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    strain="C58"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Agrobacterium tumefaciens str. C58 (U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="ftsH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translation="MPERFGVQMARRYFGTDGIRGQSNVFPMTPDLAMRVGIAVGTIF/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="GI:17742131"
                                                                                                                                                                                                                                                                                                                                        translation="MNPNFRNFALWAVIALLLIALFSMFQTSPTQTGSREIPYSQFIR"
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complement(5111. .6100)
/gene="Atu3712"
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GMADAVLYDAHLWIMRPFLACERQVIRDYVSSRSRHWLDDPSNENIRYERVRVRQTLP
HSPIALDDSTAVRRQMLSERTAVFLRERAQVFHAALARLADDDVNPDLPEERHGLAAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(3755.
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APKKKAEASPYNEATPDTDDVATIIETPOGGASVSPPESSSASTAAPGETTLGSIEL
DSKOMPVGGTLINGGAINSSGSLFGYTTGMGTERKTDPVNTAALTSEGDIYQAYCHVLS
GDYKLAEQGFQOYLOGYPKGTKAADASFWLGEAQYSQGKFNEAAKTFINGHOTYGKSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IAALGGRSYFPAASSMERVLRFLKTGETGRMTVGRVLLDRRRDGLYIFREQRNLPELQ
IESSGQAVWDDRFLVKNGSDFPINVAAGRVGTAAQAAALFPSAPSGVVKPAMAGLPQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="identified by sequence similarity; putative; ORF located using Blastx/Glimmer"
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/protein_id="AAL44524.1"
/db_xref="GI:17742136"
/db_xref="GI:17742136"
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LVTGKYVTRESDGRLRAEFRLKFOTFAGQOLGFTQPENWRRVAHIIADAIYERVTG
EKGYEDTRVVEYSESGKFTARKRQLSIMDQGGGFTQPENWRRVAHIIADAIYERVTG
YMSFEGQQPKVYLLQLETGQREVVGNFFGMTFSPRFSPDGQKVIMSLQQDGNANIYTM
TMSFEGQQPKVYLLQLETGQREVVGNFFGMTFSPRFSPDGQKVIMSLQQDGNANIYTM
DLRSRTTTRLINTAAIDTAPSYSPDGQRVAFESDRGGRQQIVMADGSGQQRVSFGU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KAPEMLMKLGMSLAALDNTETACATLREVPKRYPNASKTVLSKVASEQKRLSC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="conserved hypothetical protein"
/protein_id="AAL44522.1"
/db_xref="GI:17742134"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="identified by sequence similarity; putative;
located using Blastx/Glimmer"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="msrtnisalspmqklarnpayiamtlalalagcankknmpnsag
ELGLGGAGSATPGSQQDFTVNVGDRIFFDTDSTSIRADAQQTLQRQAQWLSRYENYAI
TVEGHADERGTREYNLALGARRAAATRDFLASQGVPASRMKTISYGKEKPVAVCDDIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(6274. .6807)
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/note="Atu3713"
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                              /note="identified by sequence similarity;
located using Blastx/Glimmer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(7018. .8325)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="omp16 protein"
/protein_id="AAL44523.1"
/db_xref="GI:17742135"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="identified by sequence similarity; putative; ORF
located using Blastx/Glimmer"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translation="MAGMLGLAACTGLSGTAVSGPLFGAGGSFGTINSQQPPIVRVQA/
MFFRQNAGAGGPQLYSIDLTGYNEQLIKTPTFASDPAWSPLLD"
                               GSYSTPVWSPRGDLIAFTKQSGGKFSIGVMKTDGSGERILTSGFHNEGPTWAPNGRVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Atu3714"
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DB:
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Best Local Similarity:
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6423 CGTGACTTCCTGGCTTCCCAGGGCGTTCCGGCCAGCCGCATGAAGACGATCTCCTACGGC 636
                                                                                                                                                                                   6543 CGCCAGGCCCAGTGGCTGTCCCGTTACCCGAACTACGCTATCACCGTCGAAGGCCATGCC 6484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6750 GCTGTCATCGCCATGACGCTCGCGCTTGCTCTCGCAGGCTGCGCGAACAAGAAGAAC---
                                                                                                                                                                                                                                                                                                                                                                                                                                50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 GlnValMetValAlaProAsnAlaProThrGlyTyrThrGlyValIleTyrThrGlyVal 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 AlaAlaAlaAlaLeuSerValLeuThrPheMetThrGlyCysAlaAsnLysSerThrSer
                                           ArgAsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGluIleIleSerPheGly 148
                                                                                         AspGluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaVal 128
                                                                                                                                                                                                                            GluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThr 108
                                                                                                                                                                                                                                                                          CGCATCTTCTTCGACACCGACTCCACTTCGATCCGCGCCGACGCCCAGCAGACCCTGCAG 6544
                                                                                                                                                                                                                                                                                                                 LeuValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAsp 88
                                                                                                                                                                                                                                                                                                                                                                                                               Ala---ProLeuValAspAsnAspGluThrValLysAlaLeuAlaSerLysLeuProSer 68
                                                                                                                                                                                                                                                                                                                                                                           GCAACGCCGGGCTCCCAGCAGGACTTCACGGTC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----ATGCCGAACAGC---GCCGGTGAACTCGGCCTTGGTGGCGCCTGGCTCC 6649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MKGSLTTSAIVHASLLAFALVSLGSPEPLDVSQAEALPVELVPI
EELSQJQQGDKNAPKAEKSAPVPTTRPDIIPNAQNIGNNVADIEAPPTPTKPNDNIA
AAAPPKOEKPOPVVDTKANEVKEIVKEETSAPKPGEMAALPQTKPEIAPQPKPEPPPO
ETKAEEPPPATQEPAEIPVPQNVPRPNSRPEPPKQAETKRAEQKPAEKKPDQAK
STDKPSDKKPGEKKQETAKSASSKESDFNADDVAALLNKQAPSGGGAKRSTQTASLGG
KKSTGGSTLSQTEMDALRGAIQKNWQIIPGMADAADVRVRVTMKLDRDGTIIGRPEIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="mgmsaggsggsggrrggrggrrggaiseinvtplvdvmlvlli
IFMVAAPMMTVGVPIDLPQTSANALNSDTQPITISVNANGQIHLQETEIQAAEVADKL
QAIATTGYNERIFVRADSVAAYGVVADVMARIQAAGFKNIGLVTQQKQDN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(10027. .10746)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="tolk protein"
/protein_id="AAL44526.1"
/db_xref="GI:17742138"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="conserved hypothetical protein"
/protein_id="AAL44525.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="identified by sequence similarity; putative; ORF
located using Blastx/Glimmer"
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262.00
55.62%
38.12%
30.43%
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Indels:
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28
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                                                                                                                                                                                                                                                                                                                                                                      ----AATGTCGGCGAC 6604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l (bases 1 to 11049)
Hinkle,G., Slater,S.C. and Goodner,B.
Complete Genome Sequence of Agrobacterium tumefaciens C58
(Rhizobium radiobacter C58), the Causative Agent of Crown
Disease in Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Street, Cambridge, MA 02139, USA Approximately 800 bp of telomeric sequence missing from the left
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (14-AUG-2001) Bioinformatics, Cereon Genomics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 11049)
Hinkle,G., Slater,S.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Agrobacterium tumefaciens str. c of 187 of the complete sequence. AE008312 AE007870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Agrobacterium tumefaciens str. C58 (Cereon). Agrobacterium tumefaciens str. C58 (Cereon)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AE008312.1 GI:15159599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the chromosome and 200 bp missing from the right end.
                                                                                                                                                                                            GSIELDSKGMPVGGTLNQGANNSSGSLPGVTTGNGTRKTDPVNTAALTSEGDIYQAAY
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/note="(AJ243808) YaeN protein"
                                                                                    /gene="AGR_L_2252"
1857. .3188
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QTGSREIPYSQFIRDVDSGRVRDVTVTGNRVLGTYTENGTAFQTYSFVIDDSLMERLQ
SKNVTIVARPESDGSSGFLSYLGTLLEMFLLLGVMLFFMRQMQGSSGAMGFGKSKAK
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RQYVVPNPDIYGRERILKVHVRNVPLAPNDLKILARGTPGFSGALAMLLVLVEALAM
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IESSGQAVWDDRFLVKNGSDFPINVAAGRVGTAAQAAALFPSAPSGVVKPAMAGLPQI
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5454. .6830
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TEVRRLIDEAYTEARRILTDNHDGFVAIAEGLLEYETLTGEEIKALLRGEKPARDLGD
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Best Local Similarity:
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      520 CGTGACTTCCTGGCTTCCCAGGGCGTTCCGGCCAGCCGCATGAAGACGATCTCCTACGGC
                                                                                                                                                                                                                                                                                                                                                                                         340 CGCATCTTCGACACCGACTCCACTTCGATCCGCGCCGACGCCCAGCAGACCCTGCAG 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 GlnValMetValAlaProAsnAlaProThrGlyTyrThrGlyValIleTyrThrGlyVal 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 AlaAlaAlaLeuSerValLeuThrPheMetThrGlyCysAlaAsnLysSerThrSer 29
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                                                                                                                                                                                                                                                               CGCCAGGCCCAGTGGCTGTCCCCGTTACCCGAACTACGCTATCACCGTCGAAGGCCATGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 LeuValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAsp 88
                                                                                                                                    GACGAACGCGGTACGCGTGAATACAACCTGGCGCTCGGCGCCCGTCGTGCCGCCGCAACC 519
                                                                                                                                                                        AspGluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaVal 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCAACGCCGGGCTCCCAGCAGGACTTCACGGTC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVLDKLRANSAIRQVKPLTFNVD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALLEKENVALDIGAYRDAPSGLRIWAGATIETADMEAVMPWLAWAYQTQKAALSKAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DVGSHMIYITNTDVPGMIGFMGTTLGEAGVNIANFQLGREKEAGDAIALLYVDGPVSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_table-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55.62%
38.12%
30.43%
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262.00
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gene

CDS

CDS

---AATGTCGGCGAC 339

294

249

CDS gene gene

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FEATURES
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ORGANISM
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LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PUBMED
                                                                                                                                                                                      CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 149 GluGluArgProIleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArgArgAla 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 10643)

Eisen, J.A., Nelson, K.E., Paulsen, I.T., Heidelberg, J.F., Wu, M.,

Dodson, R.J., Debby, R., Gwinn, M.L., Nelson, W.C., Haft, D.H.,

Dodson, R.J., Debby, R., Gwinn, M.L., Nelson, W.C., Haft, D.H.,

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Vanathevan, J., Khouri, H., White, O., Gruber, T.M., Ketchum, K.A.,

Venter, J.C., Tettelin, H., Bryant, D.A. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dodson, R.J., Debby, R., Gwinn, M.L., Nelson, W.C., Haft, D.H., Hickey, E.K., Peterson, J.D., Durkin, A.S., Kolonay, J.L., Yang, F., Holt, T., Umayam, L.A., Mason, T., Brenner, M., Shea, T.P., Parksey, D., Nierman, W.C., Feldblyum, T.V., Hansen, C.L., Czaven, M.B., Radune, D., Vanathevan, J., Khouri, H., White, O., Gruber, T.M., Ketchum, K.A., Venter, J.C., Tettelin, H., Bryant, D.A. and Fraser, C.M.

The complete genome sequence of Chlorobium tepidum TLS, a photosynthetic, anaerobic, green-sulfur bacterium Proc. Natl. Acad. Sci. U.S.A. 99 (14), 9509-9514 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chlorobium tepidum TLS
AE012837 AE006470
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GKDKSLVPKVLPPPPSSSMSSNSSGSTSAQSKEEASAATGEALLSEGLIKMKRGDYAG
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2455. .3243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(3366. .3797)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(3366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LYKQGLSFAKIGDEANAKARYKDVLNLYPQSPEAKLAQKNLDKK"
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                                                                                                                                                                                                                                                                                                                                             IDFDKRGVKWTMREIPVFYHEGKGLCVELHNKIYTLDQFFK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to PID:624955; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="conserved hypothetical protein"
/protein_id="AAM71879.1"
/db_xref="GI:21646577"
                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="pscD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="CT0641"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="pscD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MVPAIFLSACASQKDLSYVQGEVSQLKQESTVIKQQSAGSYSEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="identified by Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="CT0640"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MQKEKWQEPTKDVWFSSWIDIWFMNNKTGGWA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(2384. .2482)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(2384. .2482)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KNRRDHFVVK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GHCDERGTDEYNIALGERRAEAARMYLVNLGVSGGRLSTVSYGEEKPFDPGHNEEAWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="mrrTLTGIIGAAMIILAGCSSKSAVSTDETSRAGYGSGMGGGTGAGGVSVEDIGQGGKAGSIIGDIFFDFDSSALSSEAQEQLNQNAAWMQKNPTSAVIIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="identified by Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="CT0639"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="CT0639"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="peptidoglycan-associated lipoprotein"
/protein_id="AAM71877.1"
/db_xref="GI:21646575"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF00691"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MQVQGMMSFGADQARMTTISYSEEKPFDLGHDETAGSKNRWAHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="GI:21646574"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="identified by match to PFAM protein family HMM
                                                                                                                                                                                                                                                                .4590
                                                                                                                                                                                                           by Glimmer2;
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Best Local Similarity:
Query Match:
US-09-674-779B-2 (1-172) x AE012837 (1-10643)
                                                                                       Percent Similarity:
                                                                                                                                            Alignment Scores:
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                                                                                                                                                                                gene
                                                                                                                           NO.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(4720. .6621)
/gene="dnak"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HLSDIPPAPRGVPQIEVTFDIDANGILNVSAKDKATGKEQSIKIEASGKLTEAEIEKM
KEDAKAHAAEDQKRKEEIELKNSADSLIFSTEKQLTELGDKLPADKKAAIESALEKLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MGKIIGIDLGTTNSCVAVMQGTQPTVIENSEGSRTPSWVAFTK
TGERLYGQAAKRQAVTNPKNITIFSIKREMGRKTDEVPNEKKLASYDVVNEGGYAKVKI
GDKTYSPQEISAMILOKMKQTAEDELGEKVTERAVITVPAYENDAORQATRDAGKIAGL
EVKRIINEPTAAALAYGLDKKKENEKVAVFDLGGGTFDISILELGGGVEEVKSTDGDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(6701. .7099)
/gene="CT0644"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSTRIPKVQALVKEFFGKEPNKSVNPDEVVAIGAAIQGGVLQGDVTDVLLLDVTPLSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HLGGDDFDQVIINYLADEFKKQEGIDLRKDAIALQRLKEAAEKAKIELSSRTDTEINL
PFITATQEGPKHLVINLTRAKFEAMSAALFDKLFEPCRRAIKNSKFDIKEIDEVVLVG
                                                                                                                                                                                               /translation="MSKSMTITEEEVKKWQFNMPDEMLDAVSNRFKLLSEPMRLKILR ALCDREHTVQEIVKEVGASQANISKHLALMHDNGVVNRRKEGLKCYYRISDDSIVYAC FLISKSVVENLQDRLSWIQKVYTNLTT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="CT0645"
7118. .7228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LPGIAKEQIALNIEDDVLTIKAERTHKEEEEKKKNYHRVERTYGSFSRSFNIGEIIDQE
HIGATYDNGYLHVTLPKTQPAKKTKEIPIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="heat shock protein, Hsp20 family"
/protein_id="AAM71883.1"
/db_xref="GI:21646581"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YEVIDGDDK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EAHKSGRVDAIKPAMDELSKVWSDAASNLYGQPGAEPQPETNGHAGGSKGGDGAVNAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GIETLGGVMTKLIEANTTIPTRKQEIFSTAADNQTSVEVHVLQGERPMASDNKTLGRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAM71882.1"
/db_xref="GI:21646580"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="DnaK protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="identified by match to PFAM protein family HMM
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                                                                                                                                                                                                                                                                                                                                                                complement(7467. .7856)
                                                                                                                                                                                                                                                                                                                                                                                                  complement(7467. .7856)
                                                                                                                                                                                                                                                                                                                                                                                                                   /product="hypothetical protein"
/protein_id="AAM71884.1"
/protein_id="AAM71884.1"
/db_xref="Gi:21646882"
/translation="MFVFSREGLWRSLITSVIETSKDVPKRFFHFDSLCV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7118
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/transl_table=11
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                                                                                                                                                                                complement(8023.
                                                                                                                                                                                                                                                    /product="transcriptional regulator, ArsR family"
/protein_id="AAM71885.1"
/db_xref="GI:21646583"
                                                                                                                                                                                                                                                                                                                                                                             /gene="CT0646"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="CT0645"
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                                                                                                                                                                                                                                                                                                         /transl_table=11
                                                                                                                                                                                                                                                                                                                                             /gene="CT0646"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translation="MLMKIAKDPMRLFDDIWSGSQMAVAPSFKVDISEDENAYHLDAE/
                                                                                                                                                                                                                                                                                                                                /codon_start=1
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                                                   259.50
56.41%
35.90%
30.14%
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                                                                                                                                                                                    .8250)
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                                                                                                            Length:
Matches:
                                                                        Mismatches:
                                                                                       Conservative:
                                                        Indels:
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32
63
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                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                REFERENCE
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                                                                                                                                                                                                                                                                                                                                     MEDLINE
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                                                                                                                                  JOURNAL
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                                                                                                                                                                                                                                                                                                                 PUBMED
                                                                               source
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15 SerValLeuThrPheMetThrGlyCysAlaAsnLysSerThrSerGlnValMetValAla

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2218 CTGGTTAACCTTGGAGTAAGCGGAGGCCGTCTTTCTACCGTCAGTTACGGCGAAGAAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1918 GAAACCTCCAGAGCCGGTTATGGATCGGGAATGGGAGCGGAACTGGAGCAGGAGCAGGA 1977
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2278 CCGTTTGACCCCGGTCATAACGAAGAGGCTTGGGCAAAGAACAGAAGA 2325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 GlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArgAsnTyr 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152 ProIleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArgArg 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 LeuLeuGlyLysGlyIleAsnGlnAlaSerValGluIleIleSerPheGlyGluGluArg 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heidelberg, J.F., Eisen, J.A., Nelson, W.C., Clayton, R.A., Gwinn, M.L., Dodson, R.J., Haft, D.H., Hickey, E.K., Peterson, J.D., Umayam, L., Gill, S.R., Nelson, K.E., Read, T.D., Tettelin, H., Richardson, D., Ermolaeva, M.D., Vamathevan, J., Bass, S., Qin, H., Dragoi, I., Sellers, P., McDonald, L., Utterback, T., Fleishmann, R.D., Nierman, W.C. and White, O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heidelberg,J.F., Eisen,J.A., Nelson,W.C., Clayton,R.A., Gwinn,M.L., Dodson,R.J., Haft,D.H., Hickey,E.K., Peterson,J.D., Umayam,L.A., Gill,S.R., Nelson,K.E., Read,T.D., Tettelin,H., Richardson,D., Gill,S.R., Nelson,K.E., Read,T.D., Tettelin,H., Richardson,D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                Ermolaeva,M.D., Vamathevan,J., Bass,S., Qin,H., Dragoi,I., Sellers,P., McDonald,L., Utterback,T., Fleishmann,R.D., Nierman,W.C., White,O., Salzberg,S.L., Smith,H.O., Colwell,R.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
1 (bases 1 to 11914)
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Vibrio cholerae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AE004259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 095230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCCTGGATGCAGAAAAACCCCTACTTCTGCCGTGATCATTGAGGGACATTGCGATGAGCGG 2157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAspGluArg 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTCGATTTCGACAGTTCGGCACTAAGCTCCGAAGCACAGGAACAACTCAATCAGAATGCC 2097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAspGluGlnAla 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuValAspAsnAspGluThrValLysAlaLeuAlaSerLysLeuProSerLeuValTyr 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProAsnAlaProThrGlyTyrThrGlyValIleTyrThrGlyVal------AlaPro 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 11914)
                                                                                                                                                                                                                                                                          Center Dr, Rockville,
/note="biotype: El Tor"
                                                                                                                                     /strain="N16961"
                                                                                                                                                                                                                                          Location/Qualifiers
                            /chromosome="I"
                                                                /db_xref="taxon:666"
                                                                                                    /serotype="01"
                                                                                                                                                                         /organism="Vibrio cholerae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GI:9656353
                                                                                                                                                                                                                                                                                                                                                                                      Venter, J.C. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11914 bp DNA linear BCT 31-304-20 _{
m jome~I}, section 167 of 251 of the complete
                                                                                                                                                                                                                                                                                  MD 20850,
                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                      Research, 9712
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                  SGGLWPEPNLSATDPSLRYDSLFFNKAIDGQVDQLSSWNNPKAGGYDRESWILAAERE
AEGLIEWSPYVVDPYTRVEMITVSTPYYRNGQFAGVATVDLSLESLIQFVAATAEQYN
LGVNLKDAFGVEVVSHNFRIYNALVSIYSFGEFNWQIEVVRANGOVDEIIPDLIINI
EKGLMPILLLCVMVOYFLISHYMIFDIVLIAKKVSESREGEIIDIRYKSQDEIRHLID
TFNQKTIYLEAEKVKAQASTKAKSAFLATLSHBIRTENNGVLGTAQILLKDELITSKQR
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GLKFQLNSEITDGRWYYGDKARLRQIIFNLLSNAVKFTEAGFVAIGLSEESCDEENYL
                                                                                                                                                                                                                                                                                                                                                                                                                                complement(2163. .4373)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(2163. .4373)
                                                                                                                                                                                                                                                                                                         /transl_table=11
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/db_xref="GI:9656357"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2101. 2196
/gene="VC1830"
/note="identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="VC1830"
2101. .2196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="hypothetical protein"
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/db_xref="GI:9656356"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(2016 .2123)
/gene="VC1829"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SRTLSIPVNIAIAWPYGVFRDYVLRQGRKISPTGWMKNLSDLVAYVLFQSPVYAAILF
TVGASTDQIITAVATNALVSCGMGVLYGYFLDMCRRWFKVPGYTVSEG"
                                                                                                                                                                                                                                                                                                                                 /codon_start=]
                                                                                                                                                                                                                                                                                                                                                   identified by sequence similarity;
                                                                                                                                                                                                                                                                                                                                                                           /note="similar to GB:U07069 PID:459205 SP:P54302;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translation="MPAELGHTHKKGKKEGRNRVIYSTDGKDGSR"/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MWPSSAGKKLSHRAHRDVIKLPNVNLETDVLTKNA" 2101. .2196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="identified by Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(2016. .2123)
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/note="identified by Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(1375. .1827)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PKYMDIDELVACTQFKHKPLEQLRLKPEVIEGCEQYPIPVADFKFAIIPPTTQQTIGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="mtnpiqnyawgsktalqqlfelenpnddpqaelwmgahpngcsg
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RGFAQEEQLGIALTAAQRNYKDPNHKPELVYALTEYQAMNGFRANQEILNYFIELSID
EIQPLVNVFQSNPTEQGLRDFFSGLLSIQGEAKNRALEALMAQAKQIDLPLFQLIVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="mannose-6-phosphate isomerase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="VC1827"
89. .1255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="VC1829"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="VC1828"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(1375. .1827)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KSAEVVLPLDSSMILRHANGEQCLVRKGQSVFIPAYAEQYTIECNGRVARAFSA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENQYPNDIGLFAPLMLNVITLQPGEAMFLDAETPHAYLHGTGLEIMANSDNVLRAGLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation="MKARGPFCIRHAAADTFAMVVFCFVTGMIIEIFVSGMTFQQSLA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="VC1827"
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PID:1651333; identified by sequence similarity; putative"
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VRGEMKSPSSGAGQLFTSSNDEAAQGTFSSDANEQAAYQNAVDLILKKRDYAGAIAAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /transl_table=11
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RILMFTLEAECSLDLGCPAADKFTEFCDAHPDHTVVYYANTSAAVKARADWVVTSSIAL
EIVEHLDSEGKRIIWGFDRHLGAYIAKKTGADMLLWGGECVYHDEFSADALKRKKALY
DAALILHPESPASYVELADAVGSTSQLIKAAKTLPQKMIVATDKGIFFKMQQMVPE
KELIEAPTAGAGATCRSCAHCPWMANNGLQAIAQALREGGKQHEIFVDEALRVKSLIP
                                                                                                                                                                                               complement (7792.
                                                                                                                                                                                                                          AYAKNRRAVLVY"
                                                                                                                                                                                                                                                                                 /translation="MQLNKVLKSLLIALPVLAVTACSSSDDAANSGSQTNQSAVSTVD
SNGLNAQGQLTEQELKEQALRENQTIYFAFDNATIASDYEAMLAAHAAYLVKNPSLRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(6462. .7226)
/gene="VC1834"
/codon_start=1
                                                                                                                                                             /gene="VC1836"
                                                                                                                                                                                                                                                      TIEGHADERGTPEYNIALGERRAQAVAKYLEALGVQAGQLSIVSYGEEKPLVLGQSEE
                                                                                                                                                                                                                                                                                                                                                                                       /product="peptidoglycan-associated lipoprotein"
/protein_id="AAF94983.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(7242. .7760)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(7242. .7760)
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                                                                                                   /gene="VC1836"
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SEVGQGSCFKVRVKLAITEPVTEDVKPTKAKTYPGLRVLIVEDNRTNIMILEAFMRNK
GFECHSVMDGVQAITALQESSFDLVLMDNHMPLKDGIQATREIRQLPLPQAKILLFGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7475 AAAAACCCCAAGCCTACGCGTAACTATCGAAGGTCACGCTGATGAGCGCGGGTACTCCTGAG 7416
                                                                                                                                                                                                                                                                                                                                                           156 GlyThrAsnGluGluAlaTrpSerGlnAsnArgArgAlaGluLeuSerTyr 172
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                                                                        Pasteurella multocida.
Pasteurella multocida
                                                                                                                                             AJ271673
AJ271673.1 GI:6977945
                                                                                                                       omp 16 gene; OMP 16 protein.
                                                                                                                                                                                            Pasteurella multocida partial omp
                             Pasteurella
                                                 Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                     PMU271673
                                                                                                                                                                                                                                                                                                                                                                                                           ACCGCTTGTAGCTCAAGTGATGATGCTGCGAACTCAGGTTCTCAAACTAACCAATCAGCA 7644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AACGCAACTATCGCGAGCGACTACGAAGCAATGCTAGCTGCACACGCTGCTTACCTAGTG 7476
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(bases 1 to 393)
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TLALVISKTGNLÖVYMDLATRRLTEVTSGRSNNTEPFWHPDGKSLIFTSDRGGKPOI
YOVNLSGESTRLTMÖGSQNLGGOITDDGKFLYMYNRASDSGMLAKODLETGAMOILT-
KTLLDESPSIAPNGGMVTYSSIYNKANVLSMVSIDGRFKARLPATNGRVRAPAMSPFL
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MEGATKLPEDVSAVIASDLQRSGKFSPVPTSKMPQTPYSEEQVNFGKWTSMGVDSLLT
GTITQNAEGSVISYQLDIVEGGLTGQGOSKALSQDGGLVLSKOHVLFNKVATVPASR
MREYAHRIADLYYEELTGERGAFLTRIAYVVVNDKDYPYQLRLADYDGYNERLYLRS
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/protein_id="AAF94984.1"
/db_xref="GI:9656363"
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                                                                                                                                                                                 150 GluArgProIleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArgArgAlaGlu
                                                                                                                 170 LeuSerTyr 172
                                                                                                                                                                                                                  262 CATTATTTATCAGCGAAAGGTGTACAAGCTGGTCAAGTATCAACAGTTTCTTACGGTGAA
                                                                                  382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 ValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAspGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (10-FEB-2000) Goswami P.P., National Biotechnology Centre, Indian Veterinary Research Institute, Izatnagar, Uttar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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Pasteurella multocida outer membrane protein gene,
               PMU16849
                                                                                                                                                                                                                                                 GAACGCGGTACACCAGAATATAACATCGCATTAGGTCAACGTCGTGCAGATGCAGTAAAA
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72 c 86 g 104 t
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/protein id="CAB75338.1"
/protein id="CAB75338.1"
/db_xref="G1:6977946"
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/translation="GSSKKDESAGQMFGGYSVQDLQQRYNTVYFGFDKYNIEGEYVQI
LDAHAAFLNATPATKVVYEGNTDERGTPEYNIALGQRRADAVKHYLSAKGVQAGQVST
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/transl_table=11
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/db_xref="taxon:747"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                U16849
U16849.1
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                                                                                                                                CATTATTTATCAGCGAAAGGTGTACAAGCTGGTCAAGTATCAACAGTTTCTTACGGTGAA
                                                                                                                                                                  AsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGluIleIleSerPheGlyGlu 149
                                                                                                                                                                                                        GAACGCGGTACACCAGAATATAACATCGCATTAGGTCAACGTCGTGCAGATGCAGTAAAA
                                                                                         GluargProIleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArgArgAlaGlu 169
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66.99%
48.54%
29.97%
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Matches:
Conservative:
Mismatches:
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhang, Q. and Kapu:
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete genomic sequence of Pasteurella multocida, Pm70 Proc. Natl. Acad. Sci. U.S.A. 98 (6), 3460-3465 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      May, B.J., Zhang, Q., Li, L.L., Paustian, M.L., Whittam, T.S.
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Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
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                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
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3221 GTGTATTTCGGCTTCGATAAATACAATATCGAAGGTGAATATGTACAAATTTTAGATGCA 3162
                                                                            70 ValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAspGlu 89
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SUMMARIES

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB
Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries
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length: 2000000000
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Ygapop 10.0 , x
Fgapop 6.0 , x
Delop 6.0 , x
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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P. aeruginosa OprF Sequence of plasmi P. aeruginosa OprF P. aeruginosa OprF P. aeruginosa OprI Outer membrane pro Actinobacilius ple Virulence gene #71 Non-typable Haemop M catarrhalis MCAI Genomic fragment # Haemophilus paraga Haemophilus p	H000ZJJ. FCF	catarri catarri quence ( influen: 00 dalto agment ( aemophi: uence o:	Description M. catarrhalis BAS Genomic fragment #

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## ALIGNMENTS

M. catarrhalis BASB019 protein coding sequence #1. 01-MAR-2000 (first entry) AAZ40351 standard; DNA; 519 BP

BASB019 protein; diagnosis; infectious organism; auditive nerve damage; genetic mutation screening; antibody production; vaccine; otitis media; bacterial infection; pneumonia; sinusitis; nosocomial infection; invasive disease; delayed speech learning; bacteria adhesion prevention; upper respiratory tract infection; middle ear infection; therapy; ss.

Moraxella catarrhalis.

W09957277-A2

03-MAY-1999; 99WO-EP03038.

06-MAY-1998; 98GB-0009683

(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

WPI; 2000-062148/05 P-PSDB; AAY55089.

Novel BASB019 polynucleotides and polypeptides from Moraxella catarrhalis used to prepare vaccines against bacterial infections

 $\begin{smallmatrix} \forall \times & \circ \\ v \times & \circ \\ v \times & \circ & \circ & \circ & \circ & \circ & \circ \\ v \times & \circ & \circ & \circ & \circ & \circ \\ v \times & \circ & \circ & \circ & \circ & \circ \\ v \times & \circ & \circ & \circ & \circ \\ v \times & \circ & \circ & \circ & \circ \\ v \times & \circ & \circ & \circ & \circ \\ v \times & \circ & \circ & \circ & \circ \\ v \times & \circ & \circ & \circ & \circ \\ v \times & \circ & \circ & \circ & \circ \\ v \times & \circ & \circ \\ v$ Claim 10; Fig 2; 101pp; English.

CC screening of genetic mutations, serotype, organism or strain components of aircays which are useful for diagnostic and prognostic components of arrays which are useful for diagnostic and prognostic cumponents of arrays which are useful for diagnostic and prognostic cumponents of arrays which are useful for diagnostic and prognostic cumponents of arrays which are useful for diagnostic and prognostic cumponents of the screening of antimicrobial drugs. The polypeptides can components of the screening of antimicrobial drugs. The polypeptides can components and componists and componists and componists and componists and componists. The polypeptides, another and prevention of componists and componists and componists and componists and componists and componists. The polypeptides, and to identify agonists and considered prognosists and componists and componists and componists. The polypeptides are used for the treatment and prevention of componists and componists and componists and componists and componists. The polypeptides are used for the calcally damage, delayed speech componists of the upper respiratory tract and middle ear componists of the prevention of adhesion of bacteria componists of pathogenesis in infections initiated other than by the implantation of in-dwelling devices or by other surgical techniques. The frequency of Moraxella catarrhalis infections initiated other than by the implantation of in-dwelling devices or by other surgical techniques. The implantation that for new antibacterial compounds that may target these can be used screen for new antibacterial compounds that may target these This sequence encodes a Moraxella catarrhalis BASB019 protein of the invention. The sequences can be used for diagnosis of disease, staging of disease, or determining response of an infectious organism to drugs. The polynicleotides may be used as a source for hybridisation probes, and for resistant bacteria.

Sequence 519 BP; 139 A; 108 C; 122 G; 150 Τ,

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140	GlyGluArgArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGlyIleAsnGlnAla :	121	Qy
360		301	Db
120	ArgValLeuValAlaGlyHisThrAspGluArgGlySerArgGluTyrAsnMetSerLeu	101	Qy
300	-	241	Db
100	ProGlnAlaAlaAlaIleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAla :	81	Qy
240		181	Db
80	AlaLeuAlaSerLysLeuProSerLeuValTyrPheAspPheAspSerAspGluIleLys 8	61	Qy
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                                                                                                                                                                                                                                                                                                                         The present invention relates to a Moraxella catarrhalis genomic library comprising of a combination of 41 nucleic acid molecules (see AAF28514-AAF2854). The library has a number of uses described in the specification e.g. is useful for aidentifying diagnostic and therapeutic compositions. M. catarrhalis (Branhamella catarrhalis) is a large compositions. M. catarrhalis (Branhamella catarrhalis) is a large aerobic, gram-negative diplococcus, normally found among the bacterial flora of human upper airways. M. catarrhalis is known to cause acute, localised infections such as otitis media, sinusitis and bronchopulmonary infection and life-threatening, systemic diseases including endocarditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 369-391; 545pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genomic library for identifying diagnostic and therapeutic compositions, and for identifying virulence factors, regulatory elements and drug targets, comprises Moraxella catarrhalis nucleic
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bronchopulmonary;
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This sequence encodes a Moraxella catarrhalis BASB019 protein of the invention. The sequences can be used for diagnosis of disease, staging of disease, or determining response of an infectious organism to drugs. The polynucleotides may be used as a source for hybridisation probes, and for screening of genetic mutations, scrotype, organism or strain identification identification of mutation in BASB013 sequences, and as components of arrays which are useful for diagnostic and prognostic purposes. The polypeptides can be used to produce antibodies, and as a
                                                                                                                                                                                    Novel BASB019 polynucleotides and polypeptides from Moraxella catarrhalis used to prepare vaccines against bacterial infect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genetic mutation screening; antibody production; vaccine; otitis media; bacterial infection; pneumonia; sinusitis; nosocomial infection; invasive disease; delayed speech learning; bacteria adhesion prevention; upper respiratory tract infection; middle ear infection; therapy; ss.
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genetic mutation screening; antibody production; vaccine; otitis media; bacterial infection; pneumonia; sinusitis; nosocomial infection; invasive disease; delayed speech learning; bacteria adhesion prevention; upper respiratory tract infection; middle ear infection; therapy; ss. BASB019 protein; diagnosis; infectious organism; auditive nerve damage; genetic mutation screening; antibody production; vaccine; otitis media; M. catarrhalis BASB019

protein coding sequence

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(first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC target for the screening of antimicrobial drugs. The polypeptides can calso be used in vaccine formulations, and to identify agonists and cantagonists. The polypeptides, antibodies, agonists and antagonists and complete the properties of the treatment and prevention of complete the compl
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                                                                                                       Вþ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               can be used screen for new antibacterial compounds that may target these resistant bacteria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACAGGCTGTGCCAATAAATCAACAAGTCAAGTTATGGTTGCTCCTAATGCACCCACAGGT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ThrGlyCysAlaAsnLysSerThrSerGlnValMetValAlaProAsnAlaProThrGly 40
  GCATGGTCACAAAATCGTCGTGCTGAACTGTCTTAT 516
                           AlaTrpSerGlnAsnArgArgAlaGluLeuSerTyr 172
                                                                                                                                                                                                                GGGGAACGTCGTGCGGTGCGGTACGCAACTATTTGCTTGGTAAAGGCATTAATCAAGCC
                                                                                                                                                                                                                                                                   GlyGluArgArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGlyIleAsnGlnAla 140
                                                                                                                                                                                                                                                                                                                                                                                                                            CCGCAAGCTGCCATCTTAGACGAACAAGCACAATTTTTAACCACCAATCAAACAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TACACTGGGGTTATCTATACTGGTGTTGCACCTTTGGTAGATAATGATGAGACCGTTAAG
                                                                                                                                  SerValGluIleIleSerPheGlyGluGluArgProIleAlaPheGlyThrAsnGluGlu 160
                                                                                                         AGCGTTGAGATTATCAGTTTTGGTGAAGAACGCCCTATCGCATTTGGCACAAATGAAGAA
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99.428
99.30%
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Conservative:
Mismatches:
Indels:
Gaps:
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AAZ40353 ID AAZ XX AC AAZ

AAZ40353 standard; DNA; 519 BP

US-09-674-779B-2 (1-172) x AAZ40353 (1-519)

Query Match:

Percent Similarity: Best Local Similarity:

Mismatches: Indels:

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cc identification, identification of mutation in BASBO13 sequences, and as components of arrays which are useful for diagnostic and prognostic cc components of arrays which are useful for diagnostic and prognostic cc target for the screening of antimicrobial drugs. The polypeptides can cc target for the screening of antimicrobial drugs. The polypeptides can cc also be used in vaccine formulations, and to identify agonists and cc antagonists. The polypeptides, antibodies, agonists and antagonists cc (which are bacteristatic) are used for the treatment and prevention of cd diseases including bacterial infection, otilis media in infants and confidence of the prognession of the upper respiratory tract and middle ear cacumulation in the middle ear, auditive nerve damage, delayed speech cacumulation. They are also used in the prevention of adhesion of bacteria confections on wounds, and to thus prevent tissue damage and/or block the implantation of in-dwelling devices or by other surgical techniques. The implantation of in-dwelling devices or by other surgical techniques. The frequency of Moraxella catarrhalis infections has risen dramatically, and it is no longer common to isolate M. catarrhalis strains that are created for new artifications. The BASBO19 products of the invention of the common to isolate M. catarrhalis strains that are invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence encodes a Moraxella catarrhalis BASB019 protein of the invention. The sequences can be used for dispnosis of disease, staying disease, or determining response of an infectious organism to drugs. The polynncleotides may be used as a source for hybridisation probes, and it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel BASB019 polynucleotides and polypeptides from Moraxella catarrhalis used to prepare vaccines against bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-MAY-1998;
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                                                                                                                                                                                                                                                                                                   Sequence 519 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          screening of genetic mutations, serotype, organism or strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 10; Fig 2; 101pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                  can be used screen for new antibacterial compounds that
                                                                                                                                                                                     No.:
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1.68e-94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASB019 protein; diagnosis; infectious organism; auditive nerve damage; genetic mutation screening; antibody production; receive; oritis media; bacterial infection; pneumonia; sinusitis; nosocomial infection; invasive disease; delayed speech learning; bacteria adhasion prevention; upper respiratory tract infection; middle ear infection; therapy; ss.
Claim 10; Fig 2; 101pp; English
                                                Novel BASB019 polynucleotides and polypeptides from Moraxella catarrhalis used to prepare vaccines against bacterial infections
                                                                                                                                                 WPI; 2000-062148/05.
P-PSDB; AAY55092.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M. catarrhalis BASB019 protein coding sequence #4.
                                                                                                                                                                                                                                         Ruelle J;
                                                                                                                                                                                                                                                                                             (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
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Comprehensive of artisty which are used to produce antibodies, and as a C target for the screening of antimicrobial drugs. The polypeptides can calso be used in vaccine formulations, and to identify agonists and calso be used in vaccine formulations, and to identify agonists and calso be used in vaccine formulations, and to identify agonists and calso for the polypeptides can consist and antagonists. The polypeptides, agonists and antagonists and contagonists. The polypeptides, activations, other media in infants and consist and are bacteristatic) are used for the treatment and prevention of consists in the elderly, sinusitis, media in infants and consists endiated in infections and consists and activate diseases, chronic otitis media with hearing loss, fluid carcumulation in the middle ear, auditive nerve damage, delayed speech carcing, infections of the upper respiratory tract and middle ear confection. They are also used in the prevention of adhesion of bacteria confections on wounds, and to thus prevent tissue damage and/or block the proteins on wounds, and to thus prevent tissue damage and/or block the confinal progression of pathogenesis in infections initiated other than by the implantation of in-dwelling devices or by other surgical techniques. The frequency of Moraxella catarrhalis infections has risen dramatically, and it is no longer common to isolate M. catarrhalis strains that are cresistant to standard antiblotics. The BASBO19 products of the invention consistant bacteria. screening of genetic mutations, serotype, organism or strain identification, identification of mutation in BASB013 sequences, and as components of arrays which are useful for diagnostic and prognostic This sequence encodes a Moraxella catarrhalis BASB019 protein of the invention. The sequences can be used for diagnosis of disease, staging disease, or determining response of an infectious organism to drugs. The polynucleotides may be used as a source for hybridisation probes, and resistant bacteria. of L... , staging or The

Sequence 519 BP; 137 A; 111 C; 122 G; 149 T; 0 other

Alignment Scores:			
Pred. No.:	9.06e-94	Length:	519
Score:	844.00	Matches:	169
Percent Similarity:	98.26%	Conservative:	0
Best Local Similarity:	98.26%	Mismatches:	ω
Query Match:		Indels:	0
DB:	21	Gaps:	0

US-09-674-779B-2 (1-172) x AAZ40354 (1-519)

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                                                                                                                                                241 CCGCAAGCTGCCATCTTAGACGAACAAGCACAATTTTTAACCACCAATCAAACAGCT
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                                                                                                                                                                                                             61 AlaLeuAlaSerLysLeuProSerLeuValTyrPheAspPheAspSerAspGluI1eLys
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                                                                                                                                                                                                                                                                                                                            21
             SerValGluIleIleSerPheGlyGluGluArgProIleAlaPheGlyThrAsnGluGlu
                                                            GlyGluArgArgAlaValAlaValArgAsnTyrLeuLeuGlyLySGlyIlcAsnGlnAla
AGCGTTGAGATTATCAGTTTTGGTGAAGAACGCCCTATCGCATTTGGCACAAATGAAGAA
                                                CGTGTTTTGGTTGCAGGTCATACCGATGAGCGTGGTAGTCGTGAGTATAATATGTCACTG
                                                                                                                                                                                                                                                                                              ArgValLeuValAlaGlyHisThrAspGluArgGlySerArgGluTyrAsnMetSerLeu
                                                                                                                                                             ProGlnAlaAlaAlaIleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAla
                                                                                                                                                                                                                                                               TyrThrGlyValI1eTyrThrGlyValAlaProLeuValAspAsnAspGluThrValLys
                                                                                                                                                                                                GCTTTGGCAAGCACGCTACCCAGTTTGGTTTATTTTGACTTTGATTCTGATGAGATTAAA
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164 441 124 321 104

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RESULT 6
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                               Score
                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       purification of outer membrane protein of haemophilus influenzae
  by separation from an insoluble fraction using
detergent-contg., then detergent-free buffers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence encoding 16.6kD outer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 866 BP; 252 A; 168 C; 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H.influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Method claimed produces large quantities of in raising antibodies for detection, and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 8; 22pp; English.
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P-PSDB; AAR07145.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYNE-) STATE UNIV NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-MAR-1989;
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                                                 TCTAACAACGATGCTGCAGGCAATGGTGCTGCTCAAAGTTTTGGCGGATACTCT-----
                                                                                                                            AAATTTGTTAAATCATTATTAGTTGCAGGTTCTGTACCTGCATTAGCGGCTTGTAGTTCC 132
                                                                                                                                                                  LysSerThrSerGlnValMetValAlaProAsnAlaProThr---
                                                                                                                                                                                                       TCCAGCTTGGTCTCCATACTTAACTAAATAAAAAACTCATTTAGGAGAAATCTAATGAAC 72
             IleTyrThrGlyValAlaProLeuValAspAsnAspGluThrValLysAlaLeuAlaSer 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Apicella
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Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                        Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G; 271
                                                                                                                                                                                                                                             ----ThrPheMetThrGlyCysAlaAsn 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the purified OMP, a vaccine against
                                                                                                                                                                                                                                                                                                                        866
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29
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43
                                                                                          GlyTyrThrGlyVal 44
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                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H.influenzae DNA fragment containing the PBOMP-1 gene
                                                                                                                                                  Outer membrane protein epitopes of Haemophilus influenzae- used in the prodn. of antibodies, in vaccines and for prodn. of reagents for diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ03869 standard; DNA; 737
                                                                                                                                                                                                                               WPI; 1990-115815/15.
P-PSDB; AAR05797.
                                                                                                                                                                                                                                                                                                                                                              01-SEP-1988;
21-AUG-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        outer membrane
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                                     Sequence 737
                                                                             See
                                                                                                                Disclosure; Fig 10; 164pp; English.
                                                                                                                                                                                                                                                                                      Anilionis A,
                                                                                                                                                                                                                                                                                                                          (PRAX-) PRAXIS BIOLOGICS IN
                                                                                                                                                                                                                                                                                                                                                                                                                         31-AUG-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9002557-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haemophilus influenzae.
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                                                                         also AAQ03870,R03948 and AAR03949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 IleSerPheGlyGluGluArgProIleAlaPheGlyThrAsnGluGluAlaTrpSerGln :::|||:::||| |||:::|||:::
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LysLeuProSerLeuValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAla
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                                       BP;
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                                                                                                                                                                                                                                                                                      Seid RC,
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89US-0396572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product=PBOMP-1, outer membrane protein of H.influenzae
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                                         225
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                                         A; 134 C; 154 G; 224 T;
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H influenzae; ss.
                                                                                                                                                                                                                                                                                          Zlotnick GW,
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                                           other;
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RESULT 8
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DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                   Plasmids, E.coli, hybridomas and for use as vaccine and detection
                                                                                                                                                                                                                                           CDS
                                                                                                                                                                                                                                                                                                  Haemophilus influenzae; 16600 dalton outer membrane protein (OMP);
Disclosure; ; pp; English
                                                                                 Murphy TF, Apicella MA;
                                                                                                      (UYNY-) RES UNIV NEW YORK
                                                                                                                           08-OCT-1987;
08-NOV-1986;
                                                                                                                                                          12-NOV-1987;
                                                                                                                                                                              14-SEP-1988
                                                                                                                                                                                                   EP281673-A.
                                                                                                                                                                                                                                                                         Haemophilus influenzae
                                                                                                                                                                                                                                                                                             pneumonia; meningitis;
                                                                                                                                                                                                                                                                                                                       16600 dalton outer membrane protein of non-typable H influenzae.
                                                                                                                                                                                                                                                                                                                                                  10-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                        AAN81194;
                                                                                                                                                                                                                                                                                                                                                                                        AAN81194 standard; DNA; 867
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                                                             1988-258472/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                     691
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                                                      AAP80593
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                   antibodies from H.influenzae protein of Haemophilus influenzae
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                  Haemophilus
                 influenzae
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 18-NOV-1986;
08-OCT-1987;
                                                                                                                                                                                                                           identification; pneumonia; bacteraemia; meningitis; postpartum sepsis; acute febrile tracheobronchitis;
                                                                                                                                                                                                                                       Outer membrane protein; vaccine; antibody; treatment; detection; identification; pneumonia; bacteraemia; meningitis;
                                        18-NOV-1986;
                                                                   05-APR-1994
                                                                                              US5300632-A
                                                                                                                                                                                      Haemophilus influenzae.
                                                                                                                                                                                                                                                                              Fragment encoding outer membrane protein P6 of H. influenzae.
                                                                                                                                                                                                                                                                                                             18-OCT-1994
                                                                                                                                                                                                                                                                                                                                       AAQ45440;
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87US-0092948
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                                        86US-0932872
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/product= P6 outer membrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Purifying outer membrane protein of Haemophilus influenzae extn. with detergent buffer, treatment with RNase and solubilising by heat-treating in detergent-free buffer
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P-PSDB; AAR51161.
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12-DEC-1991;
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Genome; bacterium; Haemophilus influenzae; computer readable medium; expression modulating fragment; regulation; gene expression; vector; organism; open reading frame; ORF; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1019 BP; 310 A; 200 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 4; Column 21-22; 24pp; English.
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                                                                                                  14-SEP-1999
                                                                                                                                                             AAT42063 standard;
                                                                 Haemophilus influenzae complete genome sequence.
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                                                                                                (first entry)
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91US-0807049.
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21-APR-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents the complete genome sequence of the bacterium Haemophilus influenzae strain Rd. The invention relates to a computer readable medium (CRM) having recorded upon it the complete H.influenzae nucleotide sequence (I), a representative fragment of (I) or a nucleotide sequence at least 99% identical to (I). By providing the full-length genomic sequence in a computer readable form, it is possible to identify commercially important nucleic acid fragments and expression modulating fragments (RMFs) of the Haemophilus genome. The EMFs can be used to regulate the expression of a nucleic acid molecule. Vectors and altered organisms comprising the predicted ORFS can be used to produce any of the polypeptide fragments of the H. influenzae Rd genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haemophilus influenzae Rd genome medium - useful for identifying
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fragments by homology searching
                                                                                                                                                            401840 GTTTATTTCGGTTTTGATAAATATGACATTACTGGTGAATACGTTCAAATCTTAGACGCG
                                                                                                401660 GGTTATTTAGCTGGTAAAGGTGTTGATGCTGGTAAATTAGGCACAGTATCTTACGGTGAA
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                                 GAAAAACCTGCAGTATTAGGTCATGATGAAGCTGCATATTCTAAAAACCGTCGTGCAGTG
                                                                                                                  AsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGluIleIleSerPheGlyGlu
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95US-0426787.
95US-0476102.
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ID AAN8
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                                                                                                                                                                                                                                                                                           A pure antigenic peptide or protein related to an epitope of Haemophilus influenzae is claimed. Also claimed is a recombinant vector comprising a DNA sequence coding for an antigenic determinant of an Haemophilus influenzae outer membrane protein, the transformed cell, a subunit vaccine in a pharmaceutical carrier, a method of immunising humans and an assay for Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                            used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-DEC-1987;
02-MAR-1987;
31-DEC-1986;
                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 10; 129pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                          Sequence 737 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Deich RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vaccine; diagnosis; epitope; passive immunisation;
                                                                                                                                                                                                                                         No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PRAX-) PRAXIS BIOLOGICS IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-DEC-1987;
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                                                                                                                                                                                                                                                                                                                                                                                                                   peptide related to epitope of Haemophilus influenzae - as immunogens in vaccines and for producing antibodies for
                     110 GluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArg
                                                                                              391 GTTTATTTGGGTTTTGATAAATATGACATTACTGGTGAATACGTTCAAATCTTAGATGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1988-205305/29.
GAACGTGGTACACCAGAATACAACATCGCATTAGGCCAACGTCGTGCAGATGCAGTTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAP80665
                                                                                                                                                                                                                                                                                                                                                                                                           immunisation and assays
                                               CACGCTGCATATTTAAATGCAACACCAGCTGCTAAAGTATTAGTAGAAGGTAACACTGAT
                                                                    GlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAsp 109
                                                                                                                     ValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAspGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zlotnick G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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86US-0948364.
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259.00
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Indels:
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50
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33
                        129
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 570
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CC This sequence encodes a H. pylori outer membrane protein.
CC The protein may be used in a vaccine to prevent or treat H. pylori
CC infection or to identify H. pylori polypeptide binding compounds,
CC useful as potential H. pylori life cycle activators or inhibitors.
CC The genomic sequence of H. pylori (ATCC 55679) was determined from
CC overlapping contigs generated by mechanically shearing the bacterial
CC DNA. The sequences were analysed for ORF of at least 180 nucleotides,
CC and the predicted coding regions defined by computer evaluation. To
CC identify likely H. pylori antigens for vaccine development, the amino
CC acid sequences predicted from various ORF were analysed for significant
CC homology to other known or exported membrane proteins. Having identified
CC and determined the sequences of interest, particular regions can be
CC isolated from H. pylori by PCR amplification for recombinant polypeptide
CC isolated from H. pylori by pCR amplification for recombinant polypeptide
CC Note: This DNA sequence is not reproduced in the specification and
CC has been derived from the related specification, w09719098.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Вþ
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                                                                                                                                                                                                                                                                                           Claim 1; Page -; 1481pp; English.
                                                                                                                                                                                                                                                                                                                                          Helicobacter pylori nucleic acid sequences and polypeptide(s) - useful for vaccines to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Outer membrane; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacterium; life cycle; activator;
                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAW20394.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H. pylori outer membrane protein ORF 31262.aa.
                                                                                                                                                                                                                                                                                                                              infection, and to detect Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-DEC-1996
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or prevent H.
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                                                                                                                       Transmembrane; cytoplasmic; cell envelope; flagella; transport; secreted; periplasmic; chronic gastritis; duodenal ulcer disease; activator; inhibitor; bacterial life cycle; vaccine; immunise; detection; antisense; inhibition; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 540
                                                                                                                                                                          H. pylori outer membrane protein ORF 31262.aa
                                                                                                                                                                                                                         AAT77469;
                                                                                                                                                                                                                                             AAT77469 standard;
                                                                                                                                                                                                  11-AUG-1997
            29-MAY-1997
                                  WO9719098-A1
                                                                                                 Helicobacter pylori.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCGGCTATTGAA-----AGCGGGACTATCATCGCTTCTATTTATTTTGATTTTGACAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GluThrValLysAlaLeuAlaSerLysLeuProSerLeuValTyrPheAspPheAspSer 76
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                                                                                                                                                                                                                                                                                                             ThrAsnGluGluAlaTrpSerGlnAsnArgArgAlaGluLeu 170
                                                                                                                                                                                                                                                                                                                                    GTAGAAAAAGATATGATCAAAAACCATCAGTTTTTGGCGAAAAGCAAACCCAAATGCGTCCAA
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                                                                                                                                                                                                                                                                                                                                                                             AACCAAGCGCTTGGCGTTAAAAGGACTTTGAGCGTGAAAAAACGCTTTAGTCATTAAAGGG 423
                                                                                                                                                                                                                                                                                                                                                                                           AsnMetSerLeuGlyGluArgArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGly 136
                                                                                                                                                                                                                                                                                                                                                                                                                       AACCAC --- ATGCAAGTGCTTTTGGAAGGCAATACCGATGAATTTGGCTCTAGCGAATAC 363
                                                                                                                                                                                                                                                                                                                                                                                                                                           AsnGlnThrAlaArgValLeuValAlaGlyHisThrAspGluArgGlySerArgGluTyr 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATGAGATCAAAGAATCCGATCAAGAGACTTTAGATGAGATCGTGCAAAAAAGCTAAAGAA 306
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215.50
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This sequence encodes an H. pylori outer membrane protein. Helicobacter pylori has been strongly linked to chronic gastritis and duodenal ulcer disease. The nucleic acid sequences of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-NOV-1996;
                                                                                                                                                                                          Claim 1; Page 108; 235pp; English.
                                                                                                                                                                                                                                                                             Helicobacter pylori nucleic acid sequences and related proteins used for diagnostics and therapeutics % \left( 1\right) =\left\{ 1\right\} =\left\{ 1\right\} 
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cc are used to evaluate compounds, especially activators or inhibitors of bacterial life cycle, for the ability to bind an H. pylori nucleic acid cc sequence. The nucleic acid sequences, and corresponding proteins, are calso useful for generating vaccines for immunising subjects against H. cc pylori or for use in detecting the presence of Helicobacter species in cc a sample. Antisense nucleic acid sequences of these sequences are cc used to inhibit expression of a gene from Helicobacter species. H. cc pylori whole genomic DNA was isolated and nebulised to a median size of cpylori whole genomic DNA was isolated and nebulised to a median size of complementary to the BstXI-cut pMPX vectors, while the overhang is not cc complementary. Therefore the linkers will not concatemerise nor cc will the cut vector re-ligate itself easily. The linker-adapter inserts cc were ligated to each of the 20 pMPX vectors to construct a series of cc senienced. The ORF/protein reference number for this sequence was obtained the related specification, W09640893.

Sequence 540 BP; 190 A; 88 C; 128 G; 134 T; 0 other:

TC-00-674-770B-3: /1-1731 x AAT77460 /1-5401	Alignment Scores: Pred. No.: Score: Score: Percent Similarity: Best Local Similarity: Query-Match: DB:
Y AAT77469 (	5.83e-17 215.50 50.00% 32.76% 25.03%
1-540)	Length: Matches: Conservative: Mismatches: Indels: Gaps:
	540 57 30 66 21

72

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This invention describes a novel preparation of an agent (A) for CC detection, prevention and/or treatment of microbial infection by: (i) identifying essential genes (I) and corresponding polypeptides (II); (ii) identifying compounds that are directed against (II) and CC inactivate the microbe; (iii) testing these for suitability for use; and CC (iv) formulating selected (A). Identifying essential genes (I) comprises (II) formulating selected (A). Identifying essential genes (I) comprises (In) hittion (CAI) and/or subtractive recombination mutagenesis (SRM), CC preparation of gene-deficient microorganisms by conditional antisense (CC proparation) in the deficient microorganisms. (CC polypeptide (IIa), vector or host cell containing (Ia), derived (CC polypeptide (IIa), or fragments, (IIa) reparticularly used for diagnosis, (CC treatment or prevention of infection by Helicobacter pylori. Particularly (CC (IA)) and (IIa) are used in DNA, subunit or live vaccines. The method (CC identifies essential genes, including those that have homology in other (CC gene-deficient cells can be screened quickly, in an automated process, and the infection of the companion of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
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17-JUN-1999;
21-JUL-1999;
  Sequence 540 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 37; Page 252-253; 366pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Preparing an agent for diagnosis or control of microbial infection, useful particularly against Helicobacter, based on identification o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    essential genes in defective mutants -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apfel H,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H. pylori HPS144 encoding DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vaccine; screening;
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                                  ficient cells can be screened quickly, in an automated process, identified genes can be used for screening without purification
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99DE-1027740.
99DE-1034029.
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                            19-DEC-1996.
                                                       WO9640893-A1
                                                                                                                                                                                           Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor;
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                                                                                                                                                    Helicobacter pylori.
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No . :
                                                                                                                                                                            duodenal ulcer disease; chronic gastritis; diagnosis; envelope;
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                                                                                                                                                                                                                                                                                                                                                                                                        ThrAsnGluGluAlaTrpSerGlnAsnArgArgAlaGluLeu 170
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25.03%
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The protein may be used in a vaccine typervent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors.
The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.
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07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter
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                                                                                                                                                                                                                                                                                                                                         AlaProThrGlyTyrThrGlyValIleTyrThrGlyValAlaProLeuValAspAsnAsp 56
                                                                                                                                                                                                                                                                                                                                                                             AATAAGACTGTGGCTGGCGATGTGAGCACTAAAGCGGTTCAGACTGCGCCCTGTTACTACA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTGTATTTAGTTTCTTGGTAGCTTTTTTATTGGTAGTTGGCTGTAGTCATAAAATGGAT 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SerValLeuThrPheMet-----
IleAsnGlnAlaSerValGluIleIleSerPheGlyGluGluArgProIleAlaPheGly 156
                                                                AsnMetSerLeuGlyGluArgArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGly 136
                                                                                                     AsnGlnThrAlaArgValLeuValAlaGlyHisThrAspGluArgGlySerArgGluTyr 116
                                                                                                                                                                       TATGAGATCAAAGAATCCGATCAAGAGACTTTAGATGAGATCGTGCAAAAAGCTAAAGAA 330
                                                                                                                                                                                                                                                                         GluThrValLysAlaLeuAlaSerLysLeuProSerLeuValTyrPheAspPheAspSer 76
                                     AACCAAGCGCTTGGCGTTAAAAGGACTTTGAGCGTGAAAAACGCTTTAGTCATTAAAGGG 447
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95US-0487032
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50.00%
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Mismatches:
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                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                     antibody-detection assays, on sera, plasma, urine, saliva etc., they are highly sensitive and specific. The specification also describes 69 previously unrecognised immunogenic cluster families. H. pylori antigens are used to detect H. pylori-specific antibodies, for diagnosing infection or to confirm eradication of infection, and in vaccines to protect against H. pylori infection and related diseases (gastritis, peptic ulcer, gastric adenocarcinoma/lymphoma).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV90653 standard; DNA; 770 BP
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peptic ulcer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleotide sequence of clone Y175.ASM from cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                            The present sequence encodes a Helicobacter pylori antigenic protein that is characterised by immunoreactivity with H. pylori-positive antisera. The proteins are highly immunogenic and induce a long-lasting immune response that persists even after antimicriobial treatment. In
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chow TP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-OCT-1997;
25-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Helicobacter pylori antigens and related nucleic acid sequences useful in serological diagnosis and protective vaccines, providing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-009433/01
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                                                                                                                                                                                                                 No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunogenic cluster family; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ThrAsnGluGluAlaTrpSerGlnAsnArgArgAlaGluLeu 170
ThrSerGlnValMetValAlaPro---AsnAlaProThrGlyTyrThrGlyValIleTyr 46 ::::::: :::
                                             AlaAlaAlaAlaAlaLeuSerValLeuThrPheMetThrGlyCysAlaAsnLysSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fry KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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97US-0045107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lim MY,
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211.50
52.02%
31.21%
24.56%
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                                                                                                                                                                      Mismatches:
                                                                                                                                                                                   Conservative:
                                                                                                                                                      Indels:
                                                                                                                                                                                                    Matches:
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gastric lymphoma; ss.
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RESULT 17
AAV90843
ID AAV90
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  antibody-detection assays, on sera, plasma, urine, saliva etc., highly sensitive and specific. The specification also describes previously unrecognised immunogenic cluster families. H. pylori
                                                                         The present sequence encodes a Helicobacter pylori antigenic protein that is characterised by immunoreactivity with H. pylori-positive antisera. The proteins are highly immunogenic and induce a long-lasting immune response that persists even after antimicriobial treatment. In
                                                                                                                                                                                                                                                                                      New Helicobacter pylori antigens and related nucleic acid sequences useful in serological diagnosis and protective vaccines, providing
                                                                                                                                                                                                                   Claim 20; Page 281; 402pp; English.
                                                                                                                                                                                                                                                                      long-lasting
                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-009433/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GENE-) GENELABS TECHNOLOGIES
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25-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antigen; immunogenic cluster family; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleotide sequence of cluster
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                                                                                                                                                                                                                                                                                                                                                                                                                                ΤP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AsnGluGluAlaTrpSerGlnAsnArgArgAlaGluLeu 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAAGCGCTTGGCGTTAAAAGGACTTTGAGCGTGAAAAACGCTTTAGTCATTAAAGGGGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAC---ATGCAAGTGCTTTTGGAAGCCAATACCGATGAATTTGGCTCTAGCGAATACAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                Fry KE,
                                                                                                                                                                                                                                                                         immune response
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gastric adenocarcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-0061958
97US-0045107
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                                                                                                                                                                                                                                                                                                                                                                                                                              McAtee CP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gastritis;
lymphoma; ;
H. pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; diagnosis;
                                                                                                                                                                                                                                                                                         providing
  antigens
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RESULT 18
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                                                                                                        Antigen;
peptic ul
 27-APR-1998;
                            05-NOV-1998.
                                                    W09849314-A2
                                                                                                                                               Nucleotide sequence from clone
                                                                                                                                                                           18-FEB-1999
                                                                                                                                                                                                     AAV90545;
                                                                                                                                                                                                                               AAV90545 standard;
                                                                             Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       are used to detect H. pylori-specific antibodies, for diagnosing infection or to confirm eradication of infection, and in vaccines to protect against H. pylori infection and related diseases (gastritis, peptic ulcer, gastric adenocarcinoma/lymphoma).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1236 BP; 430 A; 220
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                                                                                                                      immunogenic cluster
                                                                                                                                                                                                                                                                                                           AsnGluGluAlaTrpSerGlnAsnArgArgAlaGluLeu
                                                                                                                                                                                                                                                                                                                                      GAAAAAGATATGATCAAAACCATCAGTTTTGGTGAAACCAAAACCCAAAATGCGCCCAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                              CAC --- ATGCAAGTGCTTTTGGAAGCCAATACCGATGAATTTGGCTCTAGCGAATACAAC
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                                                                                                                                                                        (first entry)
                                                                                                         gastric
98WO-US08487.
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                                                                                                        adenocarcinoma;
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                                                                                                                      family;
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                                                                                                                                              Gla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 253 G; 332 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
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Indels:
                                                                                                      vaccine;
a; gastric
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                                                                                                     gastritis;
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                                                                                                                  diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antibody-detection assays, on sera, plasma, urine, saliva etc., they are highly sensitive and specific. The specification also describes 69 previously unrecognised immunogenic cluster families. H. pylori antigens are used to detect H. pylori-specific antibodies, for diagnosing infection or to confirm eradication of infection, and in vaccines to protect against H. pylori infection and related diseases (gastritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence encodes a Helicobacter pylori antigenic protein that is characterised by immunoreactivity with H. pylori-positive antisera. The proteins are highly immunogenic and induce a long-lasting immune response that persists even after antimicriobial treatment. In
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New Helicobacter pylori antigens and related nucleic acid sequences - useful in serological diagnosis and protective vaccines, providing long-lasting immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-OCT-1997;
25-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 27; Page 95; 402pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENE-) GENELABS TECHNOLOGIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptic ulcer, gastric adenocarcinoma/lymphoma).
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                           1460 GAAAAAGATATGATCAAAACCATCAGTTTTGGTGAAACCAAACCCAAATGCGCCCAAAAA 1519
                                                                                                                               1343 CAC---ATGCAAGTGCTTTTGGAAGCCAATACCGATGAATTTGGCTCTAGCGAATACAAC
                                                                                                                                                                                                                                     1999-009433/01
                                                                                                                                                                                                                                                                                                                                                                                            47
                                                                                                                                                                                                                                                                                                                                                                  28 ThrSerGlnValMetValAlaPro---AsnAlaProThrGlyTyrThrGlyValIleTyr 46
                                                                                                                                                                                                                                                                                                                                                                                                                      œ
                                                                                                                                             GlnThrAlaArgValLeuValAlaGlyHisThrAspGluArgGlySerArgGluTyrAsn 117
                                                                                                                                                                                                           GluIleLysProGlnAlaAlaAlaIleLeuAspGluGlnAlaGlnPheLeuThrThrAsn 97
                                                                                                                                                                                                                                                                                      ACAGAACCAGCTCCAGAGAAAGAAGAGCCTAAACAAGAGCCAGCTCCAGTGGTTGAAGAA 1222
                                                                                                                                                                                                                                                                                                                                         GATAATAAGACTGTGGCTGGCGATGTGAGCGCTAAAACGGTTCAGACTGCACCTGTTACT 1162
                                                                                                                                                                                                                                                                                                                                                                                                                    AlaAlaAlaAlaAlaLeuSerValLeuThrPheMetThrGlyCysAlaAsnLysSer 27
AsnGluGluAlaTrpSerGlnAsnArgArgAlaGluLeu 170
                                                   AsnGlnAlaSerValGluIleIleSerPheGlyGluGluArgProIleAlaPheGlyThr 157
                                                                             CAAGCGCTTGGCGTTAAAAGGACTTTGAGCGTGAAAAACGCTTTAGTCATTAAAGGGGTA 1459
                                                                                                   MetSerLeuGlyGluArgArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGlyIle 137
                                                                                                                                                                                   GAGATCAAAGAATCCGATCAAGAGACTTTAGATGAGATCGTGCAAAAAGCTAAAGAAAAC
                                                                                                                                                                                                                                                             LeuProSerLeu---
                                                                                                                                                                                                                                                                                                             ThrGlyValAlaProLeuValAspAsnAspGluThrValLysAla---LeuAlaSerLys 65
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97US-0045107.
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211.50
52.02%
31.21%
24.56%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            328 G; 441 T; 0 other;
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Matches:
Conservative:
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                                                      Score:
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Query Match:
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                                                                                                                                                                                                                                                    This sequence represents Omp22, a novel gene encoding an outer membrane protein which exhibits antigenicity and immunogenicity against Helicobacter pylori. This bacterium is associated with inflammation of the stomach and gastilits related diseases e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Omp22 gene; outer membrane protein; antigen; immunogen; stomach; gastritis; peptic ulcers; gastric cancer; diagnostic; vaccine; d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT74194;
                                                                                                                                                                                                   ulcers and gastric cancer. Omp22 could be used in immunological therapy as a H. Pylori-specific antigen for the treatment and prevention of diseases associated with this microorganism e.g. as the active
                                                                                                                                                                                                                                                                                                                                                                                  Helicobacter pylori outer membrane protein, Omp22 - used invaccine for treatment or prevention of H. pylori infection
                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAW23592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-1996;
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                                                                                                                                              Sequence 435 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-402617/37
                                                                                                                                                                                  ingredient in a diagnostic kit or a vaccine
                                                                                                                                                                                                                                                                                                                                                Example 3; Pages 20-22; 38pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96KR-0002105
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67..72
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49..54
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82..85
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                                                                                                                                                  164 A; 73 C;
7.19e-16
205.50
58.68%
38.02%
23.87%
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                      Mismatches: Indels:
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  03-JUL-2000;
11-JUL-2000;
21-JUL-2000;
07-AUG-2000;
18-AUG-2000;
14-SEP-2000;
10-NOV-2000;
22-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                     Chlamydial infection; antigen; immunogen; vaccine; diagnosis; human respiratory disease; cardiovascular disease; atherosclerosis; coronary artery disease; carotid artery stenosis; myocardial infarce cerebrovascular disease; aortic aneurysm; claudication; stroke;
                                                                                                                   03-JUL-2001;
                                                                                                                                           10-JAN-2002.
                                                                                                                                                                    W0200202606-A2
                                                                                                                                                                                                                     mat_peptide
                                                                                                                                                                                                                                             sig_peptide
                                                                                                                                                                                                                                                                                              Key
                                                                                                                                                                                                                                                                                                                                                                                                                      Chlamydia pneumoniae cp7090 ORF DNA, SEQ ID NO:38
                                                                                                                                                                                                                                                                                                                        Chlamydia pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABL91202 standard; DNA; 579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 ATTTATTTTGATTTTGACAAGTATGAAATCAAAGAATCCGATCAAGAGACTTTAGATGAG 180
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                                                                                                                                                                                                                                                                                                                                            CWL029; open reading frame; ORF; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAATTTGGCTCTAGCGAATACAACCAAGCGCTTGGCGTTAAAAGGACTTTGAGCGTGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAsp 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AlaProLeuValAspAsnAspGluThrValLysAlaLeuAlaSerLysLeuProSerLeu 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCAAACCCAAATGCACCCAAAAAACTAGAGAGTGTTATAAAGAAAAACAGAAGAGTGGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAspGlu 89
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2000GB-0016363.
2000GB-0017047.
2000GB-0017983.
2000GB-0019368.
2000GB-0020440.
2000GB-0022583.
2000GB-00227549.
2000GB-0031706.
                                                                                                                2001WO-IB01445
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                   576
                                                                                                                                                                                         "Mature protein"
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                                                                                                                                                                                                                                                                                                                                                                      infarction;
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CC Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia CC pneumoniae (strain CWL029), and ABL91184-ABL91373 represent DNA encoding Ct them. The proteins are predicted to be immunogenic and may therefore be conserved in vaccine production and for diagnostic purposes. Chlamydia CC pneumoniae is a common cause of respiratory disease in humans, and is calso involved in the development of cardiovascular diseases such as common cause of respiratory disease in humans, and is catheroscilerosis, coronary artery disease, carotid artery stenosis, composation and stroke. The proteins and nucleic acids of the invention composation and stroke. The proteins and nucleic acids of the invention composation or treatment of chlamydial infections, particularly Chlamydia pneumoniae infections. The proteins may also be used in the detection of CP chlamydia pneumoniae, and the nucleic acids may be used in pCR, branched CC pneumoniae gene expression. The present sequence represents a compositionally claimed DNA which encodes a Chlamydia pneumoniae protein of the present sequence represents a compositionally claimed DNA which encodes a Chlamydia pneumoniae protein of the present sequence represents a compositionally claimed DNA which encodes a Chlamydia pneumoniae protein of the present sequence represents a compositional protein of the present sequence represents a composition of the presents and presents a composition of the presents and presents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel Chlamydia pneumoniae protein useful in the manufacture medicament for treatment or prevention of infection due to CP preferably Chlamydia pneumoniae, and for diagnostic purposes
       Sequence 579 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CHIR-) CHIRON SPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB90544.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Grandi G;
184 A; 131 C;
109
G;
155 T; 0 other;
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Alignment Scores:

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Percent Similarity:
Best Local Similarity:
Query Match:
                                                No.:
1.42e-15
204.50
58.82%
38.66%
23.75%
                                    Matches:
Gaps:
                  Mismatches:
                          Conservative:
         Indels:
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## US-09-674-779B-2 (1-172) x ABL91202 (1-579)

AC AC	RESU AAD ID	Db	Qy	Db	Qy	Db	Qy	Db	Qy	DЪ	Qy	Д	Qy	
AAD08593;	RESULT 21 AAD08593 ID AAD08593	502	151	442	131	382	111	322	91	262	72	202	54	
	л 21 1593 AADO8593 standard; DNA; 779 BP.	502 CATCCTTTAAATTCGGGACAAAAACTAGCATGGCAACAAAATCGCCGTACAGAG 558	ArgProlleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArgArgAlaGlu 169	CATCTCCGAAAGCAGGGAATCTCTGCAGATCGTCTATCTA	TyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGluIleIleSerPheGlyGluGlu 150	CGTGGAGCTGCATCCTATAACCTTGCTTTAGGAGCACGACGAGCCAATGCGATTAAAGAG 441	ArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArgAsn 130	322 GTTCACTACATGAAGAAAAACCCGAAAGCTACACTGTACATTGAAGGGCATACTGACGAG 381	AlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAspGlu 110	TTTGCTACAGACAGCTATACAATTAAAGGTGAAGAGACCTTGCGATTCTCACGAACTTG 321	PheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAspGluGln 90	GATTCCAAAGAAAAAAAAAAAAAAAGTCAAGCCAAGTTGCAGCATTTCGTAATATCACC 261	AspAsnAspGluThrValLysAlaLeuAlaSerLysLeuProSerLeuValTyr 71	

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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or express it in a non-toxic, mutated form. The omp P6 probes are useful in diagnostic tests as capture or detection probes and the primers are useful in diagnostic methods involving PCR (polymerase chain reaction).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of omp P6 precursor protein and their corresponding DNAs are useful in vaccine composition. The polynucleotide is useful in the construction of attenuated Chlamydia strains that can over express the polynucleotide of attenuated the polynucleotide of attenuated the polynucleotide of attenuated the polynucleotide of attenuated the polynucleotide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diseases (e.g. bronchitis, sinusitis) and acute respiratory diseases (e.g. cough, sore throat). C. pneumoniae infection is also observed to be associated with atherosclerosis and asthma. Immunogenic fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein (omp) P6 precursor gene. The omp P6 precursor polynucleotide, polypeptide and its antibody are useful for detecting, preventing and treating Chlamydia infections e.g. pneumonia, upper respiratory tractifications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is Chlamydia pneumoniae outer membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chlamydia polypeptides and polynucleotides for preventing, diagnosing and treating Chlamydia infection in mammals, especially humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murdin AD, Oomen RP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The antibody is useful for purifying polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AVET ) AVENTIS PASTEUR LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 779 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scores:
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                                                                 362 TTTGCTACAGACAGCTATACAATTAAAGGTGAAGAGAACCTTGCGATTCTCACGAACTTG
                                                                                                                                                                                      302 GATTCCAAAGAAGAAAAACAATACAAGTCAAGCCAAGTTGCAGCATTTCGTAATATCACC
         91
                                                                                                                       72 PheAspPheAspSerAspGluIleLys---ProGlnAlaAlaAlaIleLeuAspGluGln
                                                                                                                                                                                                                                           54 AspAsnAspGluThrValLysAlaLeuAlaSerLysLeuProSerLeu-----ValTyr 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fig 1; 74pp; English.
      AlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAspGlu 110
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US-09-674-779B-2 (1-172) x AAX91990 (1-1230025
                                             Query Match:
                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                              The present sequence represents the complete genome of Chlamydia pneumoniae, and encodes proteins AAY34584-Y35879. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, crythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in immunogenic compositions as vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX91990 standard; DNA; 1230025 BP
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21-NOV-1997;
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                                                                                                                                                       Sequence 1230025 BP; 367213 A; 249833 C; 249013 G; 363589
                                                                                                                                                                                 Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 291-611; 1912pp; English.
                                                                                                                                                                                                                                                                                                                                                                                      Genome sequence of Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-357842/30
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                                                                  The present sequence represents the complete genome of Chlamydia trachomatis. Open reading frames (ORFs) of the genome encode polypeptides AAY36754-Y37949. The polypeptides can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion
                                                                                                                                                                                                                                                                                                                                                                                   04-NOV-1998;
28-NOV-1997;
17-DEC-1997;
      conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, salpingitis, perihepatitis, bartholinitis; pneumopathy in breast feeding infants; and venereal lymphogranulomatosis. The polypeptides of the invention may be of use
                                                                                                                                                                                                             Claim 1; Page 373-656; 1755pp; English.
                                                                                                                                                                                                                                               Genome sequence of Chlamydia trachomatis
                                                                                                                                                                                                                                                                                   WPI; 1999-371125/31.
                                                                                                                                                                                                                                                                                                                   Griffais R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaccine; eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete genome sequence of Chlamydia trachomatis.
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these diseases
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97FR-0015041.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                              mat_peptide
          (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                    25-JUN-1999;
                                                             23-JUN-2000;
                                                                                                               WO200100836-A1
                                                                                                                                                                                                                                                               BASB311; infection; otitis media; pneumonia; gene therapy;
                                                                                                                                                                                                                                                                                          Moraxella catarrhalis DNA encoding BASB113 protein.
                                                                                                                                                                                                                    Moraxella catarrhalis
                                                                                                                                                                                                                                            vaccine;
                                                                                                                                                                                                                                                          diagnosis;
                                                                                                                                                                                                                                                                                                                          23-APR-2001
                                                                                                                                                                                                                                                                                                                                                                           AAF30043 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       No.:
                                                                                                                                                                                                                                                                                                                                                                                                                       832873 CATCCTGTTCATCCAGGCCATAATGAATTAGCTTGGCAACAAAATCGTCGTACTGAA 832817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           832993 CGTGGAGCTGCAGCTTATAACCTAGCTTTAGGAGCTCGTCGTGCGAATGCTGTAAAACAA 832934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             833113 TTCGCTACAGATAGTTATTCTATTAAAGGAGAGGATAACCTCACGATTCTTGCAAGCTTA 833054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               833173 TCCAAAGAAGAGCAGCTGTACAAAACGAGCGCACAGAGTACCTCTTTCCGAAATATCACT 833114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   833233 GGATTCGTACCTTTCTACTCCGATGAAGAATTCAACAAGCTTTTGTTGAAGATTTTGAT 833174
                                                                                                                                                                                                                                                                                                                                                                                                                                        151 ArgProIleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArgArgAlaGlu 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 ArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArgAsn 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48 GlyValAlaProLeuValAspAsnAspGluThrValLysAlaLeuAlaSerLysLeuPro
                                                                                                                                                                                                                                               SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TACCTCATCAAACAAGGAATCGCTGCAGACCGCTTATTCACTATTTCTTACGGAAAAGAA 832874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGluIleIleSerPheGlyGluGlu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PheAspPheAspSerAspGluIleLysProGln---AlaAlaAlaIleLeuAspGluGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SerLeu-----
                                                                                                                                                                                                                                                    antibacterial; antimicrobial; genetic immunisation;
                                                           2000WO-EP05851
                                                                                                                                                                                                                                                                                                                     (first entry)
                                 99GB-0015044.
                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                     /note=
                                                                                                                                                                                                                                                                                                                                                                         DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.55e-10
196.50
48.92%
35.25%
22.82%
                                                                                                                                                 "a polynucleotide having this
                                                                                                                                     also specifically claimed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (1-1038602)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      214645 C; 214259 G; 305001 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
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19
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                                                                                                                                   sequence
Claim 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptide or antibody. A claimed therapeutic composition useful in treating humans with M. catarrhalis infection comprises at least 1 antibody directed against a BASB113 polypeptide. BASB13 polynucleotides also have utility in diagnosis of the stage and type of infection, and also for therapeutic or prophylactic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polynucleotide encoding such a polypeptide. A claimed method of diagnosing a Moraxella infection involves identifying a BASB113 polypeptide or antibody. A claimed therapeutic composition useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 10; Page 67; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful for diagnosing and producing vaccines against bacterial infections such as otitis media and pneumonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAB20105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New BASB113 polypeptide isolated from Moraxella catarrhalis bacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             purposes, in particular genetic immunisation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 AAAACAGGTCGTGATGCCATTTTG----GGGGCGGCAGTTGGTGCAGCAGCAGGGGGCGTAT 240
133 LeuGlyLysGlyIleAsnGlnAlaSerValGluIleIleSerPheGlyGluGluArgPro 152
                                                                                                                                                                                                                                        355
                                                                                                                                                                                                                                                                                                                                 295
                                                                                                                                                                                                                                                                                                                                                                                                                           241 ATGGAGCGTCAAGCAAAGCAGATTGAGCAACAATGCAAGGAACGGGCGTGACT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerThrSerGlnValMetValAlaProAsnAlaProThrGlyTyrThrGlyValIleTyr 46
                                                  CAAGCGGCTTATAATCAAGAGCTGTCTGAGCGTCGAGCGGATTCAGTGCGTTATTACTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTGGGGCTGTGGCAGTGCACTTGGCGGTACTGCCATTTCAAAAGCAACTGGTGGCGAA
                                                                             SerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArgAsnTyrLeu 132
                                                                                                                                                                                          PheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAspGluArgGly 112
                                                                                                                                                                                                                                     GCTCATGATGACGATACTTTAAACAGTGCATTTTTGGGTCGTTTAAACCAGCTGGCTAAT 414
                                                                                                                                                                                                                                                                                 AspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAspGluGlnAlaGln 92
                                                                                                                                                                                                                                                                                                                               GTAACCCACGATACCGACACGGGTAATATTAATCTAACTATGCCAGGTAATATTACTTTT 354
                                                                                                                                                                                                                                                                                                                                                                          ValAspAsnAspGluThrValLysAlaLeuAlaSerLysLeuProSerLeuValTyrPhe 72
                                                                                                                                              ACGATGAATCAGTATCATGAAACAACGATTGTCATTGTAGGACATACAGACTCAACGGGT 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.5e-12
180.50
41.01%
26.97%
20.96%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----ThrGlyValAlaProLeu 52
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48
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Qy Db

4099 AAAACAGGTCGTGATGCCATTTTG----GGGGCGGCAGTTGGTGCAGCAGCAGGGGGCGTAT 4155

SerThrSerGlnValMetValAlaProAsnAlaProThrGlyTyrThrGlyValIleTyr 46

4039 ATTGGGGCTGTGGCAGGTGCACTTGGCGGTACTGCCATTTCAAAAGCAACTGGTGGCGAA

7 IleAlaAlaAlaAlaAlaLeuSerValLeuThrPheMetThrGlyCysAlaAsnLys 26

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RESULT 25
AAF28526
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US-09-674-779B-2 (1-172) x AAF28526 (1-31940)
                                                              Best Local Similarity:
                                                                            Percent Similarity:
                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                               The present invention relates to a Moraxella catarrhalis genomic library comprising of a combination of 41 nucleic acid molecules (see AAF28514-AAF2854). The library has a number of uses described in the specification e.g. is useful for aldentifying diagnostic and therapeutic compositions. M. catarrhalis (Branhamella catarrhalis) is a large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomic library; bacteria; human upper airway; otitis media; bronchopulmonary; endocarditis; meningitis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomic fragment #13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                          Genomic library for identifying diagnostic and therapeutic compositions, and for identifying virulence factors, regulatory elements and drug targets, comprises Moraxella catarrhalis nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200078968-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Moraxella catarrhalis.
                                                                                                                                                                                                   aerobic, gram-negative diplococcus, normally found among the bacterial flora of human upper airways. M. catarrhalis is known to cause acute, localised infections such as otitis media, sinusitis and bronchopulmonar infection and life-threatening, systemic diseases including endocarditis
                                                                                                                                                                                                                                                                                                                                                                Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-041427/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-JUN-1999;
                                                                                                                                                          Sequence 31940
                                                                                                                                                                                       and meningitis.
                                              Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               535 ATTAATCAAGGCGTTGATCCATATCGTATTCAGACAGTGGGGTATGGTATGCGACAACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               153 IleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArgArgAlaGluLeu 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard; DNA; 31940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTGCATCGAATGCAACCGAAGCAGGTCGTGCTCAAAATCGCCGTGTTGAGCTG
                                                                                                                                                                                                                                                                                                                                                                Page 115-123; 545pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patterson C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                           ВP;
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                                 3.22e-10
180.50
41.01%
26.97%
20.96%
                                                                                                                                                           9411 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Berg KL;
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                               Gaps:
                                                                Mismatches:
                                                                                 Conservative:
                                                   Indels:
                                                                                                Matches:
                                                                                                                                                               7140 G;
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                                                                                                                                                               T; 0 other;
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This sequence represents the complete genome sequence of the bacterium Haemophilus influenzae strain Rd. The invention relates to a computer readable medium (CRM) having recorded upon it the complete H.influenzae nucleotide sequence (I), a representative fragment of (I) or a nucleotide sequence at least 99% identical to (I). By providing the full-length genomic sequence in a computer readable form, it is possible to identify
                                                                                                                    Claim 1; Page 77.2-77.1091; 1291pp; English
                                                                                                                                                                  Haemophilus influenzae Rd genome recorded on computer readable medium - useful for identifying commercially important nucleic acid
                                                                                                                                                         fragments by homology searching
                                                                                                                                                                                                                            WPI; 1996-485782/48
                                                                                                                                                                                                                                                                                                                                               07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                               07-JUN-1995;
21-APR-1995;
                                                                                                                                                                                                                                                              Adams MD,
                                                                                                                                                                                                                                                                                                                                                                                                                  22-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome; bacterium; Haemophilus influenzae; computer readable medium; expression modulating fragment; regulation; gene expression; vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haemophilus influenzae complete genome sequence
                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
(UYJO ) UNIV JOHNS HOPKINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism; open reading frame; ORF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTGCATCGAATGCAACCGAAGCAGGTCGTGCTCAAAATCGCCGTGTTGAGCTG 4563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArgArgAlaGluLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTAATCAAGGCGTTGATCCATATCGTATTCAGACAGTGGGGTATGGTATGCGACAACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAAGCGGCTTATAATCAAGAGCTGTCTGAGCGTCGAGCGGATTCAGTGCGTTATTACTTG 4449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTCATGATGACGATACTTTAAACAGTGCATTTTTGGGTCGTTTAAACCAGCTGGCTAAT 4329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTAACCCACGATACCGACACGGGTAATATTAATCTAACTATGCCAGGTAATATTACTTTT 4269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArgAsnTyrLeu 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACGATGAATCAGTATCATGAAACAACGATTGTCATTGTAGGACATACAGACTCAACGGGT 4389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAspGluArgGly 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGGAGCGTCAAGCAAAGCAGATTGAGCAACAAATGCAAGGAACGGGCGTGACT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuGlyLysGlyIleAsnGlnAlaSerValGluIleIleSerPheGlyGluGluArgPro 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAspGluGlnAlaGln 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ValAspAsnAspGluThrValLysAlaLeuAlaSerLysLeuProSerLeuValTyrPhe 72
                                                                                                                                                                                                                                                            Fleischmann RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                             95US-0487429.
95US-0426787.
95US-0476102.
                                                                                                                                                                                                                                                                                                                                                                                                                96WO-US05320
                                                                                                                                                                                                                                                            Smith HO,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          regulation; gene expression; vector;
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Best Local Similarity:
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              16-DEC-1994;
                                               17-NOV-1995;
                                                                                                                                                Pseudomonas aeruginosa serotype 6 (ATCC 33354)
                                                                                                                                                                                 antibody; glutathione-S-transferase; GST; ds.
                                                                                                                                                                                                     Vaccine;
                                                                                                                                                                                                                                    P. aeruginosa OprF-OprI hybrid gene
                                                                                                                                                                                                                                                                         01-OCT-1996
                                                                                                                                                                                                                                                                                                                                            AAT32600 standard;
                                                                                19-JUN-1996
                                                                                                                                                                                                                                                                                                           AAT32600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            commercially important nucleic acid fragments and expression modulating fragments (EMFs) of the Haemophilus genome. The EMFs can be used to regulate the expression of a nucleic acid molecule. Vectors and altered organisms comprising the predicted ORFS can be used to produce any of the polypeptide fragments of the H. influenzae Rd genome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1235512 GTTGCTGGTTACACTGACCGTATTGGTTCTGACGCGTTCAACGTAAAACTTTCTCAAGAA 1235571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1235335 CGTTTTGGTCAAGGCGCAGCACCAGTTGTTGCAGCACCTGAAGTTGTAAGCAAAACTTTC 1235394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1235275 CCAAATACCGCACTTAACTACAACCCTTGGATTGGTTCTATCAATGCGGGTATTTCTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104 ValAlaGlyHisThrAspGluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArg 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84 AlaAlaIleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeu 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47 -----ThrGlyValAlaProLeuValAspAsnAspGluThrValLysAlaLeuAla
                                                                                                                                                                                                 fusion protein; OprF; OprI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IleIleSerPheGlyGluGluArgProIleAlaPheGlyThrAsnGluGlu------
                                                                                                                                                                                                                                                                                                                                                                                                            CGTAAAGCGCTTATCGCTTGTTTTGCTCCAGACCGTCGTGTAGAAATCGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGlu 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SerLysLeuProSerLeuValTyrPheAspPheAspSerAspGluIleLysProGlnAla
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                                             95EP-0118098
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176.50
47.77%
30.57%
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RESULT 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Von
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 13-14; 23pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fusion proteins for Pseudomonas aeruginosa fragments of outer membrane proteins I and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transformants. The oprF-oprI hybrid protein, and antibodies raised against it, conferred protection against P. aeruginosa infection in laboratory animals. The hybrid protein was significantly more immunogenic than an oprI-oprF fusion (AAR99627).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              was expressed in
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           AAQ54144;
                                       AAQ54144 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       GluThrValLysAlaLeuAlaSerLysLeuProSerLeu---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTCCGACTCCGACAACGACGGCGTCTGCGACAAC-GTCGACAAGTGCCCGGACACCCCG
                                                                                                                                                                                                                                                                                                                                                                          CTGGACGTGAAGTTCGACTTCGACAAGTCCAAGGTCAAAGAGAACAGCTACGCTGACATC
                                                                                                                                                                                                                                                                                                                                                                                                                             GCCAACGTCACCGTTGACGCCAACGGCTGCCCGGCTGTCGCCGAAGTCGTACGCGTACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AlaProThrGlyTyrThrGlyValIleTyrThrGlyValAlaProLeuValAspAsnAsp
                                                                                            CGCGTTGAAAGCAGCCAC
                                                                                                                      ArgAlaGluLeuSerTyr 172
                                                                                                                                                                            PheGlyGluGluArgProIleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArg 166
                                                                                                                                                                                                        GTTCGTGACGTACTGGTCAACGAGTACGGTGGAAGGTGGTCGCGTGAACGCTGTCGGT
                                                                                                                                                                                                                                 ValArgAsnTyrLeuLeuGlyLys----GlyIleAsnGlnAlaSerValGluIleIleSer 146
                                                                                                                                                                                                                                                              ACCGACTCCGTCGGTACCGACGCTTACAACCAGAAGCTGTCCGAGCGTCGTGCCAACGCC
                                                                                                                                                                                                                                                                                     ThraspGluargGlySerargGluTyrAsnMetSerLeuGlyGluargargAlaValAla 127
                                                                                                                                                                                                                                                                                                                   AAGAACCTGGCCGACTTCATGAAGCAGTACCCGTCCACTTCCACCACCGTTGAAGGTCAT
                                                                                                                                                                                                                                                                                                                                            AspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHis
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                                                                                                                                                  TACGGCGAGTCCCGCCCGGTTGCCGACAACGCCACCGCTGAAGGCCGCGCTATCAACCGT 444
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US-09-674-779B-2 (1-172) x AAQ54144 (1-4274)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence of plasmid pRW3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           plasmid pRW3 contains the whole P.aeruginosa outer membrane protein OprF gene with a mutated promoter in pTZ19R. It was isolated for the creation of OprF epitope insertion vectors which include a promoter and a DNA sequence encoding at least the amino terminal portion of a P.aeruginosa OprF. Inserted in the DNA sequence are one or more unique restriction sites for insertion of one or more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-MAY-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1993-405827/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hancock REW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA sequences encoding a protein or interest.
                                                                                                                                                                                                                                                                                                                                                                                           3252 CTGGCCTGGGCGTCGGCTTCAACTTCGGTGGTTCGAAAGCCGCTCCGGCTCCGGAACCGG
                                                                                                                                                                              3413
                                                                                                                                                                                                                                                   3354
                                                                                                        3473
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                                                                                                                                                                                                                                                                                   47 ThrGlyValAlaProLeuValAspAsnAspGluThrValLysAlaLeuAlaSerLysLeu
                                                                                                                                     78 GluIleLysProGlnAlaAlaAlaIleLeuAspGluGlnAlaGlnPheLeuThrThrAsn
                                                                                                                                                                                                                                                                                                                                                           27
                                                                                                                                                                                                                67 ProSerLeu----
                                                                                                                                                                                                                                                                                                                                                                                                                            7 IleAlaAlaAlaAlaAlaAlaLeuSerValLeuThrPheMetThrGlyCysAlaAsnLys 26
                                                                                                      AAGGTCAAAGAGAACAGCTACGCTGACATCAAGAACCTGGCTGACTTCATGAAGCAGTAC 3532
                                                                                                                                                                            CCGGCTGTCGCCGAAGTCGTACGCGTACAGCTGGACGTGAAGTTCGACTTCGACAAGTCC
                                                                                                                                                                                                                                                 ACAAC-GTCGACAAGTGCCCGGATACCCCGGCCAACGTCACCGTTGACGCCAACGGCTGC 3412
                                                                                                                                                                                                                                                                                                                                                         SerThrSerGlnValMetValAlaProAsnAlaProThrGlyTyrThrGlyValIleTyr 46
MetSerLeuGlyGluArgArgAlaValAlaValArgAsnTyrLeuLeuGlyLys---Gly
                                                                 GlnThrAlaArgValLeuValAlaGlyHisThrAspGluArgGlySerArgGluTyrAsn 117
                                   CCGTCCACTTCCACCACCGTTGAAGGTCACACCGACTCCGTCGGCACCGACGCTTACAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BRITISH COLUMBIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wong R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein; OprF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92US-0891495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93WO-CA00227.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.09%
31.21%
19.98%
                                                                                                                                                                                                                                                                                                                          -----TTGCCGACGTTTGCTCCGACTCCGACAACGACGGCGTTTGCG
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172.00
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative:
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                                                                                                                                                                                                                 ----ValTyrPheAspPheAspSerAsp
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3472

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                              QΥ
                                                                                                                                                                                     RESULT 29
                                                    US-09-674-779B-2 (1-172) x AAT32599
                                                                                   BB
                                                                                                                                   Score
                                                                                                                                              Alignment Scores: Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Вр
                                                                                            Query Match:
                                                                                                                      Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B
                                                                                                        Local Similarity:
                                                                                                                                                                                                       A cDNA sequence (AAT32599) codes for amino acids 190-350 (AAR99625) of the Pseudomonas aeruginosa ATCC 33354 outer membrane protein F (OprF), i.e. the C-terminal region of protein. It was obtd. by PCR amplification of the OprF gene in plasmid pFSauI (see also AAT32592-93). A hybrid gene between glutathione-s-transferase and the OprF sequence was expressed in Escherichia coli. OprF-OprI (AAT32500) and OprI-OprF (AAT32600) hybrid genes were constructed and the encoded proteins (AAR99626-27) were tested for their efficacy as vaccines against P. aeruginosa infection.
                                                                                                                                                                                  Sequence 486 BP;
                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 11-12; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                               Fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                             Von
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Broeker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BEHW ) BEHRINGWERKE AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP717106-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas aeruginosa serotype 6 (ATCC 33354).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vaccine; fusion protein; OprF; OprI;
antibody; glutathione~S-transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P. aeruginosa OprF C-terminal region cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT32599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT32599
                                                                                                                                                                                                                                                                                                                                                                                                                                           specht BU;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3593
                                                                                                                                                                                                                                                                                                                                                                                                      1996-279559/29.
DB; AAR99625.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137
        32
                                                                                                                                                                                                                                                                                                                                                               proteins for Pseudomonas aeruginosa vaccines nts of outer membrane proteins I and F.
GCTCCGACTCCGACAACGACGCGTCTGCGACAAC-GTCGACAAGTGCCCGGACACCCCG
                        AlaProThrGlyTyrThrGlyValIleTyrThrGlyValAlaProLeuValAspAsnAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IleAsnGlnAlaSerYalGluIleIleSerPheGlyGluGluArgProIleAlaPheGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAGAAGCTGTCCGAGCGTCGTGCCAACGCCGTTCGTGACGTTACTGGTCAACGAGTACGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCACCGCTGAAGGCCGCGCTATCAACCGTCGCGTTGAA 3751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ThrAsnGluGluAlaTrpSerGlnAsnArgArgAlaGlu 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTAGAAGGTGGTCGCGTGAACGCTGTTGGTTACGGCGAGTCCCGGCCCGGTTGCCGACAAC 3712
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Domdey H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94EP-0120023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95EP-0118098
                                                                                                                                                                                 109 A; 158 C;
                                                                                171.50
46.15%
33.57%
19.92%
                                                                                                                                1.2e-11
171.50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hungerer K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        486
                                                     (1-486)
                                                                                                                                                                                 138 G; 81
                                                                            Gaps:
                                                                                                       Mismatches:
                                                                                                                   Conservative:
                                                                                           Indels:
                                                                                                                                Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Knapp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      outer membrane GST; ds.
                                                                                                                                                                                 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      В,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ulrich
                                                                             486
48
18
67
11
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RESULT 30
AAT34419
ID AAT3
AC AAT3
AC AAT3
AC AAT3
AC AAT3
AC P. a
XX Vacc
KW Vacc
KW anti
XX Pseu
PN EP71
AX 15-1
PR 15-1
PR 15-1
PR WPI;
PR WPI;
PR WPI;
PR WPI;
PR Frac
XX WPI;
PR Frac
XX A cci
CC Acic
CC Acic
CC AlTC
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CC
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                                                                                              A cDNA sequence (AAT34419) codes for a fusion (AAR99627) between amino acids 21-83 of the outer membrane protein I (oprI) and amino acids 190-350 of outer membrane protein F (oprE) of Pseudomonas aeruginosa ATCC 33354, the 2 moleties being separated by a dipeptide linker. A glutathione-S-transferase fusion with the hybrid gene was expressed glutathione-S-transferase fusion with the hybrid gene was expressed
                                                                                                                                                                                                                                                                            Disclosure; Page 15-16; 23pp; English.
                                                                                                                                                                                                                                                                                                                              Fusion proteins for Pseudomonas aeruginosa fragments of outer membrane proteins I and
                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P. aeruginosa OprI-OprF hybrid gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BEHW ) BEHRINGWERKE AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-DEC-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT34419 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Specht BU;
                                                                                                                                                                                                                                                                                                                                                                                                                          1996-279559/29
DB; AAR99627.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147 PheGlyGluGluArgProIleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ValArgAsnTyrLeuLeuGlyLys----GlyIleAsnGlnAlaSerValGluIleIleSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fusion protein; OprF; OprI; outer membrane
glutathione-S-transferase; GST; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Domdey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Η,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA; 681 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hungerer K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Knapp B,
                                                                                                                                                                                                                                                                                                                                       vaccines F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ulrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein;
                                                                                                                                                                                                                                                                                                                                                            contg
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opri-oprf hybrid protein was significantly less immunogenic than oprf-oprI fusion (AAR99626).

in Escherichia coli and Saccharomyces cerevisiae transformants.

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AAN82023
ID AAN8
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DB:
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Вþ
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                                            03-JUN-1987;
                                                                                                                                         DE3718591-A.
                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                   Outer membrane protein F; OMPF; vaccination; antibodies;
                                                                                                                                                                                                                                                                                                                 Outer membrane protein F of Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                AAN82023 standard; DNA; 1253 BP
                                                                            03-JUN-1987;
                                                                                                                                                                                                                                                      Pseudomonas
                                                                                                                                                                                                                                                                                                                                                   22-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                  AAN82023;
             (BEHW ) BEHRINGWERKE AG
                                                                                                            15-DEC-1987.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGCGTTGAA 654
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ThrAspGluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ArgAlaGlu 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TACGGCGAGTCCCGCCCGGTTGCCGACAACGCCACCGCTGAAGGCCGCGCTATCAACCGT: 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PheGlyGluGluArgProIleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArg
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                                                                                                                                                                                                                                                      aeruginosa.
                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                            87DE-3718591
                                                                            87DE-3718591
                                                                                                                                                                                      /*tag=
                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                         /product=Outer membrane protein
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33.57%
19.92%
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171.50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The protein is isolated from the OMP of P. aeruginosa serotype 6 ATTCC 33354) and purified by HPLC. The amino-terminal and trypsin fragments are sequenced and a series of oligonucleotide probes constructed corresponding to the established sequences. These probes used to screen a gene bank of 15-20 kb fragments of genomic DNA in lambda EMBL 3. One positive clone includes a 15 kb insert conty. the protein gene, which can be isolated as a 2.5 kb PstI fragment. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fragment cannot be cloned int a high copy no. vector because of the toxicity of the gene prod.., so is subcloned as two fragments with an overlapping region of about 500bp. Ab's are raised by usual immunisation or cell-fusion procedures. The DNA is useful in diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; ; p; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1253 BP; 279 A; 389 C; 358 G; 227 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       outer membrane protein F of Pseudomonas aeruginosa sequences encoding it and derived antibodies, useful for cination and diagnosis.
                                                 1021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 AlaAlaAlaAlaAlaLeuSerValLeuThrPheMetThrGly------CysAla 24
                                                                                                                                        ValArgAsnTyrLeuLeuGlyLys---GlyIleAsnGlnAlaSerValGluIleIleSer 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                {\tt AlaProThrGlyTyrThrGlyValIleTyrThrGlyValAlaProLeuValAspAsnAsp}
                ArgAlaGlu 169
                                                TACGGCGAGTCCCGCCCGGTTGCCGACAACGCCACCGCTGAAGGCCGCGCTATCAACCGT
                                                                              {\tt PheGlyGluGluArgProIleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArg}
                                                                                                               GTTCGTGACGTACTGGTCAACGAGTACGGTGTGGAAGGTGGTCGCGTGAACGCTGTCGGT
                                                                                                                                                                            ACCGACTCCGTCGGTACCGACGCTTACAACCAGAAGCTGTCCGAGCGTCGTGCCAACGCC
                                                                                                                                                                                                       ThrAspGluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAla
                                                                                                                                                                                                                                          AAGAACCTGGCCGACTTCATGAAGCAGTACCCGTCCACTTCCACCACCGTTGAAGGTCAT
                                                                                                                                                                                                                                                                      AspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHis 107
                                                                                                                                                                                                                                                                                                       CTGGACGTGAAGTTCGACTTCGACAAGTCCAAAGGTCAAAGAGAACAGCTACGCTGACATC
                                                                                                                                                                                                                                                                                                                                    -----ValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeu
                                                                                                                                                                                                                                                                                                                                                                       GCCAACGTCACCGTTGACGCCAACGGCTGCCCGGCTGTCGCCGAAGTCGTACGCGTACAG
                                                                                                                                                                                                                                                                                                                                                                                                   GluThrValLysAlaLeuAlaSerLysLeuProSerLeu---
                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTCCGACTCCGACAACGACGGCGTCTGCGACAAC-GTCGACAAGTGCCCGGACACCCCG
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45.36%
30.60%
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Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                             membrane protein, ompa2, from Actinobacillus pleuropneumoniae (APP) strain Pz420 (ATCC 98930). The invention relates to the novel APP outer membrane proteins omp20, OmpA, OmpA7, OmpA1 and OmpA2 (AAY97896-Y97900) and to nucleic acids encoding them (AAA38554-A38558). APP is a Gram negative coccobacillus which is one of the most important swine pneumonic pathogens. 12 different serotypes of APP have been recognised which vary in geographic distribution. Prior art attempts at vaccinating against APP have produced mainly serotype-specific immune responses. In contrast, natural immunity to any one serotype seems to confer significant protection from disease caused by other serotypes, suggesting that natural exposure induces cross-reactive immunity to shared antigens.
                                                                                                                                                                                         The novel outer membrane proteins of the invention are present in all 12 serotypes, and may provide a target for cross protective immunisation. The novel outer membrane proteins and nucleic acids encoding them can be used as a vaccine against APP in swine. They can also be used as reagents for the diagnosis of APP infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
                                                                                                                                          Sequence 1319 BP; 428 A; 252 C; 260 G; 379 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents DNA encoding a low molecular weight outer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 32; Page 49-51; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Low molecular weight Actinobacillus pleuropneumoniae proteins and DNA encoding them, for use as vaccines against the bacteria in swine - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Warren-Stewart LM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Actinobacillus pleuropneumoniae ompA2 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ankenbauer RG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PEIZ ) PFIZER PROD INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Actinobacillus pleuropneumoniae strain Pz420.
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                                                                              NO : :
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Claim 7; Pages 306-308; 322pp; English
                                                               Attenuated Pasteurellaceae bacteria comprising mutations in virulence genes, useful as a live attenuated vaccine against bacterial infection
                                                                                                                                                                                                                                                                                                      09-APR-1999;
10-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Actinobacillus pleuropneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Virulence gene; antibacterial; vaccine; bacterial infection; septicemia; bronchopneumonia; rhinitis; wound infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Virulence gene #71.
                                                                                                                                          P-PSDB;
                                                                                                                                                                                                          Lowery DE, Fuller TE,
                                                                                                                                                                                                                                                        (PHAA ) PHARMACIA & UPJOHN INC
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99US-0153453
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21
                                                               attenuated vaccine against bacterial infections
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                                                                                                                                                                                                                                                                                                              Fimbrin protein; vaccine; otitis media;
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                           WO9426304-A
                                                                                              stem_loop
                                                                                                                                                                                                                                                                                                                                                                                                            09-AUG-1995
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                                                                                                                                                                                                                                                                 Haemophilus
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typable clinical isolates of Haemophilus influenzae share common
epitopes. Thus frimbrin isolated from non-typable Haemophilus
influenzae 1128 strain is a particularly suitable immunogen to
protect against the different non-typable HJ. influenzae that cause
otitis media. Fimbrin protein is produced by culturing a transformed
mlcroblal host , pref. E.coli, Sporodoptera frugiperda or a mucosal
pathogen. Fimbrin protein (FP) produced by this process is claimed.
The FP protein migrates in polyacrylamide genes to a posn. equiv. to
a mol. wt. of 25.5 kD or 37.5 kD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vaccine comprising non-typable Haemophilus influenza fimbrin protein - useful in studying, preventing or reducing the severity of otitis media, also fimbrin protein and DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1720 BP; 571 A;
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O
                                                                                                                                                                                                                                                                                                                   ValAlaGlyHisThrAspGluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArg
                                                                                                                                                                                                                                                                                                                                                                                                                                AlaAlaIleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeu
CGTAAAGCACTTATCGCTTGTCTTGCTCCAGACCGTCGTGTAGAAATCGCA 1467
                                                                                                                                                                                                                                                                                                                                                                                   CAAGCTACATTAGACAGCGTCTATGGCGAAATTTCACAAGTTAAAAGTCGAAAAAGTAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGC --- TTAAATTCTGATGTAACTTTCGCATTTGGTAAAGCAAACTTAAAACCTCAAGCA
                                                                                                                                             IleIleSerPheGlyGluGluArgProIleAlaPheGlyThrAsnGluGlu-----
                                                                                                                                                                                              CGTGCAGATTCAGTAGCTAACTACTTGTTGCTAAAGGTGTTGCAGCAGACGCAATCTCA
                                                                                                                                                                                                                                      ArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGlu
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                                                                                                GCAACTGGTTACGGTGAAGCAAACCCAGTAACTGGCGCAACTTGTGACCAAGTTAAAGGT
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165.50
46.50%
29.94%
19.22%
                                            ----AlaTrpSerGlnAsnArgArgAlaGluLeuSer 171
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Indels:
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RESULT 35
AAL46503
      Pred.
             Alignment Scores:
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05-SEP-2000;
05-SEP-2000;
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01-SEP-2000;
05-SEP-2000;
05-SEP-2000;
05-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                        29-AUG-2000;
29-AUG-2000;
29-AUG-2000;
                                                 The present invention provides the protein and coding sequences of proteins from Moraxella catarrhalis. These can be used to produce vaccines which protect against M. catarrhalis infection, which can otitis media, respiratory infection, sinusitus, and pneumonia. The
                                                                                                                                                                                                                            05-SEP-
     NO.:
                              Sequence 898
                                                                                             Claim 2; Fig 21; 277pp; English.
                                                                                                              Moraxella polypeptide and polynucleotides useful as vaccine for immunizing a host e.g. humans against disease e.g. otitis media pneumonia, caused by infection of the bacteria
                                                                                                                                                                                                                                                                                                              01-SEP-2000;
01-SEP-2000;
                                              present sequence
                                                                                                                                                  P-PSDB; AA017571.
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29-AUG-2000;
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29-AUG-2000;
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29-AUG-2000;
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28-AUG-2000;
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                                                                                                                                                                          Loosmore S,
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2000US - 2284 4 3 P.
2000US - 2285 1 1 P.
2000US - 2285 1 2 P.
2000US - 2287 7 4 P.
2000US - 2294 6 5 P.
2000US - 2294 7 4 P.
2000US - 2294 7 8 P.
2000US - 2294 7 8 P.
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2000US-228295P.
2000US-228296P.
2000US-228438P.
2000US-228439P.
2000US-228440P.
2000US-228441P.
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                             290 A; 171 C;
                                              is a
     1.75e-10
                                            coding sequence of
                                                                                                                                                                        Bradley
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                             182 G;
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Best Local Similarity:
The present invention relates to a Moraxella catarrhalis genomic library
                                                                                                                                                                                                                                                                         AAF28548;
                                   acids
                                                                                           Lagace RE,
                                                                                                                             18-JUN-1999;
                                                                                                                                                              28-DEC-2000.
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US-09-674-779B-2 (1-172) x AAL46503 (1-898)
                                                                    Genomic library for identifying diagnostic and therapeutic compositions, and for identifying virulence factors, regular elements and drug targets, comprises Moraxella catarrhalis
  Claim 1; Page 345-368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomic library; bacteria; human upper airway; otitis media; sinusitis; bronchopulmonary; endocarditis; meningitis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF28548 standard; DNA; 96109
                                                                                                                                                                                                                                                                   (INCY-) INCYTE GENOMICS INC
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                                                                                                                                                                                                                   Patterson C,
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English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   comprising of a combination of 41 nucleic acid molecules (see AAF28514-AAF28554). The library has a number of uses described in the specification e.g. is useful for aidentifying diagnostic and therapeutic compositions. M. catarrhalis (Branhamella catarrhalis) is a large aerobic, gram-negative diplococcus, normally found among the bacterial flora of human upper airways. M. catarrhalis is known to cause acute, localised infections such as otitis media, sinusitis and bronchopulmonary infection and life-threatening, systemic diseases including endocarditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 96109 BP; 28783 A; 18910 C;
                   mat_peptide
                                                        sig_peptide
                                                                                                                                                             Haemophilus paragallinarum
                                                                                                                                                                                               Haemagglutinin; antigen; vaccine;
hagh; gene; ds.
                                                                                                                                                                                                                                                  Haemophilus
                                                                                                                                                                                                                                                                                     18-APR-2002
                                                                                                                                                                                                                                                                                                                                                         ABA91419 standard; DNA; 1035 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTTTAGACTCAACCGAAATTCCCCCAAGAAAATAAAGAAATCTTGGATTTGGCTGCCGAA 68515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTTGAAGAAATGAGATGGATATTTTAATCAATGCATTAAATACCCAAATCATTAACTTT 68455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ValAspAsnAspGluThrValLysAlaLeuAlaSerLysLeuProSerLeuValTyrPhe 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTTGCCGATAGTATTGAAACAGCGCGTGTTGCTATTGTTTGCTTTGGGT-----GATACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ValAlaProAsnAlaProThrGlyTyrThrGlyValIleTyrThrGlyValAlaProLeu 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LeuGlyLysGlyIleAsnGlnAlaSerValGluIleIleSerPheGlyGluGluArgPro 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACGCATGAGTATAATCAAGATTTATCAGAATCTCGTGCTGCTGCTGTTAAAGAGTATTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArgAsnTyrLeu 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAspGluArgGly 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AspPheAspSerAspGluIleLysProGlnAlaAlaIleLeuAspGluGlnAlaGln 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                           IleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArgArgAlaGlu 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTATCAAAAGGTGTTGCTGCTGAACGTTTGAACACTCAAGGTGCAAGTTTTGATTATCCA
                                                                                                                                                                                                                                                paragallinarum strain 2403 haemagglutinin hagA gene
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                                                                                                                                                                                                                coryza; chicken;
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80 LysProGlnAlaAlaAlaIleLeuAsp-----

AAAACATTTGCA-----TTAAATTCAGATGTTACTTTCGCATTTGGTAAAGCAAATTTA 714 LysAlaLeuAlaSerLysLeuProSerLeuValTyrPheAspPheAspSerAspGluIle

-GluGlnAlaGlnPheLeuThr

79

Qγ 밁 QΥ 망

116 TyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArgAsnTyrLeuLeuGlyLys

 ${\tt ThrasnGlnThralaArgValLeuValAlaGlyHisThraspGluArgGlySerArgGluA$ CGTCCAGAAGCACAAAATGTATTAGACGGTATTTATGGTGAAATCGCACAGTTA-----

-AAATCAGTACAAGTAGATGTTGCTGGTTATACTGACCGTATTGGTAGCGAAGCA 822

Qy Db δÃ DЬ 8

601 GCTGGTTTATCTTACCGTTTTGGTCAAAGTGCACCAGTTGTTGAACCTAAGGTTGTTGCA 660

ThrGlyValIleTyrThr-----GlyValAlaProLeuValAspAsnAspGluThrVal 59

541 GGACGTGTGGAAAAAGATGGTAGCCGTGTAGATTATACACCAAGCATCGGTTCTGTAACT

22 GlyCysAlaAsnLysSerThrSerGlnValMetValAlaProAsnAlaProThrGlyTyr

В

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US-09-674-779B-2 (1-172) x ABA91419 (1-1035)
                                                  Query Match:
                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                       The present sequence is that of the coding region of the hagA gene CC of Haemophilus paragallinarum strain 2403 (serovar A). The gene CC was isolated from chromosomal DNA by PCR amplification. It encodes haemagglutinin (see AAM50718). The invention provides ce encodeing nucleic acids (see AAM50718). The invention provides composition nucleic acids (see AAM51417-27) from 11 strains (serovars A, B and C) of H. paragallinarum, the causative agent of infectious coryza of chickens. The polypeptides are useful in vaccines for communisation against infectious coryza, as are the nucleic acids when expressed in attenuated bacteria, especially Salmonella or CC whom expressed in attenuated bacteria, especially Salmonella or CC the mature protein, or a biologically active fragment, variant or CC derivative, that is capable of eliciting an immune response, providing protection against one or more strains of H. CC paragallinarum in chickens. Also claimed are methods of using the haemagglutninin polypeptides and nucleic acids for detection and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUL-2000; 2000AU-0008652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-JUL-2001; 2001WO-AU00822
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                                                                                                                                                                            Sequence 1035 BP; 319 A; 186 C;
                                                                                                                                                                                                              diagnosis of infectious coryza in chickens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Fig 5; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New haemagglutinin polypeptide isolated from Haemophilus paragallinarum useful as a vaccine for immunising chickens against coryza caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAM50718
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                                                                                                                                                                              234 G; 296 T;
                                   Gaps:
                                                                        Mismatches:
                                                       Indels:
                                                                                           Conservative:
                                                                                                          Matches:
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  The present sequence is that of the coding region of the hagA gene of Haemophilus paragallinarum strain 0222 (serovar B). The gene was isolated from chromosomal DNA by PCR amplification. It encodes haemagglutinin (see AAM50721). The invention provides recombinant haemagglutinin polypeptides (see AAM50716-27) and encoding nucleic acids (see ABA91417-27) from 11 strains (serovars A, B and C) of H. paragallinarum, the causative agent of infectious coryza of chickens. The polypeptides are useful in vaccines for when expressed in attenuated bacteria, especially Salmonella or Mycoplasma (claimed). The recombinant polypeptide is preferably the mature protein, or a biologically active fragment, variant or derivative, that is capable of eliciting an immune response,
                                                                                                                                                         Claim 11; Fig 5; 67pp; English.
                                                                                                                                                                                     New haemagglutinin polypeptide isolated from Haemophilus paragallinarum useful as a vaccine for immunising chickens against coryza caused by
                                                                                                                                                                                 the species
                                                                                                                                                                                                                           P-PSDB;
                                                                                                                                                                                                                                                           Terry TD,
                                                                                                                                                                                                                                                                                                    07-JUL-2000; 2000AU-0008652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haemagglutinin; antigen; vaccine; immunisation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene;
                                                                                                                                                                                                                           AAM50721.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCGAAATGTGATACGGTTAAAGGTCGCAAAGCATTAATCGCTTGTTTAGCAGACGATCGT 1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlyIleAsnGlnAlaSerValGluIleIleSerPheGlyGluGluArgProIleAlaPhe 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCCAACTTGAAATTATCACAACGTCGTGCTGATACTGTGGCTAACTACTTAGTTTCTAAA
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                                                                                                                                                                                                                                                        Tseng H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        paragallinarum strain 0222 haemagglutinin hagA gene.
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                                                                                                                                                                                                                                                       Jennings MP,
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                                                                                                                                                                                                                                                       Downes
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sig_peptide
                                 CDS
                                                                Haemophilus
                                                                                    hagA; gene;
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US-09-674-779B-2 (1-172) x ABA91422 (1-1035)
                                                                                                                                                                                                                      Haemagglutinin; antigen; vaccine; immunisation; coryza; chicken;
                                                                                                                                                                                                                                                                      Haemophilus paragallinarum strain 2671 haemagglutinin hagA gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                ABA91423 standard; DNA; 1035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1035 BP; 318 A; 186 C; 234 G; 297
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ThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAspGluArgGlySerArgGlu 115
                                                CGTCCAGAAGCACAAAATGTATTAGACGGTATTTATGGTGAAATCGCACAGTTA-----
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RESULT 40
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The present sequence is that of the coding region of the hagA gene of Haemophilus paragallinarum strain H-18 (serovar C). The gene was isolated from chromosomal DNA by PCR amplification. It encodes haemagglutinin (see AAM50724). The invention provides recombinant haemagglutinin polypeptides (see AAM50716-27) and encoding nucleic acids (see ABA91417-27) from 11 strains (serovars A, B and C) of H. paragallinarum, the causative agent of infectious coryza of chickens. The polypeptides are useful in vaccines for immunisation against infectious coryza, as are the nucleic acids when expressed in attenuated bacteria, especially Salmonella or
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hagA; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1035 BP; 318 A; 185 C; 233 G; 299 T; 0 other;
                                                                           1003 CGTGTAGAAATCTCA 1017
                                                                                                                  167
                                                                                                                                                                                                                                                                            136
                                                                                                                                                                                                                                                                                                            823 GCCAACTTGAAATTATCACAACGTCGTGCTGATACTGTGGCTAACTACTTAGTTTCTAAA 882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 GlyCysAlaAsnLysSerThrSerGlnValMetValAlaProAsnAlaProThrGlyTyr 41
                                                                                                                                                                                                                                                                   GlyIleAsnGlnAlaSerValGluIleIleSerPheGlyGluGluArgProIleAlaPhe 155
                                                                                                                                                                                                                                                                                                                                       TyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArgAsnTyrLeuLeuGlyLys 135
                                                                                                                                                                                                                                                                                                                                                                                        -----AAATCAGTACAAGTAGATGTTGCTGGTTATACTGACCGTATTGGTAGCGAAGCA 822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LysAlaLeuAlaSerLysLeuProSerLeuValTyrPheAspPheAspSerAspGluIle 79
                                                                                                                                                     GCGAAATGTGATACGGTTAAAGGTCGTAAAGCATTAATCGCTTGTTTAGCAGACGATCGT 1002
                                                                                                                                                                                                GlyThrAsnGlu------
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Command line parameters:

#MODEL=frame+_p2n.model -DEV=xlp
-Q-/cgn2_1/USPTO_spool/US09674779/runat_06072003_121614_9813/app_guery.fasta_1.327
-DB=EST -OFMT-fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END--1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=100
-DOCALION=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN-0 -ALIGN=40 -MODE=LOCAL
-DOCALION=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN-0 -ALIGN=40 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09674779_eCGN_1_1_1525_erunat_06072003_121614_9813 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Email: benning@msu.edu
Clones were originally prepared at Michigan State University.
Arabidopsis Biological Resource Center, The Ohio State University,
309 Botany & Zoology Bldg., 1735 Neil Avenue, Columbus, OH 43210
USA, FAX: 6142920603 TEL: 6142929371.
Location/Qualifiers
                                                                                                                                                    White,J.A., Todd,J., Newman,T., Focks,N., Girke,T., Martinez de Ilarduya,O., Jaworski,J.G., Ohlrogge,J. and Benning,C. A new set of Arabidopsis expressed sequence tags from developing seeds. The metabolic pathway from carbohydrates to seed oil Plant Physiol. 124 (4), 1582-1594 (2000)
                                                                                                                                                                                                                                                                                                       BE530264 247 bp mRNA linear EST 19-MAR-
M77K09STM Arabidopsis developing seed Arabidopsis thaliana cDNA
clone 600039738R1 5', mRNA sequence.
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                                                                    Tel: 517 355 1609
Fax: 517 353 9334
                                                                                                                        Contact: Benning, C
Dept. of Biochemistry & Molecular Biology
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                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           238 AACATCGTTTACTTCGATCTGGACAAGTACGATATCCGTTCTGACTTCGCTCAAATGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88 AspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHis 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 GTTAAGATGTACCTGCAGGGTAAAGGCGTTTCTGCAGACCAGATCTCCATCGTTTCT 2
                                                                                                                                                                                                                                                                                          Unpublished (2001)
Other_GSSs: AG-ND-131G1.TF
Contact: Brendan J Loftus
                                                                                                                                                                                   9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0208
Fax: 301 838 3543
                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 779)
Shetty,J., Malek,J., Koo,H., Collins,F., Gardner,M. and Loftus,B.J. Direct Submission of BAC-end sequences from Anopheles gambiae
to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M University BAC Center University, College Station, Texas 77843-2123, USA using a HindIII
                                                                               This clone is from an A gambiae BAC library (ND-TAM) provided by Fih. Collins and sequenced by The Institute for Genomic Research (TICR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae
                                                                                                                                                                                                                                               Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AG-ND-131G1.TR ND-TAM Anopheles DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                     Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoldea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anopheles gambiae
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                                                                                                                                                                 bjloftus@tigr.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib-"Arabidopsis developing seed"
/tissue_type="seed"
/dev_stage="5-13 days after flowering"
/lab_host="E.coli"
/note="Organ: Developing seed; Vector: pBluescript SK-;
Site_1: EccRI; Site_2: XhoII"
site_1: EccRI; Site_67 g 64 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:370."
/clone="600039738R1"
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206.00
69.62%
50.63%
23.93%
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Indels:
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40
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24
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RESULT 3
BF635668
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                      AUTHORS
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                                                                                                                                                                                                                                                                                                                  164 GlnAsnArgArgAlaGlu 169
                                                                                                                                                                                                                                                                                                                                                                                         144 IleIleSerPheGlyGluArgProIleAlaPheGlyThrAsnGluGluAlaTrpSer 163
                                                                                                                                                                                                                                                                                                                                                                                                                                    479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125
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                                                                                                                                                                                                                                                                                               599 CAAAACAGAAGGGTGGAA 616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47 ThrGlyValAlaProLeuValAspAsnAspGluThrValLysAlaLeuAlaSerLysLeu 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 ValMetValAlaProAsnAlaProThrGlyTyrThrGlyValIle----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            partial digest.
Seq primer: M13
Class: BAC ends.
                                                      Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Spermatophyta; Magnoliophyta; Fabaceae; Papilionoideae; Trifolieae
                                                                                                                                                                                                              NF106A12DT1F1087 Drought Medicago truncatula cDNA clone
Torrez-Jerez, I., Scott, A.D., Harris, A.R., Flores, H.R., Inman, J.T., Weller, J.W. and
                                                                                                                                                    EST
                                                                                                                                                                                                                                     BF635668
                                                                                                                                   barrel medic.
                                                                                                                                                                  BF635668.1 GI:11899826
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ala---ValAlaValArgAsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGlu 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AlaGlyHisThrAspGluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArg
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                                                                                                                                                                                                                                                                                                                                                              GCTCAATCTGCTGTGAAAGGGGAAATTACTAAGGCAGGTATTGCTGAGGATCGATTATCA 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AATGGTTATACGGATAACTCTGGTAATGCTGACCACAATCTGAAACTTTCAGATGCAAGA 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAGCGGTACTTCATATTTTGATACCGATAAGGCTACTTTGAAACCTGACGGATCC
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                                (bases 1 to 236)
                                                                                                                                                                                               mRNA sequence.
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ss: BAC ends.
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/clone="AG-ND-13161"
/clone=lib="ND-TAM"
/note="Vector: pEcBaC1; S
a 115 c 163 g 197
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/strain="PEST"
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182.50
54.11%
28.77%
21.20%
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Indels:
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197 t
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, Gonzales,R.A.,
May,G.D.
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42
37
60
7
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NF106A12DT
                                                               Trifolieae;
                 Bell, C.J.,
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RESULT 4
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Best Local Similarity:
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                                                                                             JOURNAL
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Contact: May GD
Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
                                                                                         Unpublished (2000)
                                                                                                      Torrez-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J. Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D. Expressed Sequence Tays from the Samuel Roberts Noble Foundation Medicago truncatula drought library
                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                     Medicago truncatula
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Tel: 580 221 7391
Fax: 580 221 7380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plant Biology Division
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
OK
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Insert Length: 236 Std Error: 0.1
Plate: 106 row: A column: 12
Seq primer: TCACACAGGAAACAGCTATGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlyThrAsnGluGluAlaTrpSerGlnAsnArgArgAlaGluLeuSerTyr 172
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                                                                                                                                                                                             (bases 1 to 246)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plantlets harvested in a series of days-post-watering
timepoints. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Medicago truncatula"
/db_xref="taxon:3880"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="Pooled timepoints"
/note="Vector: Lambda Zap; Contains a mixture of entire
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="NF106A12DT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Plantlets"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Drought"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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163.00
75.44%
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Medicago truncatula

Medicago; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                           Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK
Tel: 580 221 7391
Fax: 580 221 7380
                Email: gdmay@noble.org
Insert Length: 305 Std Error: 0.00
Plate: 099 row: G column: 07
Seq primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                Contact: May GD
                                                                                                                                                                                                                  Medicago truncatula drought library Unpublished (2000)
                                                                                                                                                                                                                                                     Torrez-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C. Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D. Expressed Sequence Tags from the Samuel Roberts Noble Foundation
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5', mRNA sequence.
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Insert Length: 246 Std Error: 0.0
Plate: 092 row: B column: 07
Seq primer: TCACACAGGAAACAGCTATGAC.
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/note="Vector: Lambda Zap; Contains a mixture of entire plantlets harvested in a series of days-post-watering timepoints."
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/clone="NF092B07DT"
/clone_lib="Drought"
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RESULT 6
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                                                                                                                                                                             Fax: (44) 1427 C. uk
Email: bsstfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For
This is one of identified clones (BLASTX, BLASTN and mapping to E.
annotation of identified clones (BLASTX, BLASTN and mapping to E.
214 V12 Genome) please see ffrench-Constant et al. 2000, Nucleic
                                                                                                                                                                                                                                                                                      Department of Biology and Biochemistry University of Bath South Building, Bath BA2 7AY, UK Tel: (44) 1225 826621
Fax: (44) 1225 826779
                                                                                                                                                                                                                                                                                                                                                                                                                                              ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T., Daborn,P.J., Bowen,D. and Blattner,F.R. Papen,D. and Blattner,F.R. Papen,D. ample cof the entomogenic bacterium photorhabdus luminescens w14: potential implications for viru. Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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/clone="NF099G07DT"
/clone_lib="Drought"
/tissue_type="Plantlets"
/dev_stage="Pooled timepoints"
/note="Vector: Lambda Zap; Contains a mixture of entire
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                  /strain="W14"
/db_xref="taxon:29488"
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/clone="PLG01801"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae
                                                                                                                                                                                                                                                                                                                                                                         DEL448350 arNA linear EST NF003G05DT1F1036 Drought Medicago truncatula cDNA clone 5', mRNA sequence.
                                                                                                     Unpublished (2000)
On Jul 13, 2000 th
                                                                                                                                                    Torrez-Jerez,I., Scott,A.D., Harris,A.R., Gonzale Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D. Expressed Sequence Tags from the Samuel Roberts N
                                                                                                                                                                                                                                                                                                                          EST
                                                  Plant Biology Division
The Samuel Roberts Noble Foundation
                                                                                                                                      Medicago truncatula drought library
                                                                                                                                                                                                                                                                                                          barrel medic.
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                                                                                       Contact:
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/note="Genomic DNA from strain W14 was size
kb) and then cloned into M13 Janus."
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library"
                                                                                                   2000 this sequence version replaced gi:9118410
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REFERENCE
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BH404849/c
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                                                                                                                                                                                                                                                              l (bases 1 to 801)
Shetty,J., Malek,J., Koo,H.,
Direct Submission of BAC-end
Unpublished (2001)
Other_GSSs: AG-ND-126C17.TF
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Insert Length: 866 Std Error: 0.00
Plate: 003 row: G column: 05
Seq primer: TCACACAGGAAACAGCTATGAC.
             This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC
                                                                                                                                                                                                                                            Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                               Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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library was constructed at Texas A&M Universty BAC Center
                                                                                                                            Email: bjloftus@tigr.org
                                                                                                                                                     Fax: 301 838 3543
                                                                                                                                                                                                                          Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                            Anopheles
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA sequence.
                                                                                                                                                                                                          Institute for Genomic Research
                                                                                                                                                                     Medical Center Dr., Rockville, 301 838 0208
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/dev_stage="Pooled timepoints"
/note="Vector: Lambda Zap; Contains a mixture
plantlets harvested in a series of days-post-w
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Seq primer: M13
Class: BAC ends
             The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@tlgr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by The Collins and sequenced by The Institute for Genomic Research
                                                                                                                                  Department of Eukaryotic Genomics
                                                                                                                                                  Contact: Brendan J Loftus
                                                                                                                                                                 Other_GSSs: AG-ND-160F6.TF
                                                                                                                                                                                   Unpublished (2001)
                                                                                                                                                                                                    Shetty, J., Malek, J., Koo, H., Direct Submission of BAC-end
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                                                                                                                                                                                                                                                                            Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                    African malaria mosquito.
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                                                                                                                                                                                                                                                                                                                                                                                     DNA sequence.
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(TIGR). The BAC library was generated from A. gambiae PEST strain
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ss: BAC ends.
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/clone="AG-ND-126cl7"
/clone_lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
a 157 c 124 g 283 t
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/strain="PEST"
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                                                                                                                                                                                                                                                                     Diptera; Nematocera; Culicoidea
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Gaps:
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                                                                                                                                                                                 Collins, F., Garquez, ...
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                                                                                                  COMMENT
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                                                                                                                 JOURNAL
                                                                                                                                  TITLE
                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                   ORGANISM
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US-09-674-779B-2 (1-172) x BH403497 (1-603)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       228 GACAATAACCAGGTTGCAACTGAAGTAGAAACAGAATTAAAAAAT---GTGTATTTCCAT 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           462 GCTAGAGGAGTTTCTTCCAGTACTCTTAAA 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 PheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAspGluGlnAlaGlnPhe 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54 AspAsnAspGluThrValLysAlaLeuAlaSerLysLeuProSerLeuValTyrPheAsp
                                                                                                                Shetty J., Malek, J., Koo, H.,
Direct Submission of BAC-end
Unpublished (2001)
Other_GSSs: AG-ND-170A18.TR
Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                      Anopheles gambiae
Eukaryota; Metazoa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BH386478 814 bp DNA linear GSS 10-DEC-2001 AG-ND-170A18.TF ND-TAM Anopheles gambiae genomic clone AG-ND-170A18
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                                                                     Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                             вн386478.1
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                                                                                                                                                                                                                                                                                               Neoptera; Endopterygota;
                                                                                                                                                                                                                                                                                                                                                                       African malaria mosquito.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAspGluArgGlySer 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTAATAAAGCAACAATAACAAATGAGTCAGGTGCAAAGCTAGATGTAGCTGCCAACATT 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlyLysGlyIleAsnGlnAlaSerValGlu 143
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301 838 3543
                                              Medical Center Dr., Rockville,
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/note="Vector: pECBAC1;
81 c 151 g 10
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                                                                                                                                                                                                                                                                                               Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Indopterygota; Diptera; Nematocera; Culicoidea;
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                                                                                                                                                                            Collins,F., Garumer.
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163 t
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                                                20850, USA
                                                                                                                                                                                                                       Gardner, M. and Loftus, B.J.
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169 GluLeu 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             590 AAAGCTCTTGAAGCTAGAGGTGTAAACGGTGCTCAATTGAAATCTGTAAGTGTAGGTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                410 ATCTTATTCGATTTCAACAAAGCTACTATCCAGTCTGGATCTTTATCTAAAGTAGATGCT 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90 GlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAsp 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 ValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAspGlu
                                                                                                                                                                                                                                                                                                                     GSS
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    Shetty, J., Malek, J., Koo, H., Direct Submission of BAC-end
                                                                                                                                                                                                                                     Anopheles gambiae
                                                                                                                                                                                                                                                                                                                                                          BH374389.1 GI:17320531
                                                                                                                                                                                                                                                                                                                                                                                              DNA sequence.
BH374389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BH374389 512 bp
AG-ND-177A3.TF ND-TAM Anopheles
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Seq primer: M13 For Class: BAC ends.
                                                                                                                                                                                                                                                                         African malaria mosquito
                                                                                                                                                    Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                     Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GluGluArgProIleAlaPheGlyThrAsnGluGluAlaTrpSerGlnAsnArgArgAla 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGluIleIleSerPheGly---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAGAAGCTACTGTACCAGCTACTGCTTCTTACGAGGCTAGACAAGTAGACAGAAAAGTT 709
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                                                                                (bases 1 to 512)
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/note="Vector: pECBAC1; Site_1: HindIII"
141 c 184 g 214 t
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/strain="PEST"
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Collins, F., Gardner, M. and Loftu sequences from Anopheles gambiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gambiae genomic clone AG-ND-177A3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA
                                            Gardner, M. and Loftus, B.J.
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                                                                                                                                                                                                                                                                     468 GCTAGAGGAGTTTCTTCCCAGACTCTTAAA 497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 AspAsnAspGluThrValLysAlaLeuAlaSerLysLeuProSerLeuValTyrPheAsp
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                     Anopheles gambiae
Eukaryota; Metazo
                                                                                                 вн387230.1
                                                                                                                         BH387230
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Fax: 301 838 3543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
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Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                         African malaria mosquito.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: bjloftus@tigr.org
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                                                                                                                                                                                                                                                                                                                                                  GCAGCATACAACCTTAAGCTTTCCAGAGAAAGAGCGGCTGCTGTTGTTGGAGCTCTGGAA 467
                                                                                                                                                                                                                                                                                                                                                                                      ArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArgAsnTyrLeuLeu 133
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                                                                                                                                          DNA sequence.
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/note="Vector: pECBAC1;
69 c 124 g 1
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/strain="PEST"
/db_xref="taxon:7165"
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                   Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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REFERENCE
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                         141 rValGluIleIleSerPheGlyGluGluArgProIleAla 154
                                                               486
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                                                                                                                                                                                            321 GTATTGAAT
                                                                                                                                                                                                                                                                                                                             261 AAGGTTGAAAAATTACTTCTTCCCAAATGAAAAAAGATATTAACGAGTCTGGGAAAGCT
                                                                                                                                                                                                                                                                                                                                                                                            201 TGCTGGAACGAAGAAGTGGAAAATTACTATTCTGGAGAAGGCAGCAGCTGAAGTTCCA
                                                                                                                                                                                                                                                                                                                                                          43 GlyVal---IleTyrThrGlyValAlaProLeuValAspAsnAspGluThrValLysAla
                                                                                                                                                                                                                                                                                         62 LeuAlaSerLysLeuProSerLeuValTyrPheAspPheAspSerAspGluIleLysPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 301 838 0208
Fax: 301 838 3543
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Department of Eukaryotic Genomics
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                                                                                                                                                                                                                             GlnAlaAlaIleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArg
ACTACAAACAAAAGGTTTTGGACAGGATAATCCTTTGGCT 585
                                                             ATTGGACAGAGCTACAACAATATATACTTATTTAACAGATAAAGGGATTAAATCTGATAG
                                                                                          yGluArgArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSe
                                                                                                                             CTTTCTATAGAAGGGCATACTGACAACAATGGTACAAAAGAACACAATTAGGAAATTATC
                                                                                                                                                        ValLeuValAlaGlyHisThrAspGluArgGlySerArgGluTyrAsn-MetSerLeuGl 121
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/clone_lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
/86 c 132 g 180 t
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/strain="PEST"
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TITLE
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US-09-674-779B-2 (1-172) x BH393516 (1-822)
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2001)
Other_GSSs: AG-ND-160N3.TF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 301 838 0208 Fax: 301 838 3543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Brendan J Loftus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: bjloftus@tigr.org
                                                                                                                                                                                                                                                                                                                                                                         GluThrValLysAlaLeuAlaSerLysLeuProSer------LeuValTyrPheAsp 73
GCAGCATACAACCTTAAGCTTTCCAGAGAAAGAGCGGCTGCTGTTGTTGGAGCTCTGGAA 463
                                                  ArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArgAsnTyrLeuLeu 133
                                                                                                                                                                                                                                                                                                                                           AAGACAATAACCAGGTTGCAACTGAAGTTAGAAACAGAATTAAAAAATGTGTATTTCCAT 286
                                                                                                                                                                  LeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAspGluArgGlySer 113
                                                                                                                                                                                                                           TTTAATAAAGCAACAATAACAAATGAGTCAGGTGCAAAGCTAGATGTAGCTGCCAACATT 346
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/clone_lib="ND-TAM"
/note="Vector: pEGBAC1; Site_1: HindIII"
104 c 178 g 243 t
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/strain="PEST"
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                                                                                                                -GGTGGAAATTATCTATTAACCGGACATACAGATGCTAAAGGTAGT
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ORIGIN
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                                                110
                                                                                                                                                                              275 GTGTATTTCCATTTTAATAAAGCAACAATAACAAATGAGTCAGGTGCAAAGCTAGATGTA 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 GlyLysGlyIleAsnGlnAlaSerValGlu 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      464 GCTAGAGGAGTTTCTTCCAGTACTCTTAAA 493
                                                                                                                                        90
                                                                                                                                                                                                                       70 ValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAspGlu 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M University BAC Center University, College Station, Texas 77843-2123, USA using a HindIII partial digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: M13 Rev Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shetty,J., Malek,J., Koo,H., Collins,F., Gardner,M. and Loftus Direct Submission of BAC-end sequences from Anopheles gambiae Unpublished (2001)
Other_GSSs: AG-ND-132E3.TF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 301 838 0208 Fax: 301 838 3543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BH389388.1 GI:17335529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: bjloftus@tigr.org
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                                GluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArg 129
                                                                                                                                 GlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAsp 109
    GCTAAAGGTAGTGCAGCATACAACCTTAAGCTTTCCAGAGAAAGAGCGGCTGCTGTTGTT 451
                                                                                          GCTGCCAACATTATTAAGAGCAAT----GGTGGAAATTATCTATTAACCGGACATACAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         269
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/note="Vector: pECBAC1; Site_1: HindIII"
100 c 169 g 205 t
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117.50
55.41%
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                                                                                                                                                                              39
                                                                                        90
                                                                                                                                                                                                                     87 LeuAspGluGlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGly 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: bjloftus@tigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas A&M University BAC Center
University, College Station, Texas 77843-2123, USA using a HindIII
partial digest.
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: M13 For Class: BAC ends.
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Fax: 301 838 3543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Other_GSSs: AG-ND-155H3.TR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
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AG-ND-155H3.TF
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GCGGTTAACCGATATCTACAGTCAAAAATTGGAAACAATATCAAACTGGAAAGTGTAGTA
                                                                                                                               HisThrAspGluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaVal 126
                                       AlaValArgAsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGlu---IleIle 145
                                                                                     AATTGCGATATTTCCGGAACTTTGGAATACAATAAAAAGCTGTCTGAAAATCGCGCAAAT 149
                                                                                                                                                                           CTCGACAGTTTGGCGCAA----CTTAGATATAATCTGAAATTCAGAATTTTT------GGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:7165"
/clone="AG-ND-155H3"
/clone_lib="ND-TAM"
/clone_Lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
1 c 96 g 114 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Anopheles gambiae"
/strain="PEST"
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                                                                                                                                               US-09-674-779B-2 (1-172) x BH376004 (1-800)
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                                               90 GlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: bjloftusetigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas AsM Universty BAC Center
University, College Station, Texas 77843-2123, USA using a HindIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: M13 Rev
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2001)
Other_GSSs: AG-ND-135A18.TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shetty, J., Malek, J., Koo, H., Direct Submission of BAC-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               African malaria mosquito.
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                  GCTGCTGAGATTATCAAAGGAGCTAAAGCTGAAAACTTCTTAGTAACTGGTTACACAGAT
                                                                                                             ValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAspGlu
                                                                               ATCTTATTCGATTTCAACAAAGCTACTATCCAGTCTGGATCTTTATCTAAAGTAGATGCT
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/note="Vector: pECBAC1;
/note="140 c 183 q 2)
                                                                                                                                                                                                                                                                                                                                                                                           /strain="PEST"
/db_xref="taxon:7165"
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Tel: 713 500 5437
Fax: 713 500 5499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Choudhary, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Choudhary, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rhodobacter sphaeroides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Class: shotgun.
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645 AAAGAAGCTACTGTACCAGCTACTGCTTCTAACGAGGCTAGACAAGTAGACAGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                      70 ValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAspGlu
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8327H1B83102397 Cosmid library of chromosome II Rhodobacter
sphaeroides genomic clone 8327H1B83102397, DNA sequence.
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University of Texas Medical School
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: madhu@utmmg.med.uth.tmc.edu
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AsnTyrLeuLeuGlyLys---GlyIleAsnGlnAlaSerValGluIleIleSerPheGly 148
                                                                                                                                    GluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArg 129
                                                                                                                                                                                                                                                                     GlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAsp 109
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                                                                         GCGGCGGGCAGCGAGGCCTACAACCAGCAGCTCTCGCTCCTGCGGGCCGAGGAGGTGCGC
                                                                                                                                                                                                      CTCTGCACGGTGATGAAGGCGAGCGACATCCGCCTGTTTCAGATCGTGGGCCACACCGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:1063"
/clone="8327H1B83102397"
/clone_lib="Cosmid library o
/lab_host="E. coli $17-1"
/note="Vector: pLA2917"
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/strain="2.4.1T"
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                                      234 GACAATAACCAGGTTGCAACTGAAGTAGAAACAGAATTAAAAAAAT---GTGTATTTCCAT 290
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74 PheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAspGluGlnAlaGlnPhe 93
                                                                     54 AspAsnAspGluThrValLysAlaLeuAlaSerLysLeuProSerLeuValTyrPheAsp 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M University BAC Center University, College Station, Texas 77843-2123, USA using a HindIII partial digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shetty, J., Malek, J., Koo, H., Collins, F., Gardner, M. and Loftu Direct Submission of BAC-end sequences from Anopheles gambiae Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA sequence.
BH393822
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AG-ND-169D8.TF ND-TAM Anopheles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 301 838 0208
Fax: 301 838 3543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Other_GSSs: AG-ND-169D8.TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anopheles gambiae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: bjloftus@tigr.org
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                                                                                                                                                                                                                                                                                                                                                        /strain="PEST"
/db_xref="taxon:7165"
/clone="AG-ND-169D8"
                                                                                                                                                                                                                                                                                                      /clone_lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
89 c 151 g 184 t
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                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                              BASE COUNT
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114 ArgGluTyrAsnMetSerLeuGlyGluArgArg 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/seq/gethtml.pl?tl=IL&t2=IL-BT042-008.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-Sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence tags
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AI904113
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                                                                                                                                                                                                                                                                                                           7.716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

88 c 97 g 68 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="Adult"
/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="BT042"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
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(1-296)
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US-09-674-779B-2 (1-172) x BM802521 (1-1152)
                                                                                             Best Local Similarity:
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence start: 379
High quality sequence stop: 585.
Location/Qualifiers
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12285 row: o column: 06
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Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       344
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                                                                                                                                                                                                                                                              മ
                                                                                                                                                                                                                                                  /tissue_type="duodenal adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="organ: small intestine; Vector: pCMV-SPORT6;
Site_1: NotI; Site_2: Sall; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."
a 277 c 241 g 273 t 17 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
/clone="IMAGE:5560157"
                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="NIH_MGC_88"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
                                                                   3.75
86.50
48.33%
25.00%
10.05%
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Indels:
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           626 CCAAGCAATGAATTCCTTGGCAGCTTG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151 ArgProIleAlaPheGlyThrAsnGlu-------GluAlaTrpSer 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112 GlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArgAsnTyr 131
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вJ290925 Y.
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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BJ290925 BJ290925 Y. Ogihara unpublished cDNA library, Wh_SL Triticum aestivum cDNA clone whs120n03 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2002)
Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 686)
Ogihara, Y. and Murai, K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Expressed genes in Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
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                        138
                     Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)." a 233 c 181 g 132 t 2 others
                                                                                                            library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab at the University of California, Riverside (Akhunov, Chi
                                                                                                                                                                                                                                                    /note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site_1: ECORI; Site_2: XhoI; Plants were grown under hydroponic conditions at UC Davis, salt stressed for 12 hours, and for 7 days, then dissected and frozen (Akhunov
                                                                                                                                                                                 samples, polyA was purified from the pooled RNA, a cDNA
                                                                                                                                                                                                       in J Dvorak Lab). Total RNA was prepared from sheath tissue, equal quantities of RNA were pooled from the two
                                                                                                                                                                                                                                                                                                                                                /clone_lib="Y. Ogihara unpublished cDNA library, Wh_SL"
/tissue_type="seed DPA30"
/dev_stage="Feekes' scale 11.3"
                                                                                                                                                                                                                                                                                                                                                                                                                 /cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="whs120n03"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Triticum aestivum"
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                                                                                           Close, Fenton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             411-8540, Japan
                                                                                           Kianian, Otto, Simons,
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                                                                                        zhang).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              387 GCGCATGGGACGGTTGCCGCAGTAAACGCCCTGCATCTCGGTGAGGGCCCTTTTGCTGGTG
      Fax: 301 838 3543

Email: bjloftus@tigr.org

This clone is from an A. gambiae BAC library (ND-TAM) provided by This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M University BAC Center University, College Station, Texas 77843-2123, USA using a HindIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 SerLysLeuProSerLeuValTyrPheAspPheAspSerAspGluIleLysProGlnAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28 ThrSerGinValMetValAlaProAsnAlaProThrGlyTyrThrGlyValIleTyrThr 47
                                                                                                                                                                                                                                                                                                 1 (bases 1 to 638)
Shetty,J., Malek,J., Koo,H.,
Direct Submission of BAC-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BH388977 638 bp DNA linear GSS 11-DEC-200 AG-ND-126A8.TF ND-TAM Anopheles gambiae genomic clone AG-ND-126A8. DNA sequence.
                                                                                                                                                                                                 Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                    Unpublished (2001)
Other_GSSs: AG-ND-126A8.TR
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Eukaryota; Metazo
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                                                                                                                                                                                         Tel:
                                                                                                                                                                                                                                                   Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                   African malaria mosquito.
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                                                                                                                                                                                                                                                                                                                                                                 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGlyIleAsnGlnAlaSerValGlu 143
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301 838 3543
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                                                                                                                                                                                                                                                                                                                                                                             Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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                                              1 (bases 1 to 594) Walbot, V.
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121 GlyGluArgArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGlyIleAsnGlnAla 140
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                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
Maize ESTs from various cDNA libraries sequenced at Stanford
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plate: 952035 row: D column:
Location/Qualifiers
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Stanford University
BQ678932
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                                                                                                                                                                                                MetSerLeuGlyGluArgArgAlaVal-AlaValArgAsnTyrLeuLeuGlyLysGlyIl 137
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                                                                                               rAsn---GluGluAlaTrp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   library was prepared by George Rudenko using poly (A) selected RNA and Universal Riboclone cDNA Synthesis System (Promega). cDNA was synthesized using both random and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oligo(dT) primers in separate reactions and equipped with
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/db_xref="taxon:4577"
/clone_lib="952 - BMS tissue from Walbot Lab (reduced rRNA
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US-09-674-779B-2 (1-172) x BQ678932 (1-930)
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                                                  96 ThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAspGluArgGlySerArgGlu 115
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NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, 1
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Contact: Robert Strausberg, Ph.D.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
ACTAGTGCAACCAGTAAGTTGATC-----CATCCAGATGAG--
                                                                                                              AGTACTGCAGCTAAACCA---GCGGCTTCAATAACAAGTAAGCCTGCTACACTTACAACA
                                                                                                                                                        SerAspGluIleLysProGlnAlaAlaAlaIleLeuAspGluGlnAlaGlnPheLeuThr 95
                                                                                                                                                                                                                                                                                      ProSerLeuValTyrPheAspPhe-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="melanotic melanoma, cell line"
/lab_host="DHIOB (phage-resistant)"
/note="Organ: skin; Vector: pOTF7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into ECORI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NHLMGC Library."
a 283 c 186 g 193 t 2 others
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/db_xref="taxon:9606"
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38
20
36
44
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Qy	Alignment Scores pred. No.: Score: Percent Similari: Best Local Simil, Query Match: DB: US-09-674-779B-2 Qy 9 Al	BASE COUNT	FEATURES SOUICE	JOURNAL COMMENT	ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE	RESULT 25 BM448527 LOCUS DEFINITION	Qy Db Qy
29 SerGlnValMetValAlaProAsnAlaProThrGlyTyrThrGlyValIleTyrThrGly 48	: 5.86 Length: 565 bl.00 Matches: 36 rity: 41.33% Conservative: 26 mismatches: 54 9.41% Indels: 54 13 Gaps: 5 (1-172) x BM448527 (1-565) aAlaAlaAlaLeuSerValLeuThrPheMetThrGlyCysAlaAsnLysSerThr lilili   lili:::::::::::::::::::::::::::	131 a E E		An expressed sequence tag database for the halotolerant green alga, Dunaliella salina Unpublished (2002) Contact: Cushman JC Department of Biochemistry University of Nevada MS200, Reno, NV 89557-0014, USA Tel: 775-784-1918 Fax: 775-784-1650 Email: disabmandanr.edu	BM448527 BM448527.1 GI:19854099 EST. Dunaliella salina. Dunaliella salina Eukaryota; Viridiplantac Dunaliellaceae; Dunaliel 1 (bases 1 to 565)	BM448527  DSA025B03_59675 An expressed sequence tag database for the halotolerant green alga, Dunaliella salina Dunaliella salina cDNA clone DSA025B03 5, mRNA sequence	116 TyrAsnMetSerLeuGlyGluArgArgAlaValAlaValArgAsn-TyrLeuLeuGlyLy 135 ::::::
Alignment : Pred. No.: Score:	BASE COUNT	FEATURES SOURCE	KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT	Db  RESULT 26 BE372739 LOCUS DEFINITION ACCESSION		Q D	Db Oy Db
Scores: 6.84 Length: 620 81.00 Matches: 41	/strain="FWB/N" /db_xref="taxon:10090" /dlone="iMAGE:3582660" /clone=lib="NAGE:3582660" /clone_lib="NAGE:3582660" /clone_lib="NAGE:3582660" /clone_lib="NAGE:3582660" /clone_lib="NAGE:3582660" /clone_lib="NAGE:3582660" /tissue_type="tumor, biopsy sample" /dev_stage="10" months, virgin" /lab_host="DH10B" /lab_host="DH10B" /lab_host="DH10B" /lab_host="DH10B" /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Notr: Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator .providing samples: Gilbert Smith, NIH"  137 a 179 c 175 g 129 t	Tissue Procurement: Gilbert Smith, Ph.D.  CDNA Library Preparation: Life Technologies, Inc.  CDNA Library Preparation: Life Technologies, Inc.  CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  DNA Sequencing by: Incyte Genomics, Inc.  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  Plate: LLAN80738 row: c column: 13  High quality sequence stop: 598.  Location/Qualifiers  e	EST. house r house r Mus mus Eukary Mammal 1 (bas NIH-MGG Nation Unpubl: Contact	141 SETVALIGIULIELIESETPINGLYGLUGIU 150 ::::::		:::	7070 49 ValAlaProLeuValAspAsnAspGluThrValLysAlaLeuAlaSerLysLeuPro 67 :::   :::   71ATCGATGATGACGCCAAGCTGCGCGCCTTCTACGACAAGCGCCTGTCC 118 68 SerLeuValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeu 87

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SOURCE
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                                                                                                                                                                                                                                                                                                                                         TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34 AlaProAsnAlaPro-----ThrGlyTyrThrGlyVallleTyrThrGlyValAlaPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 LeuSerValLeuThrPheMetThrGlyCysAlaAsnLysSerThrSerGlnValMetVal
                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 1591)
NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BE729857 1591 bp mrNA linear EST 15-SEP-2000 601564781F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3925917 5',
                                                                                                                                          Plate: LLCM753 row: a column: High quality sequence stop: 60.
                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                     Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                         DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
                                                                                                                                                                                                                                cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (
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                                  /clone="IMAGE:3925917"
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                     /tissue_type="melanotic melanoma"
                                                                       /db_xref="taxon:9606"
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                                                      AUTHORS
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l (bases 1 to 458)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
                                                                                                                                                                                           BF758001 458 bp mRNA lir
QV3-CT0555-101100-369-e01 CT0555 Homo sapiens
BF758001
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EST.
                                                                                     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                        Homo sapiens
                                                                                                                                            human.
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GI:12105901

cDNA,

mRNA sequence.

Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

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US-09-674-779B-2 (1-172) x BE729857 (1-1591)
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424 ACACACAC-----AGCTGGGGTGTCTCCCGGGGAGAGGAGTCTTCC
                                                        156 lyThrAsnGluGluAlaTrpSerGlnAsnArgArgAlaGluLeuSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV3&t2=QV3-CT0555-
101100-369-e01&t3=2000-11-10&t4=1)
Seq primer: puc 18 forward
Seq primer: puc 18 forward
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
908 bp mRNA linear E AGENCOURT_7575827 NIH_MGC_72 Homo sapiens CDNA clone 5', mRNA sequence.
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                                                                                                                                              AGG 127
                                                                                                                                                                                  Lys 135
                                                                                                                                                                                                                            GCAAAACAGAGTCGGAGTGAAAAGAAGGCACGGAAGGCTATGTCCAACTGGGTCTTCGGC 130
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: ATCC/DCTD/DTP
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Location/Qualifiers
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/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCNV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo c
Average insert size 2 kb. Library constructed by Life
Technologies."
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/clone_lib="NIH_MGC_72"
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497 GGCGACCTCTTCTGGGAAATCTCGCCTTCCTCG-
                                                                                                                                                                           611 -----TTGGTCTGAATCAACCAGTTTATAAAGTCCCTGGCGGCAAGATTATCAAGAATG
                                                                                                                                                                                                                                                               671 CAGGTGATGTTGTGAAGAGGATCTTGAATAGGTGATATAGTTATTTTCCTGTCAGGGATT
                                       90 GlnAlaGlnPheLeuThrThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAsp 109
                                                                                                                                                                                                                   50 AlaProLeuValAspAsnAspGluThrValLysAlaLeuAlaSerLysLeuProSerLeu 69
                                                                                                                             70 ValTyrPheAspPheAspSerAspGluIleLysProGlnAlaAlaAlaIleLeuAspGlu
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                                                                                                                                                                                                                                                                                                        30 GlnValMetValAlaProAsnAlaProThrGlyTyrThrGlyValIleTyrThrGlyVal 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 385 AGCCCAGAGGGAG 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAW12283 row: j column: 10
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
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BM475133
                                                                                     GTGTTCATCTTCATCAGAGAAAGAACCATCAGCATGTCTGCGGCCAAGTTCTTCAACAAT 498
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/lab_host="DH10B (phage=resistant)"
/note="organ: small intestine; Vector: pCMV-SPORT6;
Site_1: Not1; Site_2: Sal1; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."
a 224 c 214 g 256 t
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/clone="IMAGE:5559273"
/clone_lib="NIH_MGC_88"
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US-09-674-779B-2 (1-172) x BI670158 (1-1131)
                                                                                               Percent Similarity:
Best Local Similarity:
                                                                          Query Match:
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BI670158/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149 GluGluArgProIleAlaPheGlyThrAsnGlu 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        410 ACTTACATCACTGGTAAAGGTCCCTTCAGCATGTCTCTCAAATTCATCGTGACGTTTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         350 AATGTTATTCCTGTTCCTCTTGGTATTCATCAA 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shira
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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National institutes of Health, Mammalian Gene Collection (MGC)
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603294002F1 NIH_MGC_96 Homo sapiens
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                                                                                                                                                                                                                                                                           242
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                                                                                                                                                                                                                                                                      for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

277 c 359 g 253 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
/clone="IMAGE:5313336"
/clone_lib="NIH_MGC_96"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="hypothalamus"
/lab_host="DH10B"
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80.00
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29 SerGlnValMetValAlaProAsnAlaProThrGlyTyrThrGlyValIleTyrThrGly 48

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AQ847628.1
GSS.
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385 bp DNA linear GSS 25-MAY-2
LMAJFY1_lm35c11.yl Leishmania major FV1 random genomic library
Leishmania major genomic clone LMAJFV1_lm35c11 5', DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WashU Leishmania Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. J
                                                                                                                                                                                                                                                                                                                                          Library construction: Natalia S. Akopyants, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
If using this information please cite:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21192569
Contact: Akopyants, NS / Beverley,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               shotgun sequencing: a resource for DNA microarrays and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leishmania
                                                                                                                                                                                                                                           clone material please contact: Natalia S. Akopyants Ph.D. (natalia@borcim.wustl.edu) and/or Stephen M. Beverley Ph.
                                                                                                                                                                                                                                                                          N.S. Akopyants and S.M. Beverley 'A survey of the Leishmania major Friedlin strain VI genome by shotgun sequencing' and the Washington University Genome Sequencing Center For information on obtaining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              profiling
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Akopyants, N.S., Clifton, S.W., Martin, J., Pape, D., Wylie, T.,
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                                                                                                                                                                                                     Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: 314 286 1810
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                                                                                                                                                                                                                        (beverley@borcim.wustl.edu)
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                                                       /organism="Leishmania major"
/strain="Friedlin strain V1"
/db_xref="taxon:5664"
                                                                                                                                     ity sequence stop: 365.
Location/Qualifiers
/lab_host="TOP10 (Invitrogen)"
              /clone="LMAJFV1_1m35c11"
/clone_1ib="Leishman1a major FV1 random genomic library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    major
Euglenozoa; Kinetoplastida; Trypanosomatidae;
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                                                                                                                                                                                                                                           Beverley Ph.D.
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US-09-674-779B-2 (1-172) x AQ847628 (1-385)
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                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 480)

Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

Waterston, R. and Wilson, R.

The WashU-NCI Mouse EST Project 1999
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                                                                                 Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
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Forest Park Parkway, Box 8501, St. 314 286 1800 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49 -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 474.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGI:951408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----GluArgGlySerArgGluTyrAsnMetSerLeuGlyGluArgArgAlaValAla 127
                                                                                                                                                                                                                                                                               GTTACGAGAGTCACTATCCGAAAATCTAAAAATATCCTCTTTGTCATCACAAAACCCGAT 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGAAGTGAGAAGAAGGCAAGGAAGGCTATGTCCAAACTGGGTCTTCGACAGGTTACAGGG 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGTTGCCACAGCCTCAGGCTGAGACAGGACAGGACAGAGTCTGACAGTGATGAGTCA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATTCGTCGACATCCTTGGTTCCGTGATCTCCGCACAAAATGCCCGGT-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="8 weeks"
/lab_host="DH10B"
/lab_host
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [AATTCGGATCCTTG], digested with Not I and cloned into Not I and Eco RI sites of the modified pT7T3 vector. Source irradiated bowel harvested 72 hours after irradiation (1400 Gys). Library constructed by Bob Basetead "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Barstead bowel MPLRB9"
/tissue_type="bowel"
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                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                               score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AL Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,

2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRÂNCE. (E-mail:

Seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)

This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and varrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
                                                    250 ACATTTAGCGGTTGGGCTAGTAACACTACGTCTGAT-----GTAACATCAACAGAG 303
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241 c 156 g
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/strain="CLIB 210"
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/clone="BA0AB036F06"
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                                                                                                                                                                                                                                                                                                                                                                     Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Ld
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 460)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Thoising B., Wulle T., Tan, F., Underwood, K., Moore, B., Thoising B., William, M., Tan, F., Underwood, K., Moore, B., Thoising B., William, M., Tan, F., Underwood, K., Moore, B., Thoising B., William, M., Tan, F., Underwood, K., Moore, B., Thoising B., William, M., Tan, F., Underwood, K., Moore, B., Thoising B., William, M., Tan, F., Underwood, K., Moore, B., Thoising B., William, M., Tan, F., William, M., Willia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----AlaSerValGluIleIleSerPheGlyGlu-------GluArgPro 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTTGTCCTATCGATACCACTACCACTGAAAGTGCATCTAATGAGTATCACACTTCAAAG
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314 286 1810
                                                                                                                                                                                                                                                                                 quality sequence stop: 454
/clone="IMAGE:336778"
/clone_lib="Soares mouse p3NMF19.5"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Vector: pT7T3D (Pharmacia) with a modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GI:1297704
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US-09-674-779B-2 (1-172) x W20805 (1-460)
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                                                       NIH-MGC http://mgc.nc1.nih.gov/.
National Institutes of Health, N
                                                                                                                                                                                                                                  mRNA sequence.
BG261745
                                                                                                                                                                                                                                                                       602373532F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4481142
Email: cgapbs-r@mail.nih.gov
                      Contact: Robert Strausberg, Ph.D
                                       Unpublished (1999)
                                                                                                                     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                   BG261745.1 GI:12771561
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RESULT 37
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                                                                                                                                                                                                                                                                                                                                                                                                  133 LeuGlyLysGlyIleAsnGlnAlaSer 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94 LeuThrThrAsnGlnThrAlaArgValLeu---ValAlaGlyHisThrAspGluArgGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 PheAspPheAspSerAspGluIleLysProGln------
                                                                                                                                                                                                                    BE261626 503 bp mRNA linear BST 20-001-2601149316F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502299 5',
NIH-MGC http://mgc.nci.nih.gov/.
                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 503)
                                                                                                                                                                                              BE261626
                                                                                                                                                                                                             mRNA sequence.
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Plate: LLAM10315 row: p column: 07
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Location/Qualifiers
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/tissue_type="rettina"
/tab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pcMV-SpeTf6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
a 276 c 285 g 227 t
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/db_xref="taxon:10090"
/clone="IMAGE:4481142"
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                                                            406 AAGACGAGGACTTTTCTGGTGGGCGAACGAGTGACATTGGCTGACATCACAGTTGTC 462
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                                                                                                                                                                                                                                                                                                                                                                      81
                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 AlaSerLysLeuProSerLeuValTyrPheAspPheAspSerAspGluIleLys-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 CysAlaAsnLysSerThrSerGlnValMetValAlaProAsnAlaProThrGlyTyrThr 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence start: 3 High quality sequence stop: 502.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                             ---ProGlnAlaAlaAlaIleLeuAspGluGlnAlaGlnPheLeuThrThrAsnGlnThr 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
                                                                                                                                               LeuGlyGlu-----
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/lab_host="DH10B (phage-resistant)"
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Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 81-559-81-6854
Fax: 81-559-81-6855
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Yata 1111, Mishima, Shizuoka 411, Japan
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                                                                             LeuGlyGluArgArgAlaValAlaValArgAsnTyrLeuLeuGlyLysGlyIleAsnGln 139
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                                                                                                                                                                                                                                                                                                                GCGGATGGTTCCCGCATC----
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/dev_stage="varied"
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/strain="CB1489 him-8(e1489)"
/db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Yuji Kohara unpublished cDNA"
/sex="hermaphrodite, male"
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High quality sequence stop: 332
Location/Qualifiers
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Clemson University
100 Jordan Hall, Clemson, SC 29634, U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: rwing@clemson.edu
Seq primer: GTAAAACGACGGCCAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 864 656 7288 Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1998)
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                                                                                                                                                                                                     Anotes "Vector: pBACINDIA'O; Site_1: ECORI; Site_2: ECORI; Rice is the most important food crop in the world. Half of the world population, especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monococtyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety using EcoRI as the cloning enzyme. The library contains 55,296 clones with an average insert size of 121 Kb providing approximatley 15 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99 %. Three high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening and can be requested from the Clemson University BAC/EST Resource Center (www.genome.clemson.edu)."
                                                                                                                                                                                                              83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Leaf"
/lab_host="E. coli DH10B"
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/db_xref="taxon:4530"
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BM491955
BM491955.1 GI:18612886
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Townsend Hall, Newark, DE 19717,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         University of Delaware
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2002)
Contact: Larry A. Cogburn
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POrter, T.E. and Cogburn, L.A.
ESTS from Normalized Chicken Pituitary/Hypothalamus/Pineal cDNA
library, USDA/IFAFS Animal Genome Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           cogburn@udel.edu, www.chickest.udel.edu.
                                                                                                       മ
                                                                                                   /note="Vector: pCMVSPORT6; Library made from pools of total RNA isolated from each tissue ages. Single pass sequencing 5'-end" 230 c 227 g 105 t 15 others
                                                                                                                                                                                                                                                                                       /clone="pgp2n.pk007.o23"
/clone_lib="Normalized Chicken
Pituitary/Hypothalamus/Pineal Library (pgp2n)"
                                                                                                                                                                                                                                                                                                                                                    /organism="Gallus gallus"
/strain="Commercial broiler chickens"
/db_xref="taxon:9031"
                                                                                                                                                                                                                            /tissue_type="Pituitary Gland/Hypothalamus/Pineal Gland"
/dev_stage="Embryonic (d12,d14,d19); post-hatch (1,3,5,7,9
                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                        /lab_host="E. coli_EMDH10B"
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  Length: Matches:
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Best Local Similarity:
Search completed: July Job time : 1417 secs
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                                                                  491 CCGGAGGGTGGCCGATTTAAGAAGGAG 517
                                                                                                      142 ValGluIleIleSerPheGlyGluGlu 150
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                                                                                                                                                                                                                                                                                                                  ThrAsnGlnThrAlaArgValLeuValAlaGlyHisThrAspGlu---ArgGlySerArg 114
                                                                                                                                         AGCGGCAAGTCGGCCCTGGTGCACCGCTACCTGACCGGCACCTATGTGCAGGAGGAGTCT
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23.67%
9.06%
13
                  6
                  2003, 13:11:03
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19
74
36
                                                                                                                                                                                                                                             -----LeuGly 121
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                                                                                                                                               490
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